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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed in the bone marrow and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 10 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, 15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
REFERENCE THEREOF

20

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto\_BONE\_MARROW.txt, 25 created 24 January 2001, having 26,421,347 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome- 35 derived single exon nucleic acid probes expressed in human



bone marrow and single exon nucleic acid microarrays that include such probes.

### Background of the Invention

5           For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to  
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent  
15 biological understanding.

          For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via  
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

          More recently, however, the development of high  
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein  
30 product.

          One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed  
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,  
Science 252:1651 (1991); Williamson, *Drug Discov. Today*  
4:115 (1999)). For nucleic acids sequenced by this  
approach, often the only biological information that is  
5 known *a priori* with any certainty is the likelihood of  
biologic expression itself. By virtue of the species and  
tissue from which the mRNA had originally been obtained,  
most such sequences are also annotated with the identity of  
the species and at least one tissue in which expression  
10 appears likely.

More recently, the pace of genomic sequencing has  
accelerated dramatically. When genomic DNA serves as the  
initial substrate for sequencing efforts, expression cannot  
be presumed; often the only *a priori* biological information  
15 about the sequence includes the species and chromosome (and  
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence  
accumulation by directed, EST, and genomic sequencing  
approaches - and in particular, with the accumulation of  
20 sequence information from multiple genera, from multiple  
species within genera, and from multiple individuals within  
a species - there is an increasing need for methods that  
rapidly and effectively permit the functions of nucleic  
sequences to be elucidated. And as such functional  
25 information accumulates, there is a further need for  
methods of storing such functional information in  
meaningful and useful relationship to the sequence itself;  
that is, there is an increasing need for means and  
apparatus for annotating raw sequence data with known or  
30 predicted functional information.

Although the increase in the pace of genomic  
sequencing is due in large part to technological changes in  
sequencing strategies and instrumentation, Service, *Science*  
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),  
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

*Ismb* 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*, *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5           The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single  
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally  
15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality.  
20 Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia  
25 - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the bone marrow, particularly those diseases with polygenic etiology.

30

#### Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for  
35 predicting, confirming, and displaying functional

information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

5           In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

          The present invention also provides compositions  
10 and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

          Accordingly, in a first aspect of the invention,  
15 there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs:  
20 1 - 13,114 or a complementary sequence, or a portion of such a sequence.

          By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

25           In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

          In an alternative embodiment, each of said plurality of probes is separately and addressably  
30 isolatable from said plurality.

          In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

35           In yet another embodiment, said set of single

exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,012 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include

- polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

- In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

- In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 13,115 - 26,012, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,114.

- Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.



In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,013 - 38,628 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid

probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer; wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human bone marrow, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human bone marrow; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from

genomic sequence of said eukaryote; and then  
detecting specific hybridization of detectably  
labeled nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are  
5 derived from mRNA from the bone marrow of said eukaryote,  
said probe is a single exon probe having a fragment  
identical in sequence to, or complementary in sequence to,  
said predicted exon, said probe is included within a single  
exon microarray in accordance with the first aspect of the  
10 invention, and said fragment is selectively hybridizable at  
high stringency.

In a eighth aspect of the invention, there is  
provided a method of assigning exons to a single gene,  
comprising:  
15 identifying a plurality of exons from genomic  
sequence in accordance with the seventh aspect of the  
invention; and then  
measuring the expression of each of said exons in  
a plurality of tissues and/or cell types using  
20 hybridization to single exon microarrays having a probe  
with said exon,  
wherein a common pattern of expression of said  
exons in said plurality of tissues and/or cell types  
indicates that the exons should be assigned to a single  
25 gene.

In an ninth aspect of the invention, there is  
provided a nucleic acid sequence as set out in any of SEQ  
ID NOS: 1 - 26,012 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is  
30 provided a peptide encoded by a sequence comprising a  
sequence as set out in any of SEQ ID NOS: 13,115 - 26,012,  
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be  
encoded by a sequence comprising a sequence set out in any  
35 of SEQ ID NOS.: 1 - 13,114.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 26,013 - 38,628.

5           Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,013 - 38,628, or fragment thereof.

          In another aspect, the invention provides means  
10 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated  
15 sequence.

#### Detailed Description of the Invention

##### 20 Definitions

          As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately  
25 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

          As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach  
30 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the  
35 term "microarray" and phrase "nucleic acid microarray"

further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the

consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

5           As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons  
10 encoding the peptide are wholly contained within the exon.

          As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a  
15 nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

          As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present  
20 within a target mRNA.

          As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is  
25 meant that it is homologous to the given sequence.

          As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least  $10^7$ ,  
30 preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

          As used herein with respect to the visual display  
35 of annotated genomic sequence, the term "rectangle" means

any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

- 5           As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

#### Brief Description of the Drawings

- The present invention is further illustrated with reference to the following non-limiting figures and  
15 examples in which:

- FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in  
20 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

- 25           FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

- FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length  
30 shown in black and PCR product length shown in dotted lines;

- FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color  
35 hybridization to a genome-derived single exon microarray.

The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

5           FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured  
10   tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

15           FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a  
20   BLAST Expect ("E") value of greater than  $1e-30$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e-30$  ( $1 \times 10^{-30}$ ) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases  
25   25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30   Methods and Apparatus for Predicting, Confirming,  
Annotating, and Displaying Functional Regions From Genomic  
Sequence Data

FIG. 1 is a flow chart illustrating in broad  
35   outline a process for predicting functional regions from



genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the

- htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI).
- 5 Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.
- 10 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
- 15 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
- 20 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which

25 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

- 30 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
- 35 assay. Where the subsequent experimental assay is

bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

5           The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

10           Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by  
15 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for  
20 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process  
25 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output  
30 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational  
35 substrates for, and performance of subsequent assay, of

functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.

- 5 Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to  
10 process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

- The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be  
15 identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction  
20 analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of  
25 sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

- The exact content of query 20 will also depend  
30 upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the  
35 sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were

static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query

20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS\_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or

codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the  
5 undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence,  
10 leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered  
15 occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

20 Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived  
25 from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the  
30 input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,  
35 where sequences with the desired function are identified



within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after  
5 transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X  
10 chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment,  
15 for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described  
20 become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene  
25 prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and  
30 GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For  
35 the newly accessioned human genomic sequence input in

Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among

different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process  
5 can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence,  
10 but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done  
15 in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process  
300 for identification of a subset thereof for functional  
20 assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental  
25 verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the  
30 species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

35 Where such subsequent gene expression assay uses

amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of

verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

5 Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is  
10 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)  
15 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500  
20 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more  
25 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400  
30 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs  
35 predicted from human genomic sequence according to the

methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at  
5 amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are  
10 thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no  
15 more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20 Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit  
25 further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all  
30 amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not  
35 exceed about 25 nt in length. The "universal" priming

sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

- 5           Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 10 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 15 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

- The amplified nucleic acids can be attached 20 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

- 25           Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 30 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

- As is well known in the art, microarrays 35 typically also contain immobilized control nucleic acids.



For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 5 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural 10 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the 15 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, 20 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

25 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using 30 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid 35 probe than can be achieved with spotting or lithography

techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such

microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the

desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include

artificial sequence similar to that found in EST  
microarrays. However, the genome-derived single exon  
microarray of the present invention can be made without  
such sequences, and if so constructed, presents an even  
5 smaller amount of nonspecific sequence that would  
contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned  
material as probes in EST microarrays is that such  
microarrays contain probes that result from cloning  
10 artifacts, such as chimeric molecules containing coding  
region of two separate genes. Derived from genomic  
material, typically not thereafter cloned, the probes of  
the genome-derived single exon microarrays of the present  
invention lack such cloning artifacts, and thus provide  
15 greater specificity of signal in gene expression  
measurements.

A further consequence of the cloned origin of  
probes on many EST microarrays is that the individual  
probes often have disparate sizes, which can cause the  
20 optimal hybridization stringency to vary among probes on a  
single microarray. In contrast, as discussed above, the  
probes arrayed on the genome-derived single exon  
microarrays of the present invention can readily be  
designed to have a narrow distribution in sizes, with the  
25 range of probe sizes no greater than about 10% of the  
average size, typically no greater than about 5% of the  
average probe size.

Because of their origin from fully- or partially-  
spliced message, probes disposed upon EST arrays will often  
30 include multiple exons. The percentage of such exon-  
spanning probes in an EST microarray can be calculated, on  
average, based upon the predicted number of exons/gene for  
the given species and the average length of the immobilized  
probes. For human genes, the near-complete sequence of  
35 human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95

(1999) predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from  
5 algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-  
10 derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure  
15 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

20 Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons  
25 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic  
30 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn  
35 from noncoding regions. As discussed above, the additional

presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

5           The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

10           Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization  
15 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

          In contrast, the longer probe length of the  
20 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or  
25 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

30           A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound  
35 noncovalently to the substrate.



Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence

drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above-described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-

transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is

disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation  
5 information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in  
10 international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should  
15 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and  
20 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic  
25 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected  
30 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,  
35 SAGE ("serial analysis of gene expression") databases, and

more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -  
5 including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200,  
10 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such  
15 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or  
20 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

25 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the  
30 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively  
35 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the

sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.



Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from  
5 GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method  
10 and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to  
15 report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where  
20 display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by  
25 pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83  
30 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as  
35 many as can discriminably be displayed, depending upon the

number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions.

- 5 However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-
- 10 selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

- Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted
- 15 functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the
- 20 results of such physical assay.

- Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function
- 25 by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

- Where the function desired to be identified is
- 30 protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe
- 35 immobilized on the support surface of the microarray. As

noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

5           Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in  
10 process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically  
15 need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

          Rectangle 87 as shown in FIG. 3 includes smaller  
20 rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880  
25 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

30           Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

          For example, where the function assayed and displayed is protein coding, the degree of shading of  
35 rectangles 880 can be used to represent the degree of

sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as  
5 many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of  
10 expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which  
15 often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right  
20 borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical  
25 assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays,  
30 individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the  
35 spectra of the Cy3 and Cy5 dyes conventionally used for

respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such  
5 relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further  
10 information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

15 FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to  
20 rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return  
25 identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

30 Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

35 Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,114 of these ORFs in bone marrow.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in bone marrow is currently available for use in measuring the level of its ORF's expression in bone marrow.

Because bone marrow is the tissue in which blood cells originate, diseases of the bone marrow are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations

in single genes have in some cases been identified as causal - notably in the thalassemias and sickle cell anemia - disorders of the bone marrow are, for the most part, believed to have polygenic etiologies.

5           For example, cancers that originate in the bone marrow and lymphatic tissues such as the lymphomas, leukemias, and myeloma have been recognized as a major health concern. An estimated 632,000 Americans are presently living with lymphoma, leukemia or myeloma, and  
10 over 110,000 new cases are anticipated each year. The new cases alone account for 11% of all cancer cases reported in the United States.

          Lymphoma is a general term for a group of cancers of lymphocytes that manifest in the tissues of the  
15 lymphatic system. Eventually, monoclonal proliferation crowds out healthy cells and creates tumors which enlarge lymph nodes. Approximately 450,000 members of the U.S. population are living with lymphoma: 160,000 with Hodgkin disease (HD) and 290,000 with non-Hodgkin lymphoma.

20           Hodgkin disease (HD) is a specialized form of lymphoma, and represent about 8% of all lymphomas. HD can be distinguish in tissues by the presence of an abnormal cell called the Reed-Sternberg cell. Incidence rates of HD are higher in adolescents and young adults, but HD is  
25 considered to be one of the most curable forms of cancer. Symptoms of HD include painless swelling of lymph glands, fatigue, recurrent high fever, sweating at night, skin irritations and loss of weight.

          Although an infectious etiology has been proposed  
30 to account for the disproportionate incidence of HD among siblings reared together - particularly an association with Epstein Barr Virus (EBV) - multiple genetic contributions have also been suggested.

          As early as 1986, linkage to HLA was suggested,  
35 with Klitz et al., Am. J. Hum. Genet. 54: 497-505 (1994)

reporting an overall association of the nodular sclerosing (NSHD) group with the HLA class II region. Results of the study suggested that susceptibility to NSHD is influenced by more than 1 locus within the class II region. Through a  
 5 literature search, Shugart and Collins (2000), *Europ. J. Hum. Genet.* 8: 460-463 (2000), performed a combined segregation and linkage analysis on 59 nuclear families with HD and concluded that HD is most likely determined by both an HLA-associated major gene and other non-HLA genetic  
 10 factors, in conjunction with environmental effects.

Non-Hodgkin lymphoma (NHL) is a malignant monoclonal proliferation of the lymphoid cells in the immune system, including bone marrow, spleen, liver and GI tract. The pathologic classification of NHL continues to  
 15 evolve, reflecting new insights into the cells of origin and the biologic bases of these heterogeneous diseases. The course of NHL varies from indolent and initially well tolerated to rapidly fatal. Furthermore, common clinical symptoms of NHL, but rare in HD, are congestion and edema  
 20 of the face and neck and ureteral compression.

Non-Hodgkin lymphoma (NHL) has been linked to a variety of specific genetic defects, including 26 mutated genes and at least 9 identified chromosomal translocations. Among the mutated genes are: ALK (2p23); API2 (MIHC, cIAP2)  
 25 (11q22-q23); API4 (survivin, SVV) (17q25(?)); ATM (ATA, ATC) (11q22.3); BCL1 (11q13.3); BCL10 (CLAP, CIPER) (1p22); BCL2 (18q21.3); BCL6 (LAZ3, ZNF51) (3q27); BLYM (1p32); BMI1 (10p13); CCND1 (D11S287E, Cyclin D, PRAD1) (11q13); CD44 (MDU3, HA, MDU2) (11pter-p13); FRAT1 (10q23-q24(?)); FRAT2  
 30 (GBP) (10(?)); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LCP1 (PLS2) (13q14.1-q14.3); MALT1 (MLT) (18q21); MUC1 (PUM, PEM) (1q21); MYBL1 (AMYB, A-MYB) (8q22); MYC (CMYC, C-MYC) (8q24.12-q24.13); NBS1 (8q21); NPM1 (B23) (5q35); PCNA (20p12); TIAM1 (21q22.1); and TP53 (p53, P53) (17q13.1).

35 Among the chromosomal abnormalities are: t(1;14)



(p22;q32); t(14;18)(q32;q21); t(3;14)(q27;q32);  
t(6;14)(p25;q32); t(11;18)(q21;q21); t(1;14)(q21;q32);  
t(2;5)(p23;q35); add(14q32) / dup(14p32); and  
t(11;14)(q13;q32).

5 Additional genetic loci, as yet undiscovered, are believed to account for other occurrences of NHL.

As another example, acute leukemia is a malignant disease of blood-forming tissues such as the bone marrow. It is characterized by the uncontrolled growth of white  
10 blood cells. As a result, immature myeloid cells (in acute myelogenous leukemia (AML)) or lymphoid cells (in acute lymphocytic leukemia (ALL)) rapidly accumulate and progressively replace the bone marrow; diminished production of normal red cells, white cells, and platelets  
15 ensues. This loss of normal marrow function in turn gives rise to the typical clinical complications of leukemia: anemia, infection, and bleeding.

If untreated, ALL is rapidly fatal; most patients die within several months of diagnosis. With appropriate  
20 therapy, many patients can be cured. The survival rate for patients diagnosed with AML or ALL is 14% and 58% respectively. However, the incidences of AML is expected to be greater than ALL: an estimated 10,000 new cases of AML, predominantly in older adults, is anticipated in the  
25 U.S. alone, whereas 3,100 new cases of ALL are expected, with 1,500 of these new cases occurring among children.

The etiology of acute leukemia is not known. Although human T-cell lymphotropic virus type I (HTLV-I), a causative agent of adult T-cell leukemia, and HTLV-II,  
30 obtained from several patients with a syndrome resembling hairy cell leukemia, have been isolated, the etiologic link between HTLV and malignancy is uncertain. There is, however, evidence which suggests a genetic predisposition to incidences of acute leukemia.

35 For example, genetic disorders such as Fanconi

anemia and Down syndrome appear to increase risk of acute leukemia, specifically, AML. Evidence supporting a chromosome 21 locus for acute myelogenous leukemia (AML) includes the finding of linkage to 21q22.1-q22.2 in a family with a platelet disorder and propensity to develop AML (Ho et al., Blood 87: 5218-5224 (1996), an increased incidence of leukemia in Down syndrome, and frequent somatic translocation in leukemia involving the CBFA gene on 21q22.3. In addition, Horwitz et al., Am. J. Hum. Genet. 61:873-881 (1997), suggest that a gene on 16q22 may be a second cause of acute myelogenous leukemia. Nonparametric linkage analysis gave a P-value of 0.00098 for the conditional probability of linkage. Mutational analysis excluded expansion of the AT-rich minisatellite repeat FRA16B fragile site and the CAG trinucleotide repeat in the E2F-4 transcription factor. Large CAG repeat expansion was excluded as a cause of leukemia in this family.

Similarly, acute lymphoblastic leukemia (ALL) has been suggested to have a genetic predisposition. In particular, linkage to chromosome 9p has been reported by a number of groups. Chilcote et al., New Eng. J. Med. 313: 286-291 (1985), found that 6 of 8 patients with clinical features of lymphomatous ALL (LALL), a distinct category of ALL of T-cell lineage, had karyotypic abnormalities leading to loss of bands 9p22-p21. The mechanisms varied and included deletions, unbalanced translocations, and loss of the entire chromosome; only 1 of 57 patients without LALL had an abnormality of chromosome 9 at diagnosis. Kowalczyk et al., Cancer Genet. Cytogenet. 9:383-385 (1981), had earlier found changes in 9p in a subgroup of ALL cases. Chilcote et al. (1985) pointed out that there is a fragile site at 9p21 and raised the question of familial predisposition on this basis. This fragile site is the breakpoint in the translocation t(9;11)(p21-22;q23), which

is associated with acute nonlymphocytic leukemia with monocytic features, ANLL-AMoL-M5a. In a large series, Murphy et al., New Eng. J. Med. 313:1611 (1985), confirmed an abnormality of 9p in 10 to 11% of cases (33 out of more than 300) of acute lymphoblastic leukemia. The breakpoints in 9p clustered in the p22-p21 region. They could not, however, corroborate the specific association with T-cell origin or so-called lymphomatous clinical features. In addition, Taki et al., Proc. Natl. Acad. Sci. USA 96:14535 (1999), recently identified AF5q31, a new AF4-related gene, fused to MLL in infant ALL with ins(5;11)(q31;q13q23), and suspects that AF5q31 and AF4 might define a new family particularly involved in the pathogenesis of 11q23-associated-ALL.

As yet a further example of a disease affecting bone marrow with likely polygenic etiology is multiple myeloma (MM).

MM is a cancer of plasma cells, the final differentiated stage of B lymphocyte maturation. The malignant clone proliferates in the bone marrow and frequently invades the adjacent bone, producing extensive skeletal destruction that results in bone pain and fractures. Anemia, hypercalcemia, and renal failure are some clinical manifestations associated with MM.

MM causes 1% of all cancer deaths in Western countries. A genetic component to its etiology is suggested by disparate incidence among various groups in the country. Its incidence is higher in men than in women, in people of African descent relative to the U.S. population at large, and in older adults as compared to the young. It has been estimated that 14,000 new cases of myeloma will be diagnosed in the U.S., and over 11,000 persons will die from MM within the year.

Although, Kaposi's sarcoma-associated herpes virus has been associated with MM (Retig et al., Science

276:1851 (1997)), there is evidence that chromosomal abnormalities, such as the deletion of 13q14 and rearrangements of 14q increase the proliferation of myeloma cells.

5 Up to 30% of patients who suffer with MM have a balanced translocation, t(4;14)(p16.3;q32), that places the fibroblast growth factor receptor 3 (FGFR3) gene under the control of IgH promoter elements (Chesi et al., Nat. Genet. 16:260 (1997)). This results in increased expression of  
10 FGFR3, a member of a family of tyrosine kinase receptors implicated in control of cellular proliferation.

According to Zoger et al., Blood 95:1925 (2000), monoallelic deletions of the retinoblastoma-1 (rb-1) gene and the D13S319 locus were observed in 48 of 104 patients  
15 (46.2%) and in 28 of 72 (38.9%) patients, respectively, with newly diagnosed MM. Fluorescence in situ hybridization (FISH) studies found that 13q14 was deleted in all 17 patients with karyotypic evidence of monosomy 13 or deletion of 13q but also in 9 of 19 patients with  
20 apparently normal karyotypes. Patients with a 13q14 deletion were more likely to have higher serum levels of beta(2)-microglobulin (P=0.059) and a higher percentage of bone marrow plasma cells (P=0.085) than patients with a normal 13q14 status on FISH analysis. In patients with a  
25 deletion of 13q14, myeloma cell proliferation was markedly increased. The presence of a 13q14 deletion on FISH analysis was associated with a significantly lower rate of response to conventional-dose chemotherapy (40.8% compared with 78.6%; P =.009) and a shorter overall  
30 survival (24.2 months compared with > 60 months; P <.005) than in patients without the deletion.

There are numerous other mutated genes and chromosomal abnormalities that may predispose to MM. Examples of such genes are: B2M (15q21-q22); CCND1  
35 (D11S287E, Cyclin D, PRAD1)(11q13); CD19 (16p11.2 ); HGF

(HPTA) (7q21.1); IL6 (IFNB2) (7p21); IRF4 (MUM1, LSIRF) (6p25-p23); LTA (TNFB, LT) (6p21.3); SDC1 (2p24.1); and TNF (TNFA, TNFSF2, DIF) (6p21.3). Examples of chromosomal abnormalities include: t(6;14)(p25;q32) and  
5 t(11;14)(q13;q32).

Other significant diseases or disorders of the bone marrow are also believed, or likely to have, a genetic, typically polygenic, etiologic component. These diseases include, for example, chronic myeloid leukemia,  
10 chronic lymphoid leukemia, polycythemia vera, myelofibrosis, primary thrombocythemia, myelodysplastic syndromes, Wiskott-Aldrich, lymphoproliferative syndrome, aplastic anemia, Fanconi anemia, Down syndrome, sickle cell disease, thalassemia, granulocyte disorders, Kostmann  
15 syndrome, chronic granulomatous disease, Chediak-Higashi syndrome, platelet disorders, Glanzmann thrombasthenia, Bernard-Soulier syndrome, metabolic storage diseases, osteoporosis, congenital hemophagocytic syndrome.

The human genome-derived single exon nucleic acid  
20 probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human bone marrow, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed  
25 at detectable levels in human bone marrow, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis, grading, and/or staging  
30 of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given bone marrow disease, or to specific grades or stages thereof.

35 In one embodiment, the patient gene expression

profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's bone marrow (or cells cultured therefrom) to the genome-derived single exon microarray of the present  
5 invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the bone marrow of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the  
10 function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be  
15 used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of diseases of bone marrow to be assessed through the massively parallel determination of altered copy number, deletion, or mutation  
20 in the patient's genome of exons known to be expressed in human bone marrow. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

25 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

30 It should be appreciated, however, that the probes of the present invention, for which expression in the bone marrow has been demonstrated are useful for both measurement in the bone marrow and for survey of expression in other tissues.

35 Significant among such advantages is the presence

of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be  
5 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were  
10 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence  
15 databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes  
20 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and  
25 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. Nature 405,  
30 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct  
35 Programs Regulating Lung Inflammation and Fibrosis," *Proc.*

- Natl. Acad. Sci. USA 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," Arch. Biochem. Biophys. 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," Virology 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," Curr. Biol. 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).
- Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," Proc. Natl. Acad. Sci. USA 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," Proc. Natl. Acad. Sci. USA 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," Oncogene 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," Ann. Neurol. 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," Nat. Genet. 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer



Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in bone marrow. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity

sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA  
5 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as  
10 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

15 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity  
20 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and  
25 WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

30 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or  
35 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable

of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,115 - 26,012, respectively, for probe SEQ ID NOS. 1 - 13,114. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,115 - 26,012 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of

other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one  
5 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more  
10 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand  
15 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art  
20 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to  
25 provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic  
30 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

35 And when intended for use in solution

hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen

for the common attribute of expression in the human bone marrow.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be  
5 chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be  
10 used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

15 It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

20 The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human bone marrow. In preferred embodiments, the present invention provides human genome-derived single exon microarrays  
25 comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 13,114.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived  
30 single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression  
35 measurements. Alternatively, at a given probe density, the

same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,114 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,115 - 26,012, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,114 can be used, or that portion thereof in SEQ ID NOS. 13,115 - 26,012 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X<sup>™</sup> Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL<sup>™</sup>) System, New England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis



(Oxford Chemistry Primers, No 7) , Oxford Univ. Press  
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles  
of Peptide Synthesis (Springer Laboratory), Springer Verlag  
(December 1993) (ISBN: 0387564314).

5           It is, therefore, another aspect of the invention  
to provide peptides comprising an amino acid sequence  
translated from SEQ ID NOS.: 13,115 - 26,012. Such amino  
acid sequences are set out in SEQ ID NOS: 26,013 - 38,628.  
Any such recombinantly-expressed or synthesized peptide of  
10 at least 8, and preferably at least about 15, amino acids,  
can be conjugated to a carrier protein and used to generate  
antibody that recognizes the peptide. Thus, it is a  
further aspect of the invention to provide peptides that  
have at least 8, preferably at least 15, consecutive amino  
15 acids.

The following examples are offered by way of  
illustration and not by way of limitation.

#### 20 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted  
in Human Genomic Sequence

#### Bioinformatics Results

25           All human BAC sequences in fewer than 10 pieces  
that had been accessioned in a five month period  
immediately preceding this study were downloaded from  
GenBank. This corresponds to ~2200 clones, totaling ~350  
MB of sequence, or approximately 10% of the human genome.

30           After masking repetitive elements using the  
program CROSS\_MATCH, the sequence was analyzed for open  
reading frames using three separate gene finding programs.  
The three programs predict genes using independent  
algorithmic methods developed on independent training sets:  
35 GRAIL uses a neural network, GENEFINDER uses a hidden

Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic  
5 DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION  
10 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three  
15 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs  
20 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single  
25 gene if fewer than 7 exons were found within the 25 kb window.

#### PCR

The largest ORF from each gene bin that did not  
30 span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments  
35 fewer than 250 bp in length do not bind well to the amino-

modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

5           Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first  
10 additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit  
15 subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

          The ORFs were then PCR amplified from genomic  
20 DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

          Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard  
25 techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR  
30 amplification was classified as successful if a single band appeared.

          The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%.  
FIG. 5 graphs the distribution of predicted ORF (exon)  
35 length and distribution of amplified PCR products, with ORF

length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median  
5 size of 150 bp (n=9498). With an average amplicon size of  $475 \pm 25$  bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

10 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of  
15 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were  
20 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR  
25 and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material  
30 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was  
35 similarly found not to affect differential expression

ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-  
5 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally  
10 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt  
15 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe  
20 sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

25 All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are  
30 presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis
--

Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

## EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1)  
 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message

pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

- 5 Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer  
10 and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM  
15 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup  
20 column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

- Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a  
25 Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>0</sub>t1 DNA, and 0.5 % SDS.

- Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C  
30 overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

- 35 Slides were scanned using a Molecular Dynamics

Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

5           Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of  
10 at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

15           Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

          The relative expression signal for these probes  
20 was then plotted as function of tissue or cell type, and is presented in FIG. 6.

          FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not  
25 expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

          Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed"  
30 products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were  
35 expressed in all 10 tissues. The next most common class



(15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested

tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 5 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

10

#### Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 15 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") 20 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 25 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being 30 found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' 35 or 5' end of a gene, many of these high expression genes

will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

10 To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

15 Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR  
20 against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence  
25 AL031734\_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue  
30 type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However,  
35 in addition to the two RT-PCR results presented above, the

observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous

				system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to

				the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097  
 10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3  
 15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed

down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 $\alpha$  (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in

choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control ( n = 5)
Bone Marrow	-1.81 $\pm$ 0.11	-1.85 $\pm$ 0.08
Brain	-1.41 $\pm$ 0.11	-1.17 $\pm$ 0.05
BT474	1.85 $\pm$ 0.09	1.66 $\pm$ 0.12
Fetal Liver	-1.62 $\pm$ 0.07	-1.41 $\pm$ 0.05
HBL100	1.32 $\pm$ 0.05	2.64 $\pm$ 0.12
Heart	1.16 $\pm$ 0.09	1.56 $\pm$ 0.10
HeLa	1.11 $\pm$ 0.06	1.30 $\pm$ 0.15
Liver	-1.62 $\pm$ 0.22	-2.07 $\pm$
Lung	-4.95 $\pm$ 0.93	-3.75 $\pm$ 0.21
Placenta	-3.56 $\pm$ 0.25	-3.52 $\pm$ 0.43

10

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

20 EXAMPLE 3



Representation of Sequence and Expression Data as a  
"Mondrian"

For each genomic clone processed for microarray  
5 as above-described, a plethora of information was  
accumulated, including full clone sequence, probe sequence  
within the clone, results of each of the three gene finding  
programs, EST information associated with the probe  
sequences, and microarray signal and expression for  
10 multiple tissues, challenging our ability to display the  
information.

Accordingly, we devised a new tool for visual  
display of the sequence with its attendant annotation  
which, in deference to its visual similarity to the  
15 paintings of Piet Mondrian, is hereinafter termed a  
"Mondrian". FIGS. 3 and 4 present the key to the  
information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases  
25,000 to 130,000 shown), containing the carbamyl phosphate  
20 synthetase gene (AF154830.1). Purple background within the  
region shown as field 81 in FIG. 3 indicates all 37 known  
exons for this gene.

As can be seen, GRAIL II successfully identified  
27 of the known exons (73%), GENEFINDER successfully  
25 identified 37 of the known exons (100%), while DICTION  
identified 7 of the known exons (19%).

Seven of the predicted exons were selected for  
physical assay, of which 5 successfully amplified by PCR  
and were sequenced. These five exons were all found to be  
30 from the same gene, the carbamyl phosphate synthetase gene  
(AF154830.1).

The five exons were arrayed, and gene expression  
measured across 10 tissues. As is readily seen in the  
Mondrian, the five chip sequences on the array show  
35 identical expression patterns, elegantly demonstrating the

reproducibility of the system..

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):  
red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring  
Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in bone marrow tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical

structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the  
5 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,114 single exon probes, each fragment corresponding to an extension product from one of  
10 the two amplification primers.)

The structures of the 13,114 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,114 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not  
15 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,115 - 26,012, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than  
20 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant  
25 expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give  
30 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the  
35 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human bone marrow and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human bone marrow tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,115 - 26,012 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" ) from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs

in an exhaustive process based on the following criteria:

1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all  
5 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion  
10 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the  
15 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary:  
in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as  
20 the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  — which is probative evidence that the query sequence has previously  
25 been shown to be expressed — the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even  
30 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent  
35 a proper subset of the data present within the attached

sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 13,114) and probe exon (SEQ ID NOS.: 13,115 - 26,012, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

- 5           (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;
- (b) the most similar sequence provided by BLAST
- 10       query of the EST database, with accession number and BLAST E value for the "hit";
- (c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and
- 15       (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

## 20   EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human Bone marrow

- 25   Table 4 (546 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human bone marrow.

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived  
5 from human bone marrow comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,114 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid  
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid  
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,115 - 26,012.
5. A spatially-addressable set of single exon nucleic acid  
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid  
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid  
35 probes as claimed in any of claims 1 to 6, wherein the



average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,114 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human bone marrow.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,115 - 26,012 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human bone marrow which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
- 10 of SEQ ID NOs.: 26,013 - 38,628, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human bone marrow.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
- 25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample  
5 derived from human bone marrow, comprising:  
    contacting the microarray of claim 12, with a first  
        collection of detectably labeled nucleic acids,  
        said first collection of nucleic acids derived  
        from mRNA of human bone marrow; and then  
10 measuring the label detectably bound to each probe of  
    said microarray.

23. A method of identifying exons in a eukaryotic genome,  
comprising:  
15 algorithmically predicting at least one exon from  
    genomic sequence of said eukaryote; and then  
    detecting specific hybridization of detectably labeled  
        nucleic acids to a single exon probe,  
wherein said detectably labeled nucleic acids are derived  
20 from mRNA from the bone marrow of said eukaryote, said  
probe is a single exon probe having a fragment identical in  
sequence to, or complementary in sequence to, said  
predicted exon, said probe is included within a microarray  
according to claim 12, and said fragment is selectively  
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,  
comprising:  
    identifying a plurality of exons from genomic  
30 sequence according to the method of claim 23; and  
    then  
    measuring the expression of each of said exons in a  
        plurality of tissues and/or cell types using  
        hybridization to single exon microarrays having a  
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,012 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,012.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,013 - 38,628.

Page 1 of 546  
Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
450	13523	26455	4.57				
890	13945	26903	10.46				
1046	14092		3.88				
1305	14241	27305	7.19				
1618	14550	27528	4.21				
1642	14674	27647	6.05				
1738	14768	27753	2.88				
1784	14793	27778	1.27				
1770	14799	27785	6.94				
1808	14802	27828	1.24				
1885	15016	28023	3.44				
2715	15191	28212	2.92				
2287	15300	28524	2.97				
3200	16256	29175	3.13				
3494	16510	29431	1.32				
3327	16573	29496	10.95				
3574	16619		0.85				
3908	17008		1.15				
4225	17254	30141	1.98				
4290	17318	30188	6.25				
4310	17339	30216	0.83				
4310	17339	30219	0.83				
4364	17391		1.03				
4420	17447	30338	0.83				
4874	17891	30780	1.27				
4958	17874	30865	0.74				
5083	18053	30989	5.95				
5095	18105	30980	1.42				
5329	18435	31187	1.78				
5329	18435	31185	1.78				
5498	18598		4.07				
5878	18775		7.77				
5782	18568		3.48				
5824	18914	32097	0.95				

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5830	18920	32103	3.19				
6138	25655	32443	1.68				
6167	18242	32473	2.11				
6556	19818		1.24				
6700	19757	33034	0.89				
6700	19757	33035	0.89				
7352	20303	33647	1.82				
7352	20303	33648	1.52				
7642	20602	33698	1.45				
7642	20602	33697	1.45				
8114	21081		0.81				
8396	21365	34774	1.55				
8850	21797	35216	1.21				
9212	22178	35608	0.57				
9212	22178	35609	0.57				
9892	22845	36302	5.61				
10124	23030	36529	0.69				
10241	23168	36653	1.44				
10383	23305	36762	0.81				
10575	23597	37063	0.49				
10575	23597	37064	0.49				
10794	23715	37216	0.6				
10794	23715	37217	0.6				
11043	24007		2.14				
11366	24314		1.81				
11687	24653	38232	1.82				
11826	24712		1.94				
12888	25476		1.5				
12888	25476	31730	1.34				
6170	10245	32477	15.3	9.8E+00 AJ239028.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8339	21306	34723	1.75	9.8E+00 U32716.1	NT		Haemophilus influenzae Rd section 31 of 163 of the complete genome
10100	23026	36502	0.47	9.8E+00 Y18530.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
10100	23026	36503	0.47	9.8E+00 Y18530.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7164	20218	33549	0.66	9.6E+00 AF065630.1	NT		Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7194	20218	33550	0.66	9.0E+00	AF066530.1	NT	Gallus gallus ornithine transcarbamylase (O/C) gene, exon 1
10787	23708	37209	1.19	9.0E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gf2h2) genes, complete cds
10787	23708	37210	1.19	9.0E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gf2h2) genes, complete cds
2835	15993	28913	3.21	9.0E+00	AB043785.1	NT	Mus musculus A13 gene for antithrombin, complete cds
6457	19522	32773	0.54	9.4E+00	P75130	SWISSPROT	HYPOTHETICAL PROTEIN MG447 HOMOLOG
11911	24792	36381	2.45	9.4E+00	O36825	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
11911	24792	36382	2.45	9.4E+00	O36825	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
8435	21404	34817	0.86	9.3E+00	AF130590.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9356	22321	35748	3.15	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88)
5369	18474	31546	2.56	9.1E+00	AF035609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5369	18474	31547	2.66	9.1E+00	AF035609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9785	22726	309241	0.95	9.0E+00	P09241	SWISSPROT	RHODOPSIN
8152	19227	32456	5.62	8.0E+00	BE971808.1	EST_HUMAN	001651038T1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934692 3'
8517	19580	32837	2.21	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Op1x3 premature mRNA, partial cds
8517	19580	32838	2.21	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Op1x3 premature mRNA, partial cds
440	13574	26445	1.03	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9810	21133	34536	3.58	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11504	24446		1.54	8.0E+00	P41820	SWISSPROT	BREFFELDIN A RESISTANCE PROTEIN
8461	21459		0.82	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7599	20532		2.17	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
8704	21672	35095	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8704	21672	35096	1.58	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5986	19385	32176	3.63	7.4E+00	BF700517.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9106	22072	35498	2.72	7.4E+00	P04928	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
9106	22072	35499	2.72	7.4E+00	P04928	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2990	15048	28968	4.7	7.2E+00	L12051.1	NT	Lyoparsion esculentum Mill. GTPase (SAR2) mRNA, complete cds
2990	15048	28969	4.7	7.2E+00	L12051.1	NT	Lyoparsion esculentum Mill. GTPase (SAR2) mRNA, complete cds
7200	20252	33586	1.12	7.2E+00	BE179090.1	EST_HUMAN	RCO-HT0615-200300-031-e07 HT0613 Homo sapiens cDNA
7356	20326	33673	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7356	20326	33674	1.1	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9957	22884		6.86	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
11715	24678	38256	2.98	7.1E+00	P08880	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHB INTERGENIC REGION
11909	24780	38378	4.81	7.1E+00	P08108	SWISSPROT	MET17 PROTEIN (INCLUDES: O-ACETYLHOMOSERINE SULFHYDRYLASE (OAH SULFHYDRYLASE);
10341	23265	38744	3.43	7.0E+00	P48810	SWISSPROT	O-ACETYL-SERINE SULFHYDRYLASE (OAS SULFHYDRYLASE))
11580	24518	38074	1.7	7.0E+00	Q22469	SWISSPROT	ARGININE KINASE (AK)
8828	21594	35014	3.94	6.9E+00	P35679	SWISSPROT	WD-40 REPEAT PROTEIN MS13
10716	23638	37131	1.32	6.9E+00	P44834	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10734	23656	37149	0.44	6.9E+00	P34228	SWISSPROT	DNA MISMATCH REPAIR PROTEIN NUTS
8240	21209	34813	1.31	6.8E+00	W03412.1	EST_HUMAN	SKT6 PROTEIN
8240	21209	34814	1.31	6.8E+00	W03412.1	EST_HUMAN	zao7611.1f Soares melanocyte ZN18HM Homo sapiens cDNA clone IMAGE:291860 5'
8488	22452		1.35	6.8E+00	P36307	SWISSPROT	zao7611.1f Soares melanocyte ZN18HM Homo sapiens cDNA clone IMAGE:291860 5'
10569	23491	36983	3.31	6.8E+00	Q09370	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) (CONTAINS:
5356	18461		0.74	6.8E+00	Q69028	SWISSPROT	OUTER CAPSID PROTEINS VP6 AND VP8)
6655	19752	33026	0.72	6.8E+00	BF67212.1	EST_HUMAN	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
10434	23566	36842	1.87	6.8E+00	Q82E07	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
10434	23566	36843	1.87	6.8E+00	Q82E07	SWISSPROT	602152573FT NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4283427 5'
11453	24406		2.49	6.8E+00	Q10309	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
6535	22498	35246	7.17	6.5E+00	P03374	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10587	22559	37286	0.47	6.5E+00	BE66001.1	EST_HUMAN	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
10059	23028	36501	1.17	6.2E+00	A1010601.1	NT	ENV POLYPROTEIN (CONTAINS: COAT PROTEIN GP52, COAT PROTEIN GP36)
10927	23847	37362	0.85	6.2E+00	6754621	NT	801878435FT NIH_MGC 33 Homo sapiens cDNA clone IMAGE:3680699 5'
7236	20257	33391	1.35	6.0E+00	BE760163.1	EST_HUMAN	Schizosaccharomyces commune unknown mRNA
10175	23100	36580	0.46	6.0E+00	AF000008.1	NT	Mus musculus marnosidase 2, alpha B1 (Marn2b1), mRNA
10890	23800	37302	0.63	6.0E+00	AE001862.1	NT	801468031FT NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3871303 5'
10890	23800	37303	0.63	6.0E+00	AE001862.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (677)
							Dinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
							Dinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
							Mus musculus mixed lineage kinase 3 (MlK3) and two pore domain (K+ channel subunit (Kcnk8) genes, complete cds
6870	19727	33003	6.7	5.9E+00	AF165142.1	NT	Mus musculus DESCT1 protein (DESC1), mRNA
3538	16592		0.88	5.9E+00	7081557	NT	Homo sapiens DESCT1 protein (DESC1), mRNA
7369	20339	33690	0.65	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor (IGSR mRNA, complete cds
7369	20339	33691	0.65	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor (IGSR mRNA, complete cds
7819	20768		1.5	5.8E+00	P75600	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLII)
11805	23990	37485	2.98	5.8E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE



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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6390	19448	32689	0.78	5.6E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10138	23064		0.47	5.6E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11803	23988	37482	2.35	5.6E+00	P11880	SWISSPROT	PHENOLYLISIN (THIOL-ACTIVATED CYTOLYSIN)
7115	20049	33351	1.1	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7115	20049	33352	1.1	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7552	20515		0.84	5.4E+00	Q39435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8143	21080	34480	0.6	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
8202	21172		1.72	5.4E+00	Q91062	SWISSPROT	LIPOVITELLIN LV-2)
9151	22117	35543	0.73	5.4E+00	P40378	SWISSPROT	REPT PROTEIN
9151	22117	35544	0.73	5.4E+00	P40378	SWISSPROT	REPT PROTEIN
10396	23316	36798	1.41	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
10396	23316	36800	1.41	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4824	17841	30739	1.22	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6535	19693		0.6	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8415	21394		3.9	5.3E+00	P50108	SWISSPROT	HOMEOBOX PROTEIN CEH-20
9335	22200		0.53	5.3E+00	AB034980.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11850	24829	38425	1.84	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
12093	24964	38559	2.34	5.3E+00	Z72893.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL141w
12093	24964	38560	2.34	5.3E+00	Z72893.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL141w
5539	18636		1.22	5.2E+00	BE184940.1	EST_HUMAN	QV4-H10091-270400-185-039 HT0891 Homo sapiens cDNA
10738	23660		0.78	5.2E+00	AF248070.1	NT	Drosophila orientalis R1B retrotransposable element reverse transcriptase gene, partial cds
11527	24468		1.46	5.2E+00	Q10106	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C25E2.03C IN CHROMOSOME I
8313	22278	36709	0.85	5.1E+00	O16005	SWISSPROT	RHODOPSIN
10184	23109	36592	1.07	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
11617	24555	36117	3.01	5.1E+00	P55200	SWISSPROT	ZINC FINGER PROTEIN HRX (ALL-1)
8418	19485	32724	0.65	5.0E+00	BF31043.1	EST_HUMAN	601894910F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE4124114.5
10564	23478		0.65	5.0E+00	BF308561.1	EST_HUMAN	601894910F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE4131509.5
10796	23717	37219	3.79	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11622	24580	38122	6.39	5.0E+00	Z83890.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10592	23514		0.63	4.8E+00	U91328.1	NT	Enluc australis histone H3 (H3) gene, partial cds
4090	17124		9.81	4.8E+00	AF185255.1	NT	Enluc australis histone H3 (H3) gene, partial cds

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## Single Exon Probes Expressed In Bone Marrow

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8494	21482	34878	0.53	4.8E+00	BF39790.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8888	21852		6.15	4.8E+00	AW150067.1	EST_HUMAN	PMO-3T0547-310100-002-004 BT0547 Homo sapiens cDNA
289	13384	28311	2.03	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4039716 5'
260	13384	28311	1.69	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4039716 5'
3287	16341	29260	1.66	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21Q380
8084	21001	34397	0.53	4.8E+00	U07593.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
9551	22513	35963	1.12	4.8E+00	BE646437.1	EST_HUMAN	7c69g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 075140
9551	22513	35964	1.12	4.8E+00	BE646437.1	EST_HUMAN	KIAA0645 PROTEIN, contains element PTR5 repetitive element;
10755	23877		0.6	4.8E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8047	20884		0.61	4.8E+00	AF126177.1	NT	Isaohentkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
11930	24811	38406	2.19	4.8E+00	AE007044.1	NT	Achoaeigibbus fujidius section 63 of 172 of the complete genome
12055	24928	38526	1.87	4.8E+00	BF688841.1	EST_HUMAN	602123236F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3053	16110	29024	0.76	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
3053	16110	29025	0.76	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215284 5'
6328	19398		1.69	4.4E+00	X13414.1	NT	Murine l gene for MHG class II(a) associated invariant chain
6394	19462	32709	0.59	4.4E+00	AF156698.1	NT	Nicotiana glauca inorganic phosphate transporter (PT1) mRNA, complete cds
6240	16313		0.71	4.3E+00	AF055078.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7672	20630	33994	3.63	4.3E+00	Y13402.1	NT	Plasmodium falciparum R25R+var1 gene, exon 1
7874	20818	34186	0.81	4.3E+00	AE001222.1	NT	Tricoma pallidum section 38 of 87 of the complete genome
11210	24164	37894	7.01	4.3E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11279	24230		1.93	4.3E+00	11528311	NT	Homo sapiens Digeorge syndrome critical region gene 2 (DSCR2), mRNA
5595	18661		3.57	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-4) (RENAL DIPEPTIDASE) (ROP)
6978	18770	31942	1.35	4.2E+00	P51628	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
5954	18945		0.58	4.2E+00	O27830	SWISSPROT	POTATIVE ATP-DEPENDENT HELICASE MTH1802
6938	20162	33483	1.89	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6938	20162	33484	1.68	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9311	22278	36708	5.1	4.2E+00	AB090113.1	EST_HUMAN	W67003.X1 Scores, NFL_1 GRC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
10278	23203	36888	1.1	4.2E+00	P13368	SWISSPROT	NUBIN PROTEIN (TYAN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOGT11)
10506	23430		0.93	4.2E+00	P40888	SWISSPROT	HEXOSE TRANSPORTER HXT8

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## Single Exon Probes Expressed in Bone Marrow

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6046	25652	32334	0.64	4.1E+00	Q08185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
6048	25652	32335	0.64	4.1E+00	Q08185	SWISSPROT	CELLULAR TUMOR ANTIGEN P53
7319	20290	33633	0.76	4.1E+00	BE235888.1	EST_HUMAN	60110727F1 NIH_MGC. 10 Homo sapiens cDNA clone IMAGE:3351534.5'
7420	20387	33738	0.55	4.1E+00	BF247939.1	EST_HUMAN	60186030F1 NIH_MGC. 58 Homo sapiens cDNA clone IMAGE:4069756.5'
7923	20366	34254	7.67	4.1E+00	Q23810	SWISSPROT	YY1 PROTEIN PRECURSOR
8081	20398		0.64	4.1E+00	AB041523.1	NT	Pallidipes yessoensis mRNA for calcineurin A, complete cds
8086	21002	34398	3.95	4.1E+00	P28654	SWISSPROT	GENE 68 PROTEIN
8085	21002	34398	3.95	4.1E+00	P28654	SWISSPROT	GENE 68 PROTEIN
8249	21218	34628	2.5	4.1E+00	U57503.1	NT	Pent troglodytes novel repetitive solo LTR element in the RNU2 locus
8808	22851	36310	0.52	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
10031	22958	36426	2.43	4.1E+00	BF682425.1	EST_HUMAN	602247338F1 NIH_MGC. 62 Homo sapiens cDNA clone IMAGE:4333209.5'
10669	23591		0.45	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27)
10981	23901	37414	0.47	4.1E+00	O84242	SWISSPROT	3-OXOACYL-ACYL-CARRIER-PROTEIN SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
11231	24184		2.3	4.1E+00	P09716	SWISSPROT	HYPOTHEICAL PROTEIN HVLFI
11317	24287		13.22	4.1E+00	BE85880.1	EST_HUMAN	601607510F1 NIH_MGC. 71 Homo sapiens cDNA clone IMAGE:3903051.5'
3556	16602		0.7	4.0E+00	P36229	SWISSPROT	GLUT-INTERACTING PROTEIN 1
5534	20057	33381	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTAZE]
5534	20057	33382	0.94	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTAZE]
7123	20057	33361	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTAZE]
7123	20057	33362	1.01	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTAZE]
7395	20363	33715	1.47	4.0E+00	Q33010	SWISSPROT	SUCRASE-ISOMALTAZE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTAZE]
9225	22191	35621	0.44	4.0E+00	Q14157	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10303	23228	36711	0.43	4.0E+00	O61309	SWISSPROT	HYPOTHEICAL PROTEIN KAA0144
10526	23448	36946	0.8	4.0E+00	AE002132.1	NT	NITRIC-OXIDE SYNTHASE (NOS, TYPE II) (NEURONAL NOS) (NNOS)
10920	23542	37041	0.48	4.0E+00	Q00511	SWISSPROT	Ureaplasma urealyticum section 33 of 56 of the complete genome
10620	23542	37042	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11802	23957	37481	1.87	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11875	24757	38340	2.68	4.0E+00	P07554	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11875	24757	38341	2.88	4.0E+00	U07564	SWISSPROT	
3513	18559	29493	4.66	3.9E+00	XG4518.1	NT	Nucleocapsid protein gene 50 for class I chitinase C
4349	17376		0.90	3.9E+00	AF055486.1	NT	Mus musculus seminal vesicle secretory protein 82 (MSVSP82) gene, promoter region
5741	18835	32015	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-105 BN0070 Homo sapiens cDNA
5741	18835	32016	2.98	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-105 BN0070 Homo sapiens cDNA
6791	18845	33129	0.95	3.9E+00	AF296209.1	NT	Dicystidium discoideum non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6848	18601	33195	0.87	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, R6R1 gene, and sodium phosphate transporter (NPT3) gene, complete cds
7057	20079	33388	4.24	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSP INTERGENIC REGION
7587	20548	33608	4.15	3.9E+00	M23607.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8660	21628	35049	2.34	3.9E+00	XG5895.1	NT	Xlaevia mRNA for M4 muscarinic receptor
11720	23917	37434	2.93	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11742	24627	38206	1.89	3.9E+00	AA691489.1	EST_HUMAN	nr18a2.at NCI_CGAP_Ewt Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2637	15939		1.27	3.9E+00	AE007652.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6630	19593	32654	0.93	3.9E+00	Q57850	SWISSPROT	HYPOTHETICAL PROTEIN M10385
6937	20161	33482	0.59	3.9E+00	AI493946.1	EST_HUMAN	q251807.at NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2030437 3'
8775	21742	35164	1.03	3.9E+00	D44725.1	EST_HUMAN	HUMSUP135 Human brain cDNA Homo sapiens cDNA clone 148
10154	23079		0.66	3.9E+00	AI390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
12119	24989		15.21	3.9E+00	9031294	NT	Melanoplus sanguinipes entomovirus, complete genome
4049	17086	29682	9.75	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7372	20342		0.9	3.7E+00	AL44065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
9055	22022		0.46	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
6532	22495	35643	0.92	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11760	24868	38269	1.73	3.7E+00	BF666278.1	EST_HUMAN	602120551.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11760	24868	38270	1.73	3.7E+00	BF666278.1	EST_HUMAN	602120551.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12256	25082		2.6	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
565	13602	29375	4.04	3.9E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5286	18292	31153	0.63	3.8E+00	289709.1	NT	<i>Bacillus subtilis</i> complete genomes (section 8 of 21): from 899501 to 1208940
5327	18433	31185	0.73	3.8E+00	BF316318.1	EST_HUMAN	601501866F NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4131018 5'
8897	21693	35285	0.93	3.8E+00	D12867.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone t808
8897	21693	35286	0.93	3.8E+00	D12867.1	EST_HUMAN	HUM0001B08 Liver HepG2 cell line. Homo sapiens cDNA clone t808
8992	21958	35383	4.21	3.8E+00	AE004447.1	NT	<i>Pseudomonas aeruginosa</i> PAO1, section 8 of 529 of the complete genome
8992	21958	35384	4.21	3.8E+00	AE004447.1	NT	<i>Pseudomonas aeruginosa</i> PAO1, section 8 of 529 of the complete genome
10022	22949	36416	0.44	3.8E+00	U72775.1	NT	<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
10022	22949	36417	0.44	3.8E+00	U72775.1	NT	<i>Ciconia episcopus</i> cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11200	24155		3.18	3.8E+00	M96795.1	NT	<i>Escherichia coli</i> O157:H7 enterohemorrhagic EHEC strain 26869 complete cds
6116	19183		1.1	3.8E+00	L42898.1	NT	<i>Borrelia burgdorferi</i> (strain 25015) outer surface protein (ospC) gene, partial cds
6337	19406	32647	0.99	3.8E+00	R16745.1	EST_HUMAN	Yg00008.r1 Scores Infant brain TNIB Homo sapiens cDNA clone IMAGE:34940 5'
8087	21023	34422	0.6	3.8E+00	P97608	SWISSPROT	5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE) (5-OPASE)
8094	21030	34428	0.54	3.8E+00	A4992102.1	EST_HUMAN	cd37f10.31 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1618887 3' similar to gb-J04213
8124	21051	34459	0.56	3.8E+00	4505284	NT	CELLULAR RETINALDEHYDE-BINDING PROTEIN (HUMAN);
8929	21796		0.6	3.8E+00	P24557	SWISSPROT	Homo sapiens macrophage stimulating 1 receptor (c-met-related tyrosine kinase) (MST1R) mRNA
6387	22352	35782	0.91	3.8E+00	AA190598.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9387	22352	35783	0.91	3.8E+00	AA190598.1	EST_HUMAN	zp8604.s1 Stratagene HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:827055 3' similar to
9950	22768	36240	0.96	3.8E+00	AL161553.2	NT	contains Alu repetitive element:contains element MSR1 repetitive element ;
1514	14546	27517	5.3	3.4E+00	AF254677.1	NT	contains Alu repetitive element:contains element MSR1 repetitive element ;
6993	19945	33241	0.49	3.4E+00	U77617.1	NT	<i>Arabidopsis thaliana</i> DNA chromosome 4, contig fragment No. 53
7588	20347	33907	2.89	3.4E+00	P04052	SWISSPROT	<i>Brassica napus</i> RP85d mRNA, complete cds
7688	20907	34288	0.9	3.4E+00	P04052	SWISSPROT	Chloramphenicol transferase (chloramphenicol acetyltransferase) (CAT) complete cds
9025	21991		0.68	3.4E+00	U65406.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9428	22392	35831	0.73	3.4E+00	AJ220042.1	NT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
9467	22431	35989	0.95	3.4E+00	AJ250567.1	NT	Human alternatively spliced potassium channel ROMK1, ROMK2, ROMK3, ROMK4, ROMK6, and ROMK6 (KCNJ1) gene, complete cds
10627	23549	37049	2.59	3.4E+00	AF013187.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 23
						NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
						NT	<i>Stechanomys cerevisiae</i> MSST1 gene, complete cds



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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10700	23622	37118	5.2	3.1E+00	P49385	SWISSPROT	DEOXYHYDROLYSINE SYNTHASE (DHS)
11791	23948		1.96	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)
11811	24698		2.76	3.1E+00	S56680.1	NT	retinoid acid nuclear receptor isoform beta 2 [homo, embryonal carcinoma cell line, PCOT-MZ1, mRNA, 2871 nt]
2848	13509	28433	1.5	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PR00898 (PRO0898), mRNA
5411	18514	31392	1.33	3.0E+00	X53056.1	NT	S. aureus genes encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6708	19764	33043	0.79	3.0E+00	X60037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6708	19764	33044	0.79	3.0E+00	X60037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7363	20333		9.66	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7402	20370		0.59	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8258	22224		1.21	3.0E+00	X57838.1	NT	B. reus DNA for mycelinase
10657	23579	37078	0.54	3.0E+00	Q58905	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11008	23973	37497	1.65	3.0E+00	Q16181	SWISSPROT	ODC10 PROTEIN HOMOLOG
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
11351	24301	37827	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
11351	24301	37828	4.64	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE 2) (GC-F)
2028	13048	28059	2.33	2.9E+00	A5002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of the complete genome
6192	19256		0.6	2.9E+00	AB078033.1	NT	Chlamydomonas reinhardtii AR39, section 53 of the complete genome
7084	20028	33332	1.97	2.9E+00	Z36979.1	NT	F. fragilis gdcA gene for P-protein of the glycine cleavage system
7418	20385	33734	5.15	2.8E+00	Q14614	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7418	20385	33735	5.15	2.9E+00	Q14614	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7699	20647	34011	5.32	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8200	21170	34580	0.61	2.9E+00	PC5844	SWISSPROT	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2, NONSTRUCTURAL PROTEIN VP4, MINOR STRUCTURAL PROTEIN VP3)
8200	21170	34581	0.61	2.9E+00	PC5844	SWISSPROT	STRUCTURAL POLYPROTEIN (CONTAINS: MAJOR STRUCTURAL PROTEIN VP2, NONSTRUCTURAL PROTEIN VP4, MINOR STRUCTURAL PROTEIN VP3)
8434	27403	34816	0.82	2.9E+00	BF344171.1	EST_HUMAN	NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3
1461	14484	27460	4.16	2.8E+00	AF186398.1	NT	602017413F1 NC1_CGAP_Bra64 Homo sapiens cDNA clone IMAGE4153069 F'
							Blood human matrikase K (matK) gene, partial cds; chloroplast gene for chloroplast product

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1637	14659		2.57	2.8E+00	AL161652.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7529	20492	33854	4.93	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9972	22699		0.56	2.8E+00	BE695182.1	EST_HUMAN	601342758F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3684807.5
11048	20492	33854	1.73	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
233	13333	26256	13.36	2.7E+00	6679308	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
233	13333	26257	13.36	2.7E+00	6679308	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5631	18727	31868	1.11	2.7E+00	L14005.1	NT	Homo sapiens apoa polymorphism Kringle IV gene, exons 1 and 2
8485	21453		0.68	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9319	22284		1.69	2.7E+00	AL116459.1	NT	Bacillus cereus strain T4 cDNA library under conditions of nitrogen deprivation
9787	21110	34510	0.64	2.7E+00	AW088191.1	EST_HUMAN	xc89t12.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374.3 similar to gbM17733
10566	23786		1.56	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4701	17722	30815	0.29	2.6E+00	AF068749.1	NT	GM0-BT0281-031196-087-004 BT0281 Homo sapiens cDNA
6627	18723	31883	2.06	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
6627	18723	31884	2.06	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5925	19011		3.6	2.6E+00	Y17052.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7603	26002		0.7	2.6E+00	AJ224559.1	NT	Mycobacterium fortuitum furA II gene
							Homo sapiens Surf-5 and Surf-6 genes
7997	20806		32.15	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (SHIP) gene, exons 10 through 27, and complete cds
8394	21363	34770	1.12	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
8394	21363	34771	1.12	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10015	22842	36408	3.12	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10720	23542		2.61	2.6E+00	8055183	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12841	25977		1.58	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1460	14493	27466	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1460	14493	27467	3.73	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5911	18997	32186	2.32	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5911	18997	32187	2.32	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6901	18997	32186	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6901	18997	32187	1.49	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6982	19844	33240	0.66	2.5E+00	D30052.1	NT	Vibrio cholerae cna gene and cnaB gene for cholera toxins, complete cds
7960	20901	34293	0.55	2.5E+00	P17898	SWISSPROT	LATENCY-RELATED PROTEIN 1
8035	20972	34366	0.67	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-295-g07 FT0005 Homo sapiens cDNA
8095	21031	34426	0.51	2.5E+00	4602602	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9459	22423	35861	1.48	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10211	23136	36623	0.73	2.4E+00	BE297758.1	EST_HUMAN	801175797F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
12214	28053	29008	2.9	2.5E+00	AF298685.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3026	16083	28008	1.1	2.4E+00	IM24292.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' and
4944	17960	30851	5.31	2.4E+00	4603352	NT	Homo sapiens double C2-like domains, alpha (DCC2A) mRNA
6126	18204	32427	3.62	2.4E+00	P02843	SWISSPROT	VITELLOGENIN PRECURSOR (YOLK PROTEIN 1)
7608	20567	33227	0.71	2.4E+00	BF667502.1	EST_HUMAN	802120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
7609	20567	33928	0.71	2.4E+00	BF667602.1	EST_HUMAN	802120856F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278012 5'
8479	21448	34894	2.09	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8479	21448	34895	2.08	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8554	21522		2.82	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8988	21984		1.48	2.4E+00	AY875128.1	EST_HUMAN	RC2-PT0004-031268-011-405 PT0004 Homo sapiens cDNA
6180	22148	35573	9.52	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHNB)
10398	23320	36803	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10398	23320	36804	2.34	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10466	23388	36882	2.1	2.4E+00	X62511.1	NT	H.sapiens CTGF gene and promoter, region
10604	23528		6.1	2.4E+00	P06090	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10685	23607	37100	1.87	2.4E+00	BE326702.1	EST_HUMAN	hr63066.xt.NCI_CGAP_Kir11 Homo sapiens cDNA clone IMAGE:3133187 3'
10685	23607	37101	1.87	2.4E+00	BE326702.1	EST_HUMAN	hr63066.xt.NCI_CGAP_Kir11 Homo sapiens cDNA clone IMAGE:3133187 3'
10955	23875	37389	1.14	2.4E+00	Q51481	SWISSPROT	IDENTIFICATION REGULATORY PROTEIN NIRQ
11415	24359	37884	2.2	2.4E+00	Y14078.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFDK operon and downstream
11617	24458		1.66	2.4E+00	AF06872.1	NT	Capra hircus alphaS2-casein type G gene, intron 15
11686	24652	38231	2.14	2.4E+00	AF168652.2	NT	Fraxinus x arnassana cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1258	14293	27257	11.33	2.3E+00	Z46724.1	NT	G domesticus artificial single chain antibody gene (L3)
4147	17176		1.46	2.3E+00	A1401081.1	NT	Bos taurus partial cyto gene for cytochrome b
8934	19020		0.99	2.3E+00	N86245.1	EST_HUMAN	PROLYL-CARBOXYPEPTIDASE
7687	20645	34009	2.42	2.3E+00	0978554	NT	Rattus norvegicus ATPase, Cat++ transporting, ubiquitous (Atp2a3) mRNA
7853	20003		2.70	2.3E+00	P07169	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
8059	20906	34392	1.12	2.3E+00	X60265.1	NT	M.musci dnaf and dnaf genes homologs coding for DnaK and DnaJ
9465	22429	35888	0.54	2.3E+00	5833517	NT	Polydora ornithinis mitochondrion, complete genome
9525	22488	35936	2.03	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10958	23878	37390	0.45	2.3E+00	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
11153	24113	37638	7.84	2.3E+00	Q07076	SWISSPROT	ANNEXIN VII (SYNEXIN)
11887	24778	38304	1.99	2.3E+00	P45981	SWISSPROT	HYPOTHETICAL 171.0 KD PROTEIN IN SPOLIC-CWLA INTERGENIC REGION
12072	24945	38539	2.34	2.3E+00	BF541987.1	EST_HUMAN	G02089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12072	24945	38540	2.34	2.3E+00	BF541987.1	EST_HUMAN	G02089121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12443	25205	31828	6.31	2.3E+00	BE895237.1	EST_HUMAN	G01433678F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
13077	25609		1.3	2.3E+00	AF281882.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4048	17084	29981	1.42	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4342	17369	30251	3.8	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4342	17369	30252	3.8	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5415	18518	31395	11.02	2.2E+00	O98307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) <>
5415	18518	31398	11.02	2.2E+00	O98307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) <>
5953	19038	32234	1.83	2.2E+00	BE827220.1	EST_HUMAN	RC3-CT0264-300800-022-068 CT0264 Homo sapiens cDNA
5953	19038	32235	1.83	2.2E+00	BE827220.1	EST_HUMAN	RC3-CT0264-300800-022-068 CT0264 Homo sapiens cDNA
6180	19255	32488	8.78	2.2E+00	BE250383.1	EST_HUMAN	G00943407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6469	19594	32804	3.91	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6750	19804	33085	3.14	2.2E+00	P61459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SONATOMEDIN A)
7149	19381		3.5	2.2E+00	AA594574.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SONATOMEDIN A)
7539	20502	33851	0.95	2.2E+00	AA137027.1	EST_HUMAN	z06704.r1 Stralagene fetal retina B37202 Homo sapiens cDNA clone IMAGE:108379 3'
7665	20809	34187	18.24	2.2E+00	AA449012.1	EST_HUMAN	z06510.r1 Soares, fetal, N252Hf8_5w Homo sapiens cDNA clone IMAGE:566143 5'
7953	20894	34287	0.96	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8439	21408	34620	0.69	2.2E+00	BE301590.1	EST_HUMAN	b617H12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
8439	21408	34621	0.69	2.2E+00	BE301590.1	EST_HUMAN	b617H12x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2863207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting complex component of (MOUSE);
9897	22650		11.22	2.2E+00	BE741678.1	EST_HUMAN	G01594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948661 5'
9827	25698		2.53	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A

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## Single Exon Probes Expressed in Bone Marrow

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	23335	36816	1.57	2.2E+00	A1200373.1	EST_HUMAN	qmg9003.x1 Soares_pleocenta_8tcdweeks_2N6HP8t09W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10413	23335	36820	1.57	2.2E+00	A1200373.1	EST_HUMAN	qmg9003.x1 Soares_pleocenta_8tcdweeks_2N6HP8t09W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10456	23378	36871	2.22	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10822	23743	37244	3.06	2.2E+00	AF183416.1	NT	160785591FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075591 5'
11768	23923	37442	3.32	2.2E+00	P07911	SWISSPROT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11837	24818	38415	8.31	2.2E+00	P10407	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) [THP]
571	15844	29555	12.39	2.1E+00	AF132612.2	NT	EARLY E1A 28 KD PROTEIN
3601	16946		0.83	2.1E+00	AW449388.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
6255	19328		0.86	2.1E+00	P76357	SWISSPROT	U1-HBIS-ald-e08-QULS1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6860	20203	33532	3.45	2.1E+00	O70159	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
7225	20247	33581	0.61	2.1E+00	4503430	NT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7246	19981	33278	5.97	2.1E+00	N28575.1	EST_HUMAN	Homo sapiens dystrophin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, end translated products
8942	21809	27197	1.82	2.1E+00	AU123630.1	EST_HUMAN	y06a10.x1 Soares_melanocyte_2N6HM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIIID (HUMAN);
1201	14240	27198	1.39	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000971 5'
1201	14240	27198	1.39	2.0E+00	AF180527.1	NT	Homo sapiens p22Dcdcl (DOKDEL) mRNA, complete cds
1338	14372	27342	1.19	2.0E+00	AF204927.1	NT	Homo sapiens p22Dcdcl (DOKDEL) mRNA, complete cds
1578	14611		3.42	2.0E+00	P25592	SWISSPROT	Oryctolagus cuniculus Na <sup>+</sup> /K <sup>+</sup> -ATPase beta 1 subunit mRNA, complete cds
2159	15175	28195	4.88	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SP81
2159	15175	28195	4.88	2.0E+00	Z78279.1	NT	R norvegicus mRNA for collagen alpha1 type 1
4127	17160	30048	2.24	2.0E+00	AW694495.1	EST_HUMAN	R norvegicus mRNA for collagen alpha1 type 1
4127	17160	30049	2.24	2.0E+00	AW694495.1	EST_HUMAN	h13a05.x1 NCI CGAP GUT Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7798	20750		0.85	2.0E+00	P07599	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8358	21327	34739	3.84	2.0E+00	AB030876.1	NT	STRUCTURAL POLYPEPTIDE CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2
8358	21327	34739	3.84	2.0E+00	AB030876.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8358	21327	34740	3.84	2.0E+00	AB030876.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9274	22240	35668	3.22	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12756	25838	31427	4.52	2.0E+00	5834843	NT	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4823	17846	30746	0.98	1.9E+00	AF209408.1	NT	Danio rerio Rho50-like protein mRNA, complete cds
5679	18174	31648	4.52	1.9E+00	6754389	NT	Mus musculus Irf1l1 1,4,5-triphosphate receptor 1 (Irf1l1), mRNA
5878	18174	31848	4.52	1.9E+00	6754389	NT	Mus musculus Irf1l1 1,4,5-triphosphate receptor 1 (Irf1l1), mRNA
6219	19283	32827	1.05	1.9E+00	BE960695.1	EST_HUMAN	601879639F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6810	19884		1.78	1.9E+00	AW845899.1	EST_HUMAN	MRO-CT0063-07109-02-g02 CT0063 Homo sapiens cDNA
6912	19884		2.37	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8802	21769	35193	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8802	21769	35194	1.72	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9006	21872		3.8	1.9E+00	BF360206.1	EST_HUMAN	CW3-MT0114-010900-323-H12 MT0114 Homo sapiens cDNA
9245	22211		1.52	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9888	22915	35380	0.53	1.9E+00	AA669125.1	EST_HUMAN	ab9404.s1 Stratigene lung (4637210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element/contains element L1.1 repetitive element ;
10929	23849	37364	0.63	1.9E+00	AF242289.1	NT	Homo sapiens gep-proc-pol precursor protein gene, partial cds
3109	16166	28077	1.5	1.9E+00	P21004	SWISSPROT	PROTEIN BB PRECURSOR
3137	16194	28103	10.81	1.9E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3137	16194	28104	10.81	1.9E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5997	19052		1.84	1.9E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6224	19298	32532	2.2	1.9E+00	BF311869.1	EST_HUMAN	601887854F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4127364 5'
6538	19500		1.19	1.9E+00	BF883327.1	EST_HUMAN	602159470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6904	19958	33255	1.02	1.9E+00	BF305682.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7260	19995	33292	1.07	1.9E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7476	20442		0.7	1.9E+00	P27127	SWISSPROT	LIPOLYSACCHARIDE 1,6-GALACTOSE-4-GLUCOSE-6-POLYPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE (GLUCOSYL POLYPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8454	21423	34838	0.9	1.9E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8454	21423	34839	0.9	1.9E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8812	21779	35204	0.46	1.9E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35205	0.46	1.9E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8812	21779	35206	0.46	1.9E+00	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9206	22172	35803	2.21	1.9E+00	O43281	SWISSPROT	EMBRYONAL FN-ASSOCIATED SUBSTRATE (HEFS)
9530	22463	35941	0.66	1.9E+00	R31042.1	EST_HUMAN	h712c08.t1 Scars placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9617	22561	39009	0.64	1.8E+00	AW880004.1	EST_HUMAN	QVQ-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
10208	23133	39620	0.93	1.8E+00	P227050	SWISSPROT	CHITINASE D PRECURSOR
10648	23568		2.88	1.8E+00	AF111849.1	NT	Homo sapiens PRO0630 mRNA, complete cds
10919	23839		0.76	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12563	25808		8.17	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12642	25928		5.93	1.8E+00	9606404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpctb) mRNA
1110	14164	27104	2.43	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2270	15292	28317	3.08	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2382	15390	28415	1.97	1.7E+00	A1141087.1	EST_HUMAN	oz3105.XT Soares_NIHMP2_S1 Homo sapiens cDNA clone IMAGE:1678137.3
4487	17512	30400	0.9	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5694	18769	31980	1.68	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171298-127-a05 BT0282 Homo sapiens cDNA
5694	18789	31960	1.98	1.7E+00	BE063546.1	EST_HUMAN	CMO-BT0282-171298-127-a05 B10282 Homo sapiens cDNA
5955	19040	32238	0.49	1.7E+00	R56748.1	EST_HUMAN	G4846 Fetal heart Homo sapiens cDNA clone G4846.5' end
6133	19210	32468	3.14	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6703	19759	33038	0.59	1.7E+00	P36816	SWISSPROT	PYRUVATE DEHYDROGENASE (LPOAMIDE)PHOSPHATASE, MITOCHONDRIAL PRECURSOR
7428	20395	33746	1.01	1.7E+00	Q03703	SWISSPROT	(POP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)
7428	20395	33747	1.01	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8187	21157	34666	0.81	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8387	21836	34748	1.21	1.7E+00	6755716	NT	Mus musculus T cell acute lymphocytic leukemia 1 (Tat1) mRNA
8397	21966	34775	0.64	1.7E+00	BF630630.1	EST_HUMAN	80201977F1 NCL CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214669.5'
8897	21853	35273	0.45	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus Interferon inducible Mx protein (MX) mRNA, complete cds
8974	21640		1.92	1.7E+00	BF308000.1	EST_HUMAN	801894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084.5'
9032	22018	35442	0.51	1.7E+00	X69083.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9032	22018	35443	0.51	1.7E+00	X69083.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9166	22132	35558	0.43	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9504	25697	35909	2.37	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9604	25697	35910	2.37	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9695	22892		1.4	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10532	23454		0.5	1.7E+00	AW953681.1	EST_HUMAN	EST366751 IMAGE reassurances, MAGC Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12518	25249	31803	1.78	1.7E+00	AI878443.1	EST_HUMAN	tu82d07.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
2049	15068	28088	14.89	1.5E+00	AF198339.1	NT	MSR1, repetitive element;
2059	15078	28097	3.29	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2055	15083	28102	1.62	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2292	15304		1.33	1.6E+00	X58373.1	NT	Mus musculus ST6GaiNAcIII gene, exon 2
			1.33	1.6E+00	X58373.1	NT	B-napus gene encoding endo-polygalacturonase
2972	16030	28953	1.88	1.6E+00	W58426.1	EST_HUMAN	cd25f01.1 Soares, fetal, heart, NIH/19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
4063	17069		7.07	1.6E+00	BF570077.1	EST_HUMAN	40228805 N-Acetylglucosamine SYNTHASE (HUMAN);
4379	17407	30287	1.29	1.6E+00	AF155927.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SNARCA8) mRNA, complete cds
4379	17407	30288	1.29	1.6E+00	AF155927.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SNARCA8) mRNA, complete cds
5120	18130	31008	2.98	1.6E+00	Y11344.1	NT	Mus musculus ST6GaiNAcIII gene, exon 2
5120	18130	31007	2.98	1.6E+00	Y11344.1	NT	Mus musculus ST6GaiNAcIII gene, exon 2
5926	19012	32204	2.21	1.6E+00	LQ4903.1	NT	Brachydanio rerio HFC class II DA-beta-2'01 gene, 3' and
6020	19103	32305	0.82	1.6E+00	AF005931.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
6614	19872	32850	0.83	1.6E+00	BF390703.1	EST_HUMAN	LI2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6888	19921	33217	0.97	1.6E+00	AW224881.1	EST_HUMAN	LI-HB12-ahr-5-04-QJ.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7456	20422	33777	2.47	1.6E+00	BE97287.1	EST_HUMAN	RCB-CT0415-200700-032-ct0 C10415 Homo sapiens cDNA
8354	21333		1.1	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MYN1 HOMOLOG
8722	21690	35117	3.42	1.6E+00	AL297131.1	NT	Mus musculus SLL_MAP_17_CYP_a_SQL & CYP_b genes
9251	22217	35647	0.9	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PR00971 (PRO0971), mRNA
9251	22217	35648	0.9	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PR00971 (PRO0971), mRNA
9815	25695	34540	1.54	1.6E+00	X52046.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
9815	25695	34541	1.54	1.6E+00	X52046.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
9945	22872		0.48	1.6E+00	AF043465.1	NT	Thermotogaarabacter ethanolicus D-xylase-binding protein (xyfP) gene, complete cds
10091	23017	35493	1.23	1.6E+00	T41280.1	EST_HUMAN	phB55_19/11TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone phB55_19/11TV
			0.48	1.6E+00	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IaL), and
10546	23428	36925	0.48	1.6E+00	AF121381.1	NT	zinc finger protein (DNZ1) genes, complete cds
10546	23467	36961	1.12	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-080200-100-007 LT0016 Homo sapiens cDNA
10545	23467	36962	1.12	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-080200-100-007 LT0016 Homo sapiens cDNA
10709	23931	37126	0.78	1.6E+00	AF037352.1	NT	Mus musculus 1 cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
11123	24083	37609	1.73	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE), CAPSID ASSEMBLY PROTEIN]
11192	19103	32305	6.78	1.6E+00	AF005931.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
12017	24894	38491	2.83	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
35	13155	26056	3.54	1.5E+00	U93449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
234	13334	26258	2.63	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AFR39, section 32 of 84 of the complete genome
622	13687		2.04	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metageldin) (Adam15), mRNA
2420	15427	28450	3.2	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2521	15525	28547	2.17	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3155	15427	28450	2.96	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3386	16435	29362	0.92	1.5E+00	AE001845.1	NT	Dermococcus radiodurans R1, section 82 of 229 of the complete chromosome 1
5817	18907	32090	0.82	1.5E+00	AI065301.1	EST_HUMAN	h1210.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.1
5817	18907	32091	0.82	1.5E+00	AI065301.1	EST_HUMAN	h1210.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 000237 HKF-1.1
6546	19607	32859	2.71	1.5E+00	RI17879.1	EST_HUMAN	y9 (00271) Soare infant brain INIB Homo sapiens cDNA clone IMAGE:31693 5'
7335	20306		1.48	1.5E+00	BE785356.1	EST_HUMAN	601478748FT NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3381555 5'
7368	20338	33688	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL T18.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7368	20338	33689	16.72	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL T18.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR
7568	20531	33990	0.6	1.5E+00	AA880259.1	EST_HUMAN	ak2610.s1 Soare, testis, NIH Homo sapiens cDNA clone IMAGE:1407115 3'
7850	20796	34172	0.73	1.5E+00	AI003254.1	EST_HUMAN	ai07011.s1 Stragene echizo brain S11 Homo sapiens cDNA clone IMAGE:1884893 3' similar to gb:556838 SERO TRANSFERRIN PRECURSOR (HUMAN); Homo sapiens WDR4 gene for WD repeat protein, complete cds
8459	21428	34845	0.81	1.5E+00	BE887446.1	EST_HUMAN	601503585FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8514	21482	34996	0.48	1.5E+00	AB040587.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8991	21957	35382	1.08	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9370	22335		0.47	1.5E+00	AB038516.1	NT	Homo sapiens IGFBP alpha gene for platelet glycoprotein IIb/IIIa, complete cds
9489	22453	35693	0.55	1.5E+00	BF217818.1	EST_HUMAN	601482652FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9838	22714	36229	0.91	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soare placenta N2b2HP Homo sapiens cDNA clone IMAGE:147697 5'
9983	22920	36387	1.08	1.5E+00	AW375697.1	EST_HUMAN	CV3-GT0192.281088-008-009 GT0192 Homo sapiens cDNA
10218	23144	36833	1.42	1.5E+00	BF376764.1	EST_HUMAN	RCD-TN0078-15900-034-g05 TN0078 Homo sapiens cDNA
10412	23334		1.42	1.5E+00	BF337844.1	EST_HUMAN	602035771FT NCI_CGAP_Brrd4 Homo sapiens cDNA clone IMAGE:4183655 5'
10556	23478	36972	2.92	1.5E+00	AA017698.1	EST_HUMAN	z63806.r1 Soare retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10556	23478	36973	2.92	1.5E+00	AA017698.1	EST_HUMAN	z63806.r1 Soare retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11727	24613	38190	5.98	1.5E+00	AI134197.1	EST_HUMAN	DKFZ47P243.s1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ47P243 3'
11859	24751		6.39	1.5E+00	X07380.1	NT	Mazze mitochondrial RNA-Ser gene and RNA-Phe pseudogene
12112	24882		1.63	1.5E+00	BE257652.1	EST_HUMAN	601106921FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3350477 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12362	25151		1.87	1.6E+00	8753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
12510	25599	31420	1.61	1.6E+00	D89480.1	NT	Human mRNA for KIAA0148 gene, partial cds
12723	25376		4.94	1.8E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
12821	25443		1.33	1.9E+00	6978492	NT	Rattus norvegicus 5'-Lipoxygenase (ALOX5), mRNA
32	13152	26052	1.41	1.4E+00	7661685	NT	Homo sapiens DKFZP566M0122 protein (DKFZP566M0122), mRNA
32	13152	26053	1.41	1.4E+00	7661685	NT	Homo sapiens DKFZP566M0122 protein (DKFZP566M0122), mRNA
2285	15298		0.9	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2341	15551		8.77	1.4E+00	U67922.1	NT	Osteo arles prion protein gene, complete cds
2677	15673	26693	1.83	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2784	15776	28794	2.75	1.4E+00	AF064554.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2784	15776	28794	2.75	1.4E+00	AF064554.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3345	16306		0.63	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4284	17313	30181	1.38	1.4E+00	AW600455.1	EST_HUMAN	CNC-NN1005-140300-286-R08 NN1005 Homo sapiens cDNA
4284	17313	30182	1.38	1.4E+00	AW600455.1	EST_HUMAN	CNC-NN1005-140300-286-R08 NN1005 Homo sapiens cDNA
4580	16144	28056	0.82	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 65 of the complete genome
4590	16144	28057	0.82	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 65 of the complete genome
4615	17636		1.71	1.4E+00	BF881547.1	EST_HUMAN	802195687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE4297556 5'
5446	18548	31461	1.58	1.4E+00	AW054976.1	EST_HUMAN	w45907.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE21510460 3'
5608	18702		5.52	1.4E+00	AB032683.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6410	19478	32725	3.08	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6427	26996		4.2	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6552	18613	32875	2.85	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6552	18613	32876	2.85	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6781	19836	33119	0.56	1.4E+00	BE007870.1	EST_HUMAN	CNC-NN1005-215-b11 BN0148 Homo sapiens cDNA
6781	19836	33120	0.56	1.4E+00	BE007870.1	EST_HUMAN	CNC-NN1005-215-b11 BN0148 Homo sapiens cDNA
6996	20122	33439	0.86	1.4E+00	AW863057.1	EST_HUMAN	CNC-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA
7503	20468	33929	2.02	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, DT5822, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7521	20488	33848	1.15	1.4E+00	AW467780.1	EST_HUMAN	h23105.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE2818873 3' similar to contains Alu repetitive element
7592	20544	33904	0.58	1.4E+00	P65288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7592	20544	33905	0.58	1.4E+00	P65288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7811	20571	33635	0.65	1.4E+00	Q80905	SWISSPROT	MINOR CAPSID PROTEIN L2
8078	21648		0.6	1.4E+00	P07883	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE)(1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9146	22112		4.8	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudocytosine region, segment 1/2
9449	22413	35849	1.56	1.4E+00	R20489.1	EST_HUMAN	Y33712.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:34345 5'
9552	22514	35955	3.48	1.4E+00	BE064687.1	EST_HUMAN	RC1-BT0313-301295-012-103 BT0313 Homo sapiens cDNA
9587	22549	36000	0.45	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10568	23400	36982	0.89	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288137 5'
10613	23535	37033	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291059-008-C04 HT0198 Homo sapiens cDNA
10613	23535	37033	0.69	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291059-008-C04 HT0198 Homo sapiens cDNA
10802	23812	37320	0.92	1.4E+00	D63441.1	NT	Pandorina coelestis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10882	23812	37320	0.92	1.4E+00	D63441.1	NT	Pandorina coelestis chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
11059	24489	38055	4.43	1.4E+00	AB006882.1	NT	Homo sapiens APECE2 mRNA for AIRE-1, complete cds
11733	24619	38196	2.83	1.4E+00	BE982107.2	EST_HUMAN	601655184RT NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3845805 3'
11733	24619	38197	2.83	1.4E+00	BE982107.2	EST_HUMAN	601655184RT NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3845805 3'
11756	24684	38263	2.16	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. retri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11756	24684	38263	2.16	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. retri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11798	24894	38284	2.15	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. retri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12360	25927		1.7	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
13068	26002		1.4	1.4E+00	7557624	NT	Homo sapiens staufen (Drosophila, RNA-binding protein) homolog 2 (STAU2), mRNA
572	13841		1.56	1.3E+00	Z75640.1	NT	M. musculus gene encoding 4-dihydroxyethyl-lysine dehydrogenase
903	13958	26915	3.12	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
131	14174		32.4	1.3E+00	Y19213.1	NT	Homo sapiens putative tsfHBA pseudogene for hair keratin, exons 2 to 7
1300	14339	27239	19.22	1.3E+00	4507698	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1300	14339	27239	19.22	1.3E+00	4507698	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1358	14393		0.89	1.3E+00	U61730.2	NT	Cox1 leucine-rich dihydrodipicolinate synthase (dapA) gene, complete cds
1814	14846		2.59	1.3E+00	AE002398.2	NT	Chlamydia muridarum, section 65 of 85 of the complete genome
2255	15269		1.22	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASP genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2415	15422	28445	1.03	1.3E+00	P26391	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2557	15559		2.6	1.3E+00	BE968735.2	EST_HUMAN	601661233RT NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3916945 3'
2950	16007	28831	0.67	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythrocyte (Sptn1), mRNA

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Table 4

### Single Exon Probes Expressed in Bone Marrow

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10286	23211		0.64	1.3E+00	AI659944.1	EST_HUMAN	tg77at12.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:U4723
10509	23431	36827	0.45	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10509	23431	36928	0.45	1.3E+00	AF061251.1	NT	Escherichia coli aerolysin O157:H7 O antigen gene cluster
10594	23431	36989	1.53	1.3E+00	AE004392.1	NT	Escherichia coli aerolysin O157:H7 O antigen gene cluster
10594	23431	37008	1.53	1.3E+00	M29593.1	NT	Vibrio cholerae chromosome 11, section 49 of 93 of the complete chromosome
10594	23431	37008	1.53	1.3E+00	M29593.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10948	23669		0.85	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10975	23895	37409	0.49	1.3E+00	AI990946.1	EST_HUMAN	wc22410.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
10987	23907		0.43	1.3E+00	8922637	NT	Q19881 THIOREDOXIN REDUCTASE ;
11052	24015		3.83	1.3E+00	O14117	SWISSPROT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
11252	24203	37727	2.35	1.3E+00	P25299	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11273	24225	37751	1.71	1.3E+00	Z18692.2	NT	MRNA 3'-END PROCESSING PROTEIN RNA15
11867	24749	38331	2.61	1.3E+00	D42042.1	NT	Mus musculus desmin gene
11845	24825	38420	2.1	1.3E+00	Z98982.1	NT	Human mRNA for KIAA0085 gene, partial cds
12001	24878		1.45	1.3E+00	I31891.1	NT	Bacillus subtilis glutamic acid decarboxylase (CD) gene, complete cds
12498	25239		3.37	1.3E+00	AF187873.1	NT	Arabidopsis thaliana 3-kelocaly-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12869	25344	31762	6.47	1.3E+00	BF346043.1	EST_HUMAN	Caixa porcellus twardy-rectifying potassium channel Kir2.2 (KCNJ2) gene, complete cds
12879	25724		3.24	1.3E+00	P33464	SWISSPROT	6020231 65FT NCL CGAP_Bin87 Homo sapiens cDNA clone IMAGE:2158452 5'
12765	25407		1.83	1.3E+00	AF187035.1	NT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
651	13717	26639	13.29	1.2E+00	AA576248.1	EST_HUMAN	Sturria illium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
824	13882	26833	1.37	1.2E+00	P05228	SWISSPROT	2322408.st Scores: fetal liver, spleen, 1NFLS S1 Homo sapiens cDNA clone IMAGE:431535 3'
824	13882	26834	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
824	13882	26834	1.37	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
879	13934		0.95	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRQ3077 (PRQ3077), mRNA
1166	14206	27160	7.4	1.2E+00	AF080245.2	NT	Elaia oleifera sesquiterpene synthase mRNA, complete cds
1210	14248	27206	1.43	1.2E+00	AJ262242.1	NT	Pea seed-borne mosaic virus complete genome
1210	14248	27207	1.43	1.2E+00	AJ262242.1	NT	Pea seed-borne mosaic virus complete genome
2025	15045	28058	1.05	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3127	16184	28093	0.99	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3178	16234	28151	6.14	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3178	16234	28152	6.14	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3259	16352		3.07	1.2E+00	P64910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3337	16417	28343	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3725	16787	29678	8.46	1.2E+00	U76902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4012	17051	29957	1.76	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4327	16417	29343	1.09	1.2E+00	AF185740.1	NT	Homo sapiens LHX3 gene, intron 2
4498	17523		2.12	1.2E+00	M87060.1	NT	Rattus reticulatus cardiac AEs gene, exons 1-23
4551	17574	30484	1.33	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 21
4592	17613	30507	2.1	1.2E+00	AF156495.1	NT	Homo sapiens postsynaptic density 95 (DLG4) gene, complete cds
4619	17640		5.6	1.2E+00	X95200.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5052	18064	30942	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30943	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5052	18064	30944	2.36	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
5512	18512	31544	1.06	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5534	18730	31892	1.88	1.2E+00	AF1813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5934	18982		0.57	1.2E+00	X81879.1	NT	Calcitonin cDNA for cfr1, cfr2 and cfr3
5974	19059	32280	0.78	1.2E+00	AF010052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6276	19348	32580	2.39	1.2E+00	X74885.1	NT	D/hyd1 av1 repeat cluster DNA, fragment D
6338	19407	32648	4.12	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0085-270400-190-ac03 BN0080 Homo sapiens cDNA
6423	19490	32741	1.41	1.2E+00	X85084.1	NT	C glutamylum pla gene and ackA gene
6423	19490	32742	1.41	1.2E+00	X85084.1	NT	C glutamylum pla gene and ackA gene
6467	19532	32780	38.6	1.2E+00	AA759254.1	EST_HUMAN	shd412.21 Soares, "beta1_NHT" Homo sapiens cDNA clone 1322374.3'
6575	19935	32901	0.6	1.2E+00	N33265.1	EST_HUMAN	y939612.1t Soares melanocyte ZNF11M Homo sapiens cDNA clone IMAGE:273589.3' similar to
6950	19708	32984	0.71	1.2E+00	PI17671	SWISSPROT	gblm76515 HUMANALL472 Human carcinoma cell-derived AU RNA transcript, (RNA); gb.J04970
6954	19711	32988	2.01	1.2E+00	AF1813276.1	EST_HUMAN	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
7100	20034	33337	1.17	1.2E+00	AB026010.1	NT	ECODYSONE-INDUCIBLE PROTEIN E75-A
7113	20047	33346	2.98	1.2E+00	AI002141.1	NT	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7485	20431		0.64	1.2E+00	AI271735.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7810	20585	33934	1.64	1.2E+00	AF1734585.1	EST_HUMAN	Mus musculus DSSP gene
7912	20555	34243	2.6	1.2E+00	X74207.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8122	21059	34457	0.53	1.2E+00	BE787646.1	EST_HUMAN	AY734585 cDNA Homo sapiens cDNA clone cDNA:EH03.5'
8915	21881	35307	3.24	1.2E+00	AB033030.1	NT	Lactis pyD and pyF genes
							601481761F NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3894270.5'
							Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE [UDP-FORMING] 123 KD SUBUNIT
							(TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
							GLUCOSYLTRANSFERASE)
9010	21978		0.65	1.2E+00	P38427	SWISSPROT	

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9228	22194		0.58	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
9360	22345	35777	1.68	1.2E+00	AW377210.1	EST_HUMAN	MR2-C10222-201095-001-e07 C10222 Homo sapiens cDNA
9594	22568	36008	0.47	1.2E+00	H43599.1	EST_HUMAN	X58060.1 Scarsa fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202065 5'
9753	22893	36150	3.63	1.2E+00	Z32950.1	NT	R community gene for pyrophosphate-dependent phosphofructokinase beta subunit
9834	22891	39353	1.71	1.2E+00	D11746.1	EST_HUMAN	HUHM010401 Liver HepG2 cell line. Homo sapiens cDNA clone hmo1601
10291	23216	39700	3.62	1.2E+00	X69832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10889	23811		0.73	1.2E+00	AB009669.1	NT	Homo sapiens Klf10 gene, exon 1
11674	24676	38219	1.89	1.2E+00	AW617817.1	EST_HUMAN	PMA-ST0284-161199-001-401 ST0284 Homo sapiens cDNA
11713	24676		7.68	1.2E+00	BE160791.1	EST_HUMAN	PMT-H10422-160200-007-g10 H10422 Homo sapiens cDNA
11785	23940	37462	2.59	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12466	25799	31524	18.09	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12487	25232		2.7	1.2E+00	AP001651.1	NT	Bacillus halodurans genomic DNA, section 9/14
464	13537	26463	1.43	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1777	14806	27792	1.97	1.1E+00	AW695393.1	EST_HUMAN	QVD-BN0042-170360-163-g12 BN0042 Homo sapiens cDNA
1915	14839	27635	1.08	1.1E+00	AW675689.1	EST_HUMAN	UI-HF-BR0P-alk-F-02-UJ-51 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3341	16392	26313	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3341	16392	26314	7.34	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3498	16545	28471	0.78	1.1E+00	862284.1	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3593	16638	26568	3.94	1.1E+00	AB08360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW-P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3731	16773	26584	1.62	1.1E+00	AE003868.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3731	16773	26585	1.52	1.1E+00	AE003868.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3831	16871		0.86	1.1E+00	X85374.1	NT	H. parahaemolyticus hph104A, hph104C, hph104R and menB genes
3904	17004	26318	0.87	1.1E+00	892284.1	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4050	17087	26983	1.02	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4243	17272		6.76	1.1E+00	583533.1	NT	R. unicornis complete mitochondrial genome
5028	18042	30925	3.15	1.1E+00	U18468.1	NT	African swine fever virus, complete genome
5085	18095	30971	3.91	1.1E+00	U34740.1	NT	Emertella nidulans sterigmatocystin biosynthetic gene cluster: (staA), (staB), (staC), (staE), (staF), (staG), (staH), (staI), (staJ), (staK), (staL), (staM), (staN), (staO), (staP), (staQ), (staR), (staS), (staT), (staU), (staV) and (staW) genes, complete cds
5109	18119	30993	1.04	1.1E+00	X78425.1	NT	E. faecalis pbp5 gene
5269	18276	31139	0.9	1.1E+00	6680080	NT	Homo sapiens putative GR6 protein (GR6), mRNA
5390	18484	31159	1.53	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5565	18790	31191	13.39	1.1E+00	BE960184.1	EST_HUMAN	60165277871 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3829835 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5715	18809	31087	0.99	1.1E+00	AI138582.1	EST_HUMAN	qf6503.XT Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738260 3'
6211	19285	32517	1.93	1.1E+00	11419739	NT	Homo sapiens acute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA
6405	19473	32721	0.94	1.1E+00	AF197851.1	NT	Macroglossia pulchra cytochrome b gene, complete cds, mitochondrial gene for mitochondrial product
6547	19609	32870	0.93	1.1E+00	R06037.1	EST_HUMAN	ye89e03.1T Soares fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:124924 5'
6876	19829	33226	1.21	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7468	20434	33840	0.88	1.1E+00	AF101091.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exons 28 through 28
7514	20479	34050	0.92	1.1E+00	X55981.1	NT	Malva mRNA for endolase (2-phospho-D-glycerate hydrolase)
7732	20687	34050	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7732	20687	34051	1.83	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7754	20707	34076	8.13	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7833	25691	34158	0.94	1.1E+00	11967980	NT	Mus musculus silent mating type information regulation 2, (S cerevisiae homolog)-like (Sir2), mRNA
8470	21439	34857	2.95	1.1E+00	BF689966.1	EST_HUMAN	602082692FT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4266628 5'
8563	21531	34861	0.73	1.1E+00	AJ478339.1	EST_HUMAN	tm39h11.XT NCI CGAP_KidT1 Homo sapiens cDNA clone IMAGE:2160549 3'
9089	22055	35479	0.93	1.1E+00	AB003068.1	NT	Acetabularia calliculus mitochondrial COXI-like gene
9167	22133	35559	1.42	1.1E+00	S80750.1	NT	VH-Fanti-cytomegalovirus glycoprotein B antibody cD4 heavy chain variable region [human, mRNA Partial, 375 nt]
9278	22244	35673	0.45	1.1E+00	AJ076946.1	EST_HUMAN	oz34f05.XT Soares_NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9762	21115	36378	0.84	1.1E+00	BE384876.1	EST_HUMAN	602176278FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9886	22913	36378	0.93	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
10040	22987		0.99	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
10130	23056	36534	0.95	1.1E+00	Y12227.1	NT	Yersinia pseudotuberculosis psaeE, psaeF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10192	23117	36501	1.38	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIA0934 protein, partial cds
10287	23222	36706	6.56	1.1E+00	AL161915.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10367	23291	36757	20.52	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10867	23781	37287	1.09	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10869	23909	37422	0.83	1.1E+00	BF343644.1	EST_HUMAN	602074488FT NCI CGAP_Bmt64 Homo sapiens cDNA clone IMAGE:4150508 5'
10869	23909	37423	0.83	1.1E+00	BF343644.1	EST_HUMAN	602074488FT NCI CGAP_Bmt64 Homo sapiens cDNA clone IMAGE:4150508 5'
11012	23977	37502	2.03	1.1E+00	11087384	NT	[Homo sapiens KIA0628 gene product (KIA0628), mRNA
11094	24027		3.83	1.1E+00	AF066942.1	NT	Klebsoridium thaliana cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11435	18340		4.65	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
11439	24392	37821	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11439	24392	37922	3.12	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11883	24649	38227	3.44	1.1E+00	AB006566.1	EST HUMAN	wf9e11.x1 Soares. NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361643
12439	25002		3.12	1.1E+00	P07868	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12539	25263	31807	1.95	1.1E+00	AF216966.1	NT	Tarbia sellum immunogenic protein Tz78 mRNA, partial cds
12661	25798		2.26	1.1E+00	AF234169.1	NT	Dicystosellum discoidium isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
99	13215		1.55	1.0E+00	U23903.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	13224	28148	1.68	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for carnitine kinase, complete cds
418	13491		3.03	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 16S rRNA, 5.8S rRNA and 26S rRNA
578	13647	28580	2.22	1.0E+00	AJ281660.1	NT	Gracilaria tikvahiae mRNA for homocodomin transcription factor (so gene)
678	13741	28688	6.74	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
679	13742		1.35	1.0E+00	AF125894.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1388	15808		3.53	1.0E+00	X80416.1	NT	V. caritai Algal-GAM mRNA
1771	14800	27786	0.97	1.0E+00	AB006531.1	NT	Plasmodium falciparum virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2493	15499	28521	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2493	15499	28522	1.42	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2887	15946	28981	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2887	15946	28982	4.42	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2978	16038		0.81	1.0E+00	O14228	SWISSPROT	HYPOPHOSPHATE 67.9 KD PROTEIN C9F12.08C IN CHROMOSOME 1
3212	16287	29190	1.08	1.0E+00	AA029453.1	EST HUMAN	af29c08.st Soares. total_fetus_Nb2Hf8.9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3613	13215		0.93	1.0E+00	U23808.1	NT	WfP-C42D8.3 CEO-4204 contains element MER22 MER22 repetitive element;
3693	16736	29649	1.33	1.0E+00	AJ233816.1	NT	Xenopus laevis rhodopsin gene, complete cds
						NT	Agaricus bisporus mRNA for tyrosinase
4097	17131	30024	1.16	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4304	17333		0.73	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10138 (FLJ10138), mRNA
4843	17680	30785	1.54	1.0E+00	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5063	18065		0.9	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5354	18469	31328	3.23	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine protease
5949	19035	32228	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5949	19035	32229	5.05	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6057	19148	32360	1.44	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FGA contig fragment No. 6
6238	19309	32541	4.52	1.0E+00	PO4501	SWISSPROT	FIBER PROTEIN
6243	19316	32548	1.77	1.0E+00	AW452782.1	EST_HUMAN	U1-HB3-alk-2-09-0-JUL11 NC1_CGAP_Sup5 Homo sapiens cDNA clone IMAGE:3068969 3'
6637	19695	32872	2.12	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6691	19748	33025	0.98	1.0E+00	AF104659.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6766	19841		0.98	1.0E+00	P46505	SWISSPROT	SRB-11 PROTEIN
6813	19867	33155	0.71	1.0E+00	BE797718.1	EST_HUMAN	601581881F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3936382 5'
6813	19867	33156	0.71	1.0E+00	BE797718.1	EST_HUMAN	601581881F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3936382 5'
6944	20168	33491	1.17	1.0E+00	Y11204.1	NT	V. carteri gene encoding valvocoplin
7033	18365	31252	0.94	1.0E+00	U63721.1	NT	Human desalin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds
7345	20316	33661	1	1.0E+00	S92770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7719	20876		8.7	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7979	20918	34309	1.32	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7987	20938	34330	8.07	1.0E+00	AA775191.1	EST_HUMAN	ac79208.s1 Stragene Lung (4937210) Homo sapiens cDNA clone IMAGE:368791 3'
8165	21103		0.57	1.0E+00	BF679213.1	EST_HUMAN	602163792F1 NIH_MGC.83 Homo sapiens cDNA clone IMAGE:4294727 5'
8284	21263	34673	1.49	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC.85 Homo sapiens cDNA clone IMAGE:3848005 5'
8284	21263	34674	1.49	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC.85 Homo sapiens cDNA clone IMAGE:3848005 5'
8481	18065		1.22	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
							PEROXISOMAL HYDROLYTASE-DEHYDROGENASE-EPIMERASE (HDE) [MULTIFUNCTIONAL BETA-OXIDATION PROTEIN] (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8993	21891	35084	2.31	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDROLYTASE-DEHYDROGENASE-EPIMERASE (HDE) [MULTIFUNCTIONAL BETA-OXIDATION PROTEIN] (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8993	21891	35085	2.31	1.0E+00	Q02207	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBQUITIN THIOLESTERASE 11) (UBQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8921	21788		0.83	1.0E+00	P57194	SWISSPROT	



Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8855	21822	35242	0.44	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8855	21822	35243	0.44	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE UBP-M)
8883	25595		2.37	1.0E+00	EE147331.1	EST_HUMAN	RC1-H10229-1810395-011-008 HT0229 Homo sapiens cDNA
8923	21889	35316	0.89	1.0E+00	U42720.2	NT	Sin1an immunodeficiency virus Gag protein (gag) gene, complete cds; Ptd protein (pot) gene, partial cds; and Vpr protein (vpr), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
9075	22041	35484	1.55	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9028	22570	38019	2.14	1.0E+00	BE807592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9838	22772	39227	1.25	1.0E+00	6753423	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9838	22772	39228	1.25	1.0E+00	6753423	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9899	22896	39359	1.84	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKCC Homo sapiens cDNA clone GRCCY111 5'
9974	22501	38384	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9974	22501	38385	1.23	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10212	23137	39624	0.98	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10212	23137	39624	0.98	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10471	23593	36880	0.72	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10471	23593	36880	0.72	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10364	23486	36880	0.98	1.0E+00	A077920.1	EST_HUMAN	oyf1607 at Soares, senescent, fibroblasts NBH5F Homo sapiens cDNA clone IMAGE:1669501 3'
10890	23612	37106	3.7	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone B16FAW04 6'
10842	23762	37282	20.08	1.0E+00	AA004682.1	EST_HUMAN	2954402.1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10842	23762	37283	20.08	1.0E+00	AA004682.1	EST_HUMAN	2954402.1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10876	23768	37297	1.18	1.0E+00	111910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
12046	18459	31328	1.68	1.0E+00	Z97022.1	NT	Hordium vulgare gene encoding cyclidine proteinase
12327	25129		3.28	1.0E+00	P16306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12650	25333		2.49	1.0E+00	AW876184.1	EST_HUMAN	EST388283 IMAGE resources, MAGN Homo sapiens cDNA
1575	14608	27580	3.22	9.0E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOC1011 mRNA, complete cds
1575	14608	27581	3.22	9.0E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOC1011 mRNA, complete cds
2845	16842	28866	1	9.9E-01	AL163002.2	NT	Homo sapiens chromosome 21 segment HS21C102
3619	16663		1.1	9.0E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5717	18811	31890	8.82	9.0E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5989	19054	32254	0.70	9.8E-01	U06832	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9818	22580		1.4	9.8E-01	U85687.1	NT	Lysoarabonon esculetinon putative MIT copy 1 nematode-resistance gene
9913	22734		3.02	9.8E-01	Q28842	SWISSPROT	B2-OPARININ RECEPTOR (BK-2 RECEPTOR)
11069	24032	37556	1.48	9.8E-01	AJ005029.1	NT	Danio rerio mRNA for EHF-like receptor tyrosine kinase rtk3
524	13585	29513	1.12	9.8E-01	P22597	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2305	15317		1.28	9.8E-01	AJ003108.1	NT	Caillibacillus UBE1 gene derived retroposon on the Y chromosome
2913	15806		1.29	9.8E-01	AF174844.1	NT	Xenopus laevis rat GTPase mRNA, complete cds
7406	20374	33725	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7406	20374	33726	4.12	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7907	20550	34258	0.99	9.8E-01	BF034018.1	EST_HUMAN	601468337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7907	20550	34237	0.99	9.8E-01	BF034018.1	EST_HUMAN	601468337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
9069	22035	35468	0.88	9.8E-01	P38852	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10804	23725		0.83	9.8E-01	AA925555.1	EST_HUMAN	cd5504.at NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371947 3'
11339	24289	37813	2.06	9.8E-01	BE265705.1	EST_HUMAN	601110258F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350750 5'
11339	24289	37814	2.06	9.8E-01	BE265705.1	EST_HUMAN	601110258F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350750 5'
12545	26268		1.41	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adenylylase (adenylylase) protein >
7968	20338	33686	2.3	9.7E-01	U28716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8848	21815	35235	1.81	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8854	21821	35241	1.33	9.7E-01	M60544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
11805	24447		3.87	9.7E-01	BF611209.1	EST_HUMAN	UHH-B14-ae-e-07-Q.U1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
12117	24687	38589	2.29	9.7E-01	U87514.1	NT	Drosophila discoidium CAR3 gene, promoter region
4486	17511	30399	1.68	9.6E-01	AW76974.1	EST_HUMAN	PA2-UN00353-240300-005-f12 UN00353 Homo sapiens cDNA
5179	18168	31065	0.9	9.8E-01	7682378	NT	Homo sapiens KIA00614 gene product (KIA00614), mRNA
5847	18937	32121	3.85	9.6E-01	Z770556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5847	18937	32122	3.85	9.6E-01	Z770556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6810	19862	33259	0.97	9.6E-01	Z77341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FICA contig fragment No. 6
8735	21703		1.21	9.6E-01	X93275.1	NT	P. falciparum complete gene map of placid-like DNA (IR-A)
9203	22169	35599	0.51	9.6E-01	U81138.1	NT	Rattus norvegicus (strain R21) Rpe21 gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9446	22410	35847	0.44	9.9E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cytosolic fibrosis transmembrane conductance regulator (OFR) genes, section 1 of 2 of the complete cds; and unknown gene
11848	24731	38317	3.04	9.9E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAC08 5'
11848	24731	38318	3.04	9.9E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAC08 5'
12223	25060		2.16	9.9E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12839	25874	31416	3.03	9.9E-01	U01423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2484	15489	28512	1.03	9.9E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3766	16836	29741	2.39	9.9E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3988473 5'
3766	16836	29742	2.39	9.9E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3988473 5'
8654	22318	35745	0.86	9.9E-01	AI190162.1	EST_HUMAN	9457407.X1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:1733581 3'
8481	22425	35653	1.1	9.9E-01	AW681102.1	EST_HUMAN	RC1-CT0295-241198-011-b02 CT0295 Homo sapiens cDNA
11674	24512	38069	1.5	9.9E-01	BF218771.1	EST_HUMAN	601685163F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4103630 5'
11760	23935	37456	1.52	9.9E-01	AW293799.1	EST_HUMAN	UI-H-812-ahp-F03-Q-JUI.s1 NCJ CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727877 3'
3214	16269		3.77	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3231	16286		1.93	9.4E-01	AF080595.1	NT	Pinipinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9217	22183	35916	0.99	9.4E-01	M90724.1	NT	Human Fc-gamma-receptor1A (FCGR2A) gene, exon 4
12480	25235		2.09	9.4E-01	BE781251.1	EST_HUMAN	601469703F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866929 5'
12838	25790		1.93	9.4E-01	11418857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1745	14774		1.34	9.9E-01	AF242382.1	NT	Homo sapiens phyenyl-CoA hydroxylase (PHYH) gene, exon 5
2841	16539	29683	1.01	9.9E-01	BE071172.1	EST_HUMAN	RC5-B10503-271198-011-B01 B10503 Homo sapiens cDNA
4065	17102	29593	0.92	9.9E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4065	17102	29594	0.92	9.9E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5873	18768	31940	1.47	9.9E-01	AF219884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5761	18854	32034	3.92	9.9E-01	U36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7554	20517		0.76	9.9E-01	AF270548.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8402	21371	34779	1.75	9.9E-01	AA847040.1	EST_HUMAN	ce608033.1 NCJ CGAP OX2 Homo sapiens cDNA clone IMAGE:1385357
9165	22131		0.95	9.9E-01	AF001981.1	NT	Xenopus laevis COCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9289	22255	35685	0.91	9.9E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12833	25528	31713	1.34	9.9E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12665	25634		3.29	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds
3253	18307	29231	3.14	9.2E-01	BE622702.1	EST_HUMAN	601441339T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5008	18666		1.73	9.2E-01	7106410	EST_HUMAN	Mus musculus adult carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6101	19180	32399	4.04	9.2E-01	BF037586.1	EST_HUMAN	601461133F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3964661 5'
6789	19843	33127	0.51	9.2E-01	M84703.1	NT	N. crassa var1-RNA synthetase (GyF-200ur-3) gene
10018	22645	36412	0.77	9.2E-01	AL161655.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
10105	23031	36509	1.21	9.2E-01	6871877	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10628	23550	37050	3.42	9.2E-01	11430683	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10780	23701	37199	1.84	9.2E-01	BF568251.1	EST_HUMAN	765605X1 NCI_GGAP_K611 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
12031	24807	38501	1.54	9.2E-01	BF132402.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
1629	14682	27638	2.31	9.1E-01	T08675.1	EST_HUMAN	601820312F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:4052018 5'
2134	15151		2.08	9.1E-01	8923056	NT	xs6201.s1 Soares fetal liver splice 1N1LS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2582	15583	28602	1.12	9.1E-01	AF062319.1	NT	Alu repetitive element;
							Homo sapiens fluoresceins DNA polymerase III (dnaE) gene, complete cds
3218	16273	29195	1.11	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
3218	16273	29196	1.11	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
6291	18363	32602	1.68	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF-1b) mRNA, complete cds
6555	19712	32869	2.84	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7827	20775	34152	16.4	9.1E-01	AA006823.1	EST_HUMAN	db1g08.s1 NCI_GGAP_GC81 Homo sapiens cDNA clone IMAGE:1326862 3'
8011	20949	34342	2.68	9.1E-01	U72985.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10336	23458	36955	0.46	9.1E-01	P38432	SWISSPROT	P80-COLIN
12580	25897		10.31	9.0E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
4408	17434	30319	1.77	9.0E-01	AF069810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
7622	20552	33946	0.85	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim3) mRNA, complete cds
7652	20812		1.32	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
9704	22857	36112	0.55	9.0E-01	AF086761.1	NT	Danio rerio semaphorin 12a mRNA, complete cds
10189	23114		0.44	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5761	18873	32054	2.37	8.9E-01	AF026198.1	NT	Rabbit MHC fragment RLA-DF DNA
6377	19445		1.28	8.9E-01	X60695.1	NT	

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	25663	32637	0.69	8.9E-01	BF217939.1	EST_HUMAN	601862708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:406216 5'
6605	25663	32638	0.69	8.9E-01	BF217939.1	EST_HUMAN	601862708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:406216 5'
7408	20375		0.54	8.9E-01	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoylthetrahydropterin synthase, complete cds
8553	21521		0.43	8.9E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8769	21736	35157	1.09	8.9E-01	AF259967.1	NT	Orthoana nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
12074	24946	39541	2.99	8.9E-01	AEO03944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
12420	25190		5.46	8.9E-01	AE002188.2	NT	Chlamydomonas reinhardtii AR39, section 21 of 94 of the complete genome
5238	18246	30489	1.58	8.8E-01	O28950	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5447	18246	31118	0.9	8.8E-01	L41854.1	NT	Typhlocyba brucei microtubule-associated protein (MAPP15) mRNA, 3' end of cds
11418	24382	37897	2.31	8.8E-01	AF310817.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
12082	24954	38549	6.51	8.8E-01	AA808055.1	EST_HUMAN	Maeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12237	25952		2.3	8.8E-01	D90911.1	NT	6c38t11.st NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
465	13538	26464	1.78	8.7E-01	AF106953.2	NT	Synedrocystis sp. PC06803 complete genome, 13127, 1576593-1719843
2411	15418	28442	0.91	8.7E-01	5901803	NT	Homo sapiens S0S1 (S0S1) gene, partial cds
2885	15944	28859	6.42	8.7E-01	AA695663.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
5043	18066		2.78	8.7E-01	AF121970.1	NT	m08f11.st NCL CGAP_P44.1 Homo sapiens cDNA clone IMAGE:1076877
5247	18265	31125	0.97	8.7E-01	BF219308.1	EST_HUMAN	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
8374	21343	34754	0.95	8.7E-01	AW697335.1	EST_HUMAN	601863175F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065378 5'
9282	22248	35977	0.71	8.7E-01	A1239456.1	EST_HUMAN	RC4-NH0067-120500-013-c07 NN0057 Homo sapiens cDNA
9282	22248	35678	0.71	8.7E-01	A1239456.1	EST_HUMAN	q33606.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1946766 3'
10095	23021	38466	1.32	8.7E-01	A004663.1	NT	q33606.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1946766 3'
11081	24137	37669	4.68	8.7E-01	BF563970.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
12042	24917	38512	3.97	8.7E-01	BF107694.1	EST_HUMAN	OVG-NH1021-100800-337-c03 NN1021 Homo sapiens cDNA
12042	24917	38513	3.97	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
475	13547		2.95	8.6E-01	X17012.1	NT	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
859	13916	28874	4.32	8.6E-01	W69086.1	EST_HUMAN	Rat IGFI gene for insulin-like growth factor II
2278	15291	29316	1	8.6E-01	4533210	NT	Homo sapiens cyclochrome P450, subfamily XXIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3635	16673	29592	0.97	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3813	18853	29750	1.38	8.9E-01	U49724.1	NT	Drosophila melanogaster mef1 (Dmef1) mRNA, complete cds
5207	18216	31091	2.6	8.9E-01	BE147809.1	EST_HUMAN	RC3-H10228-160300-019-c05 H10228 Homo sapiens cDNA
6001	19084	32283	7.79	8.9E-01	X60347.1	NT	Chicken lipoprotein lipase gene
6001	19084	32284	7.79	8.9E-01	X60347.1	NT	Chicken lipoprotein lipase gene
6515	25661	32835	0.54	8.9E-01	S78772.1	NT	polyprotein [Coxsackie B4 virus CB4, host-mice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6867	19020	33215	1.7	8.9E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6867	19020	33216	1.7	8.9E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
8260	21229	34757	0.81	8.9E-01	AE000591.1	NT	Helicobacter pylori 26695 strain 68 of 134 of the complete genome
8377	21346	34757	1.29	8.9E-01	AF001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
10044	22971		0.51	8.9E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
12798	25717		0.46	8.9E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
6888	19940	33236	1.44	8.9E-01	AL112162.1	NT	Bovine chimeric strain T4 cDNA library under conditions of nitrogen deprivation
7766	20721	34093	1.5	8.9E-01	AF165214.1	NT	Bacteriophage D3, complete genome
8323	21292	34708	2.49	8.9E-01	BE542912.1	EST_HUMAN	601067107FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463503 5'
8761	21728	35150	0.93	8.9E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8849	21816	35151	0.93	8.9E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
10715	23637	37120	1.35	8.9E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
10715	23637	37130	1.35	8.9E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
12565	25699		2.29	8.9E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
12572	26283		1.37	8.9E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
4782	17902	30093	0.95	8.9E-01	AF083975.2	NT	Homo sapiens partial c-Ha-ras receptor gene, exon 2 to 5
5571	25641	31627	2.68	8.9E-01	L78726.1	NT	Oryzidium callidum gene for SigC, complete cds
5571	25641	31628	2.68	8.9E-01	L78726.1	NT	Oryzidium callidum gene for SigC, complete cds
8707	21044	34443	0.61	8.9E-01	AF051142.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
10317	23241		3.25	8.9E-01	AF051142.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
12005	24952	39478	1.54	8.9E-01	M55584.1	NT	Mammalia basitarsae phorbolone binding protein 2 precursor (PBP2) mRNA, complete cds
743	13904	26743	3.01	8.9E-01	M63437.1	NT	Pyrococcus abyssi complete genome, segment 5/6
3111	16188	29078	0.83	8.9E-01	AF161509.2	NT	Human collagenase type IV (CLG4) gene, exon 4
3823	16883	29767	3.15	8.9E-01	AF161509.2	NT	Thermus thermophilus cytochrome c-552 (cytC) and CytB (cytB) genes, complete cds
4040	17078	29976	3.15	8.9E-01	Y19177.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
5341	18446	31189	2.42	8.9E-01	AL161540.2	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
						NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10028	22955		4.53	8.3E-01	AF071852.1	EST_HUMAN	nm011212.y6 NCL CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.L1 THR repetitive element;
10469	23391	38886	1.1	8.3E-01	AF088070.1	NT	Drosophila melanogaster L11 homolog mRNA, complete cds
10579	23391	38993	3.97	8.3E-01	AF108133.1	NT	Mus musculus neuro-44 gene, exons 3 through 12 and partial cds
11033	23997	37524	2.97	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
11050	24013		1.92	8.3E-01	Z121472	NT	Phytophthora infestans mitochondrion, complete genome
11634	24571	38135	2.22	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2069	15085	28103	2.24	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2101	15118		1.08	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2688	15584		1.06	8.2E-01	AF076990.1	EST_HUMAN	IL3-CT0218-181169-031-C08 CT0219 Homo sapiens cDNA
3918	16958	28971	0.78	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3940	16990	29895	0.92	8.2E-01	AF083417.1	NT	Tenysylum orbicular elongation factor 1-alpha mRNA, partial cds
6800	19854	33139	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6800	19854	33140	0.57	8.2E-01	X95283.1	NT	G.gallus mRNA for C-Serrat-1 protein
6941	20165	33468	0.85	8.2E-01	AJ010142.1	NT	Acanthamoeba muscaria mRNA for SC1125 protein
7082	20103	33414	3.89	8.2E-01	AF037643.1	EST_HUMAN	CM4-HT0243-081109-037-ec1 HT0243 Homo sapiens cDNA
7494	25982	33907	4.38	8.2E-01	Z12128.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8787	21754	35176	0.58	8.2E-01	BE283145.1	EST_HUMAN	6011448852 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10385	23307	35765	0.68	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
10419	23341	35827	1.59	8.2E-01	AF052659.1	NT	Homo sapiens threodoxin-related protein mRNA, complete cds
10593	23505	36998	0.59	8.2E-01	AF223888.1	NT	Oncofuchus ishawytscha isolate T-20 somatolactin precursor gene, exon 1
10593	23505	36998	0.59	8.2E-01	AF223888.1	NT	Oncofuchus ishawytscha isolate T-20 somatolactin precursor gene, exon 1
10593	23505	36998	0.59	8.2E-01	AF223888.1	NT	ONCOKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10781	23673	37169	3.84	8.2E-01	CB0170	SWISSPROT	ONCOKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10781	23673	37170	3.84	8.2E-01	CB0170	SWISSPROT	ONCOKUSICK-KAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11957	24838	39432	2.87	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12038	24913	38507	4.82	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12043	24918	38514	8.1	8.2E-01	H87388.1	EST_HUMAN	YW14402.1 Scars, placenta, 806weeks, ZNBP180gW Homo sapiens cDNA clone IMAGE:252185 5' similar to cDNA36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12586	25290	31781	2.88	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2769	15761		1.48	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBKT (Tbk1) mRNA, complete cds
3472	16518	29439	3.97	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3472	18518	29440	3.87	8.1E-01	AF05068.1	NT	Homo sapiens MHC class 1 region
5792	18884	32088	0.51	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSHR) (MELANOTROPIN RECEPTOR)
6448	19513	32783	0.84	8.1E-01	U16790.1	NT	MELANOCORTIN-1 RECEPTOR (MC1-R)
6777	19832	33114	2.47	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2(X) chain (COL1A2) gene, partial cds
6777	19832	33115	2.47	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
7755	20708	34077	0.55	8.1E-01	Q04747	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
							CYTOCHROME B
8243	21212	34618	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nech) and putative amylase-related protein (Amyel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8243	21212	34619	1.12	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Pico) gene, partial cds; putative sodium channel (Nech) and putative amylase-related protein (Amyel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8968	21822	35349	0.81	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 1174
8968	21822	35350	0.81	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 1174
9122	22088	35516	1.13	8.1E-01	AW242647.1	EST_HUMAN	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN ; contains MER22 b1 PTR6 repetitive element
10484	23406	36902	0.84	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10776	23697	37195	0.42	8.1E-01	N84541.1	EST_HUMAN	KK987F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872 5' similar to EST(1) CLONE C-0PE11
11812	24997	38277	4.05	8.1E-01	BE93558.1	EST_HUMAN	RCQ-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11812	24997	38278	4.05	8.1E-01	BE93558.1	EST_HUMAN	RCQ-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
12298	25109	31839	1.73	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 139 of the complete genome
178	13279		3.32	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phospho acetyltransferase allele 19
288	13983	29310	5.97	8.0E-01	AJ132772.1	NT	Box taurinus full and rif genes
2051	15070		1.72	8.0E-01	BF93062.1	EST_HUMAN	602072473F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE4215091 5'
3093	16151	29056	1.41	8.0E-01	AF127897.1	NT	Salmonella enterica serovar typhimurium (SBO27) gene, partial cds
3324	16375	29298	1.3	8.0E-01	AB001193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3717	16760		2.36	8.0E-01	AB182758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4593	17586	30478	6.45	8.0E-01	X83759.2	NT	Gallus gallus for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
8322	21281		2.31	8.0E-01	AW601449.1	EST_HUMAN	RCQ-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8970	21837	35259	1.05	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
11303	24253	37779	1.58	8.0E-01	Q82793	SWISSPROT	CREB-BINDING PROTEIN



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
454	13527	26457	0.78	7.9E-01	D11478.1	NT	Lymantia dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
716	13778		0.78	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 69 of the complete genome
1609	14847		23.05	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1432 protein, partial cds
1693	14895		1.28	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2272	15265	28311	7.38	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitoguinin28, complete cds
2273	15268	28312	2.36	7.9E-01	AF130459.1	NT	Danio rerio Tira4-associated protein, Tira1A (lep1A) mRNA, complete cds
3328	16574	28497	3	7.9E-01	AF228564.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4330	17358		0.88	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_JMGC_7 Homo sapiens cDNA clone IMAGE:3555785 5'
4842	17663	30551	1.15	7.9E-01	6763745	NT	Mus musculus embigin (Emb), mRNA
4842	17693	30552	1.15	7.9E-01	6763745	NT	Mus musculus embigin (Emb), mRNA
5244	18252	31123	1.03	7.9E-01	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative enkyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
6479	18544	32792	0.76	7.9E-01	D35145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8448	21415	34828	3.37	7.9E-01	X60598.1	NT	P. salivum GR gene
9005	22857	36319	4.3	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3MA-B (vspG3MA-B) mRNA, partial cds
10409	23331	36816	4.3	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10451	23373	36864	0.82	7.9E-01	AV700960.1	EST_HUMAN	AV700860 GK6 Homo sapiens cDNA clone GK06R12 3'
10877	23787	37298	0.82	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-ribose reductase, complete cds
11550	24300		2.81	7.9E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11546	24487	38041	2.22	7.9E-01	P16022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (NCADHERIN)
877	13932		1.66	7.9E-01	Z43785.1	EST_HUMAN	HSC17K1041 normalized infant brain cDNA Homo sapiens cDNA clone c-1K104
2283	15286	28320	6.12	7.9E-01	AW959587.1	EST_HUMAN	HSCT1837 MAGE resequences, MAGEF Homo sapiens cDNA
4730	17760	30842	1.33	7.9E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5078	18085		0.8	7.9E-01	AW753353.1	EST_HUMAN	RC3-C10254-130100-023-c02 C10254 Homo sapiens cDNA
9187	19262	32498	2.5	7.9E-01	AF119859.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6344	19413	32655	1.04	7.9E-01	P05231	SWISSPROT	INTERLEUKIN-3 PRECURSOR (IL-3) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYDRIDON GROWTH FACTOR)
6005	19564	32939	0.72	7.9E-01	AL445069.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8838	21893	35221	1.28	7.9E-01	BF108627.1	EST_HUMAN	756405.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9589	22551	36002	1.34	7.9E-01	Y10189.1	NT	D. discoideum racGAP gene
5887	22840	36087	0.52	7.9E-01	4628873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10483	23405		1.01	7.9E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12559	25546		2.32	7.8E-01	L28260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS8) gene, complete cds
145	13248	26177	6.69	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
727	13786		3.26	7.7E-01	AF00157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (A2beta) and major histocompatibility protein class II beta chain (I2beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lb
2724	15718	28736	2	7.7E-01	Q33915	SWISSPROT	GITRATASE SYNTHASE
3968	16418		0.76	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetyl-galactosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7), mRNA
3814	16558	29576	3.83	7.7E-01	AF118085.1	NT	Homo sapiens PRO1878 mRNA, complete cds
4425	17452	30343	3.04	7.7E-01	AF189488.1	NT	Colurnix columbin japonica sub-species japonica beta-actin mRNA, partial cds
4425	17452	30344	3.04	7.7E-01	AF189488.1	NT	Colurnix columbin japonica sub-species japonica beta-actin mRNA, partial cds
5540	18738	31689	1.25	7.7E-01	P16553	SWISSPROT	RAFINOSE INVERTASE (INVERTASE)
5540	18738	31690	1.23	7.7E-01	P16553	SWISSPROT	RAFINOSE INVERTASE (INVERTASE)
6066	19147	32359	0.53	7.7E-01	R08500.1	EST_HUMAN	Y24602.61 Scores fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:127755 3'
10204	23129	36916	0.72	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12447	25207		5.53	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
6218	19292	32526	4.49	7.8E-01	AF058510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCC8) mRNA, complete cds
6218	19292	32526	4.49	7.8E-01	AF058510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCC8) mRNA, complete cds
6667	19724	32699	0.65	7.8E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA 24
7029	18561	31248	0.98	7.8E-01	A1253398.1	EST_HUMAN	seq14b12xt Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7029	18561	31248	0.98	7.8E-01	A1253398.1	EST_HUMAN	seq14b12xt Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7252	19037	33295	0.89	7.8E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-tetradotoxin receptor mRNA, complete cds
8400	21389	34778	1.33	7.8E-01	AF146793.2	NT	Mus musculus neurexin U precursor (Nmu) gene, partial cds; PHLP (Tphip) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT21 (PFT2) gene, complete cds; and H5AR (H5ar) gene, complete cds
8464	21433	34849	1.92	7.8E-01	6857752	NT	Mus musculus actinin (Actin) gene, complete cds
8464	21433	34850	1.92	7.8E-01	6857752	NT	Mus musculus actinin (Actin) gene, complete cds
8668	21636	35056	0.43	7.8E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL-D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8668	21636	35056	0.43	7.8E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL-D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9318	22283	38714	1.01	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2B6, phenobarbital inducible, type a (Cyp2b6), mRNA
9634	22578	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9634	22578	36028	5.25	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11685	24651	38229	2.09	7.6E-01	X68347.1	NT	Haeperia mRNA for neurofilament NF70
11685	24651	38229	2.09	7.6E-01	X68347.1	NT	Haeperia mRNA for neurofilament NF70
12020	24697	38229	3.05	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
12203	25045		3.8	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
514	13585		1.67	7.6E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
566	13664	29508	1.01	7.6E-01	AF020608.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FH1) gene, exon 5
7764	20717	34090	0.78	7.6E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (epi) mRNA, complete cds
12516	25247		4.53	7.6E-01	AF163151.2	NT	Homo sapiens dentin sialoprotein precursor (DSPP) gene, complete cds
13027	25576	31697	1.57	7.6E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328782 (section 29 of 148) of the complete genome
1132	14175	27124	1.35	7.4E-01	AI598146.1	EST_HUMAN	repative element contains element MIR repetitive element :
2350	15358	28381	0.93	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3739	16781	29693	18.81	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
3919	16959	29872	2.01	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4340	17387	30250	6.99	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8176	21146	34553	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8176	21146	34554	1.04	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8980	21946	35370	0.78	7.4E-01	BF346266.1	EST_HUMAN	002018456F1 NC1 CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4154340 5'
9003	22029		0.94	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9452	22416	35854	7.09	7.4E-01	BE147503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9511	22474	35918	1.14	7.4E-01	AA187988.1	EST_HUMAN	z6977001 s1 StrataGene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:6252397 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10767	23898	37185	0.74	7.4E-01	11424933	NT	Homo sapiens NY-REN-48 antigen (LOC61133), mRNA
12171	25021		4.46	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
12284	25101		1.64	7.4E-01	AI472641.1	EST_HUMAN	z613901 x1 NC1 CGAP_Lym5 Homo sapiens cDNA clone IMAGE:20439815 3'
3999	17038		0.94	7.3E-01	AP000062.1	NT	Aeropyrum pernix genome DNA, section 57
4647	17968	30555	0.97	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4729	17748	30641	4.57	7.3E-01	AF25421.1	NT	Homo sapiens HT017 mRNA, complete cds
5135	18144	31024	1.18	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6761	19815	33094	5.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6761	19815	33095	5.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7301	25579	33608	0.92	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7692	20650	34014	0.53	7.3E-01	Z14133.1	NT	D melanogaster Cdc mRNA for diaphanin heavy chain
7704	20746	34119	7.46	7.3E-01	M26511.1	NT	V alginolyticus sucrose (scrB) gene, complete cds
7794	20746	34120	7.46	7.3E-01	M26511.1	NT	V alginolyticus sucrose (scrB) gene, complete cds
8115	21052	34450	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
8115	21052	34450	0.51	7.3E-01	U34631.1	NT	Mus musculus alpha-4 integrin gene, exon 7
11759	24697	38267	3.11	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares fetal liver spleen, 1NPLS_S1 Homo sapiens cDNA clone IMAGE:437799 3'
11759	24697	38268	3.11	7.3E-01	AA678019.1	EST_HUMAN	z125b08.s1 Soares fetal liver spleen, 1NPLS_S1 Homo sapiens cDNA clone IMAGE:437799 3'
832	13889	27997	2.03	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1874	14995	27997	3.23	7.2E-01	X79140.1	NT	N tabacum NeIF-4A13 mRNA
2468	15472	28495	1.91	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3080	18137	29048	1.47	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3467	15513	29434	2.44	7.2E-01	AF065608.1	NT	Glerdia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-5/A-1 allele, complete cds
4803	17620	30714	2.99	7.2E-01	D90314.1	NT	L mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5159	18168	31046	1.57	7.2E-01	AF196778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel alpha
5159	18168	31046	1.57	7.2E-01	AF196778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel alpha
5159	18168	31047	1.57	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel alpha
7421	20388	33739	0.78	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8797	21764	35186	1.24	7.2E-01	AF236051.1	NT	Oryzopsis cuniculatus RING-finger binding protein mRNA, partial cds
9314	22279	37123	0.62	7.2E-01	AF743773.1	EST_HUMAN	AF743773 CB Homo sapiens cDNA clone CBMAFD05 5'
10705	23627	37123	2.59	7.2E-01	BF070061.1	EST_HUMAN	602118381.F1 NIH_JGCG_35 Homo sapiens cDNA clone IMAGE:4275881 5'
11091	24051	37574	3.38	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome P-450 mRNA, complete cds
12523	18343	31291	4.43	7.2E-01	U02568.1	NT	Dicopycaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
12700	23590		5.56	7.2E-01	AF0000363.1	NT	Aeropyrum pernix genomic DNA, section 617
693	13755	26695	13.3	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RYR1), complete cds
3075	16132	29045	13.21	7.1E-01	AJ270777.1	NT	Homo sapiens partial TGF-beta gene for T-cell transcription factor-4, exons 1-5-16

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4236	17265	30151	3.29	7.1E-01	7305360	NT	Mus musculus obolgin (Obol), mRNA
4236	17265	30152	3.29	7.1E-01	7305360	NT	Mus musculus obolgin (Obol), mRNA
6058	19139	32350	1.55	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:426344 5'
6058	19139	32351	1.55	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:426344 5'
7137	20113	33426	6.92	7.1E-01	U36232.1	NT	Drosophila melanogaster 8-pyruvate/hydroxyphenyl synthase (pf) gene, complete cds
8533	21501	34916	0.48	7.1E-01	H54244.1	EST_HUMAN	Y63609.01 Soares fetal liver spleen TNP15 Homo sapiens cDNA clone IMAGE:202961 3'
9088	22054	35477	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-LB10567.301269.011-409 B10567 Homo sapiens cDNA
9088	22054	35478	0.85	7.1E-01	BE074185.1	EST_HUMAN	RC1-LB10567.301269.011-409 B10567 Homo sapiens cDNA
10214	23139	36528	1.28	7.1E-01	BE094405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3858495 5'
10774	23695	37193	1.13	7.1E-01	M12961.1	NT	Human T-cell receptor gamma chain, J2 gene
12499	25773	37193	2.34	7.1E-01	AA421462.1	EST_HUMAN	Human T-cell receptor gamma chain, J2 gene
1233	14270	27229	1.13	7.0E-01	AB014614.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
1233	14270	27230	1.13	7.0E-01	AB014614.1	NT	Homo sapiens mRNA for KIAA0814 protein, partial cds
2455	15460	28482	1.09	7.0E-01	N62412.1	EST_HUMAN	Y27907.01 Soares, multiple sclerosis_2N6HNSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2455	15460	28483	1.09	7.0E-01	N62412.1	EST_HUMAN	Y27907.01 Soares, multiple sclerosis_2N6HNSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5096	18106		2.11	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6092	19143		0.95	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8721	21989		8.51	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
8871	22824	36077	0.82	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
9871	22824	36078	0.82	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mliA, mliR, mliF, and mliD genes, complete cds
11454	24397	37943	1.71	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11454	24397	37944	1.71	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13035	25811	37628	1.35	7.0E-01	9530484	NT	Bacteriophage N15 vifon, complete genome
971	14023	25976	12.59	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	14023	25977	12.59	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1313	14349	27315	2.22	6.9E-01	AA593530.1	EST_HUMAN	m28409.s1 NCL_CGAP_Gac1 Homo sapiens cDNA clone IMAGE:1085176 3'
3233	16288	29210	1.8	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5249	18257	31126	0.92	6.9E-01	AV714502.1	EST_HUMAN	AV714502 DOB Homo sapiens cDNA clone DOBATD12 5'

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5878	18687	32158	0.8	6.9E-01	AB035962.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord cell, complete cds
6104	19183	32402	0.55	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP850, partial
6806	19570	32822	1.5	6.9E-01	BE298183.1	EST_HUMAN	601177333F1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:352328 5'
8512	21281	34682	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8512	21281	34693	3.39	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8526	22469		0.73	6.9E-01	AF148046.1	NT	Entamoeba dispar calpon transporting ATPase (dipase) gene, partial cds
10053	22680	39447	0.55	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10053	22680	39448	0.55	6.9E-01	AF208319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
11587	24925	38081	2.03	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
11587	24925	38082	2.03	6.9E-01	D88013.1	NT	Homo sapiens DAN gene, complete cds
12145	25766		3.91	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFK-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
958	14011	26964	1.32	6.9E-01	AF017794.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2682	15678		1.26	6.9E-01	D50617.1	NT	Synchytrium sp. PC05803 complete genome, 2727, 3418552-3573470
2840	14651	27627	1.5	6.9E-01	AA854475.1	EST_HUMAN	q75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:2568411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4602	17623	30516	1.75	6.9E-01	J00762.1	NT	Rat(hooded) prolactin gene: exon iii and flanks
9998	22823	36388	1.67	6.9E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
11424	24593	37903	1.77	6.9E-01	AJ276975.1	NT	Staphylococcus aureus bgl1 gene for beta-glucosidase, exons 1-4
11424	24593	37904	1.77	6.9E-01	AJ276975.1	NT	Staphylococcus aureus bgl1 gene for beta-glucosidase, exons 1-4
11450	24593	37538	1.82	6.9E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11450	24593	37939	1.82	6.9E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11931	24812	39407	1.49	6.9E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lipasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
11931	24812	39408	1.49	6.9E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lipasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Secm21 gene, partial>
298	13392	26320	25.45	6.7E-01	AF213984.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
339	13428	26350	28.03	6.7E-01	AF213984.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1927	14951		1.07	6.7E-01	M12132.1	NT	Quail fast skeletal muscle tropinin 1 gene, complete cds

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2157	15173	28192	1.79	6.7E-01	AA451884.1	EST_HUMAN	zK12g12.s1 Soares, total, fetal, NB2H-F9, gw Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2176	15866	28213	2.65	6.7E-01	AF196073.1	NT	Drosophila melanogaster Mat85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Raisin) gene, complete cds, alternatively spliced
3009	19087	28937	3.95	6.7E-01	6678560	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4481	17508	30395	0.78	6.7E-01	X74421.1	NT	S.tuberculosis mRNA for glucose-6-phosphate dehydrogenase
5002	18016	30603	0.97	6.7E-01	AW078110.1	EST_HUMAN	x859712.x1 NCL CGAP_C017 Homo sapiens cDNA clone IMAGE:2574568 3'
5597	19693	31651	0.7	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (alpA and alpB) genes, complete cds
5597	19693	31652	0.7	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (alpA and alpB) genes, complete cds
6073	19154	32366	0.93	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6458	19521	32771	1.28	6.7E-01	6535035	NT	Galid herpesvirus 2, complete genome
6458	19521	32772	1.28	6.7E-01	6535035	NT	Galid herpesvirus 2, complete genome
7637	20500		4.57	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 187 of 628 of the complete genome
7693	20528	33984	0.98	6.7E-01	AE001488.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10503	23425		0.82	6.7E-01	M34048.1	NT	Human placental protein 14 (PP14) gene, complete cds
11300	24250	37776	2.62	6.7E-01	BF354648.1	EST_HUMAN	CM3-HT0769-010600-187-cd3 HT0769 Homo sapiens cDNA
11787	23942	37464	3.23	6.7E-01	OT14357	SWISSPROT	N-ACETYL-GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11
11969	24847	38444	1.62	6.7E-01	AA342521.1	EST_HUMAN	EST148065 Fetal spleen Homo sapiens cDNA 3' and
2509	15512	28538	1.92	6.8E-01	AF075240.1	NT	Homo sapiens SLT1 protein (SLU12) mRNA, partial cds
2711	15705	28721	1.4	6.8E-01	AF158339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3501	16548	29474	1.41	6.8E-01	4500880	NT	Homo sapiens scna domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (serpentin) 5A (SEMA5A) mRNA
3670	18713	29628	4.37	6.8E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
4138	17168		0.88	6.8E-01	U091328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofel gene, and sodium phosphate transporter (NPT3) gene, complete cds
5258	18266	31134	1.73	6.8E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
5282	18286	31130	0.95	6.8E-01	Z82002.1	NT	S.pneumoniae pcpB and pcgC genes
5282	18288	31151	0.95	6.8E-01	Z82002.1	NT	S.pneumoniae pcpB and pcgC genes
6486	19531	32779	3.93	6.8E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7849	20890	34281	3.57	6.8E-01	AV680508.1	EST_HUMAN	AV680508 GLC Homo sapiens cDNA clone GLC1D04.3'
8912	21878	35304	0.98	6.8E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11.5'
10023	22950		1.56	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12746	25395	31758	1.76	6.5E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 83 of the complete chromosome
624	13689	28608	0.96	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
624	13689	28607	0.96	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3446	16493	29412	4.46	6.5E-01	AB041225.1	NT	Mus musculus gene for Tdb2, complete cds
4311	17340	30220	4.28	6.5E-01	AJ272265.1	NT	Homo sapiens SIPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5102	18112	30084	3.71	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5204	18213	31088	1.13	6.5E-01	Z70528.1	NT	H. sapiens mRNA for immunoglobulin heavy chain variable region (8D4.A8, VH4, 4-59IDP-71)
5518	25640	31551	2.13	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
5802	18894	32077	0.58	6.5E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6887	19539	33234	1.24	6.5E-01	D88348.1	NT	Chicken mRNA for 11B-KDa melanosomal matrix protein, complete cds
7841	20788	34163	0.84	6.5E-01	X04789.1	NT	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7930	20873	34262	0.89	6.5E-01	A1769882.1	EST_HUMAN	wc6802.XT NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:2321642.3'
10197	23122		1.03	6.5E-01	T76904.1	EST_HUMAN	y21504.at Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108847.3'
10599	23821	37117	2.2	6.5E-01	AF118876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10997	23993	37487	2.19	6.5E-01	H87583.1	EST_HUMAN	yw1706.r1 Soares, placenta, 80weeks, 2NHP860W Homo sapiens cDNA clone IMAGE:252515.5'
11045	24009	37535	2.88	6.5E-01	AA601287.1	EST_HUMAN	not507.at NCI CGAP_P967 Homo sapiens cDNA clone IMAGE:1100748.3'
11143	24103		3.43	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACET Homo sapiens cDNA clone PLACE1007810.5'
11925	24806	38399	2.3	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit 1, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
11970	24845	38445	1.47	6.5E-01	AF146987.1	NT	Fugu ubripes U2 small nuclear ribonucleoprotein auxiliary factor subunit-related protein (U2AF1-RS2), 19 kDa Golgi adaptor protein adaptin (AP19), and phosphotyrosine kinase alpha 2 subunit (PHKA2) genes, complete cds; kelch protein (KELCH1) and kelch p>
12130	24909	38604	1.61	6.5E-01	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 78
12554	25276		2.66	6.5E-01	BE480590.1	EST_HUMAN	h774410.xt NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178130.3'
252	13349	26275	10.51	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3470	16516	29437	3.26	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3875	16514	29823	1.34	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4518	17544	30430	0.89	6.4E-01	Y12488.1	NT	Musculus whn gene
4519	17544	30431	0.89	6.4E-01	Y12488.1	NT	Musculus whn gene
5182	18201	31073	1	6.4E-01	H85337.1	EST_HUMAN	y95008.r1 Soares retina N265HR Homo sapiens cDNA clone IMAGE:222086.5'
8590	21929	35363	1.57	6.4E-01	AE001247.1	NT	Trepome pallidum section 63 of 87 of the complete genome



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10449	23371	38863	6.94	6.4E-01	U82928.1	NT	Homo sapiens atoxia telangiectasia (ATM) gene, complete cds
10464	23386	38879	1.18	6.4E-01	BF670405.1	EST_HUMAN	602150299F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:429128 5'
12866	23422	38879	5.76	6.4E-01	A7769212.1	EST_HUMAN	A7766212 MDS Homo sapiens cDNA clone MDCGC09 5'
434	13508	28442	3.27	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
536	13607	28525	2.19	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2171	15187	28203	3.4	6.3E-01	U81138.1	NT	Shigella flexneri multi-antibiotic resistance locus
2583	15584	28603	2.72	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2593	15584	28604	2.72	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
6182	19587	32490	0.8	6.3E-01	Y17276.1	NT	Lycopodium obscurum psba gene, complete cds
3029	19587	33088	0.87	6.3E-01	BE093906.1	EST_HUMAN	PMP-BT0757-010500-002-4035 BT0757 Homo sapiens cDNA
6753	19587	33088	1.07	6.3E-01	L27768.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6753	19587	33088	1.07	6.3E-01	L27768.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
8666	21633	36636	3.17	6.3E-01	BE02044.1	EST_HUMAN	50167689F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:395935 5'
9238	22204	36636	0.8	6.3E-01	S62927.1	NT	Glycoprotein Ila (AII.1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9575	22537	35989	0.74	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102593 5'
9775	22716	36171	2.86	6.3E-01	9627521	NT	Varicella virus, complete genome
9775	22716	36172	2.86	6.3E-01	9627521	NT	Varicella virus, complete genome
10298	23223	37216	0.63	6.3E-01	AE002326.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10782	23713	37216	1.55	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10895	23815	37322	0.66	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
11400	24345	37878	1.52	6.3E-01	A4877745.1	EST_HUMAN	nr0906.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR-002916 002916
11663	24599	38173	6.95	6.3E-01	A4877745.1	EST_HUMAN	HLAR.1
11754	24892	39291	1.79	6.3E-01	A4877745.1	EST_HUMAN	CM-BT043-000295-046 BT043 Homo sapiens cDNA
11915	24769	38387	2.09	6.3E-01	P36073	SWISSPROT	HYPOPHETICAL T3.7 KD PROTEIN IN INO1-HS2 INTERGENIC REGION
12258	25628	31309	5.44	6.3E-01	9810283	SWISSPROT	HYPOPHETICAL T5.3 KD PROTEIN IN VMA12-AP1 INTERGENIC REGION
12359	25149	31309	1.81	6.3E-01	AF05227.1	NT	Mus musculus keratin complex 2, gene 5g (K42-6g), mRNA
12570	25845	319	3.19	6.3E-01	X63528.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
15970	19055	32255	2.37	6.2E-01	Q10135	SWISSPROT	Climbup pscd gene
7737	20592		2.75	6.2E-01	AF022553.1	NT	HYPOPHETICAL 142.6 KD PROTEIN C2A2E2.02 IN CHROMOSOME 1
7791	25690	34117	1.12	6.2E-01	AL021127.2	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
8844	21612	35034	5.41	6.2E-01	H72255.1	EST_HUMAN	Mus musculus chromosome X contig4; putative Magea5 gene, Catractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
							yeo160d.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:213542 3'

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9208	22174	36605	0.54	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds, and dehydroquinase dehydrated/shikimate:NADP oxidoreductase gene, complete cds
9804	21127	34551	1.67	6.2E-01	BE02697.1	EST_HUMAN	601335146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3650010 5'
9868	22804		2.17	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10438	23360	38849	7.04	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10902	23822	37332	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P30 ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10902	23822	37333	5.32	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P30 ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2404	15411		5.9	6.1E-01	6678078	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Spac), mRNA
5614	18710	31868	1.3	6.1E-01	M65940.1	NT	Caenorhabditis elegans N2 CcMyoD (hlt-1) alternatively spliced genes, complete cds
7053	20075	33382	3.64	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7053	20075	33383	3.54	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7216	20238	33672	0.7	6.1E-01	AW105653.1	EST_HUMAN	x55003.x1 NCL CGAP_O723 Homo sapiens cDNA clone IMAGE:2697237 3' similar to gbX12671_rnet
7312	20283	33624	0.64	6.1E-01	Q63769	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8675	21543	34065	3.96	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
9147	22113	35537	1.17	6.1E-01	T1431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4) mRNA
9147	22113	35538	1.17	6.1E-01	T1431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4) mRNA
9170	22711	36165	23.08	6.1E-01	AF235117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9170	22711	36166	23.08	6.1E-01	AF235117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10202	23277	36613	0.99	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of E28 of the complete genome
10406	23328	36812	1.53	6.1E-01	AF19117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11306	24256		1.81	6.1E-01	X74507.1	NT	P. aethiops mdh mRNA for chloroplast malate dehydrogenase (NADP+)
12041	24916	38510	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, mRNA, 2408 nt]
12041	24916	38511	1.63	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, mRNA, 2408 nt]
12355	25731	31616	2.77	6.1E-01	AB041350.1	NT	Mus musculus Col4a5 mRNA for type IV collagen alpha 5 chain, complete cds
495	13697	26400	1.41	6.0E-01	DB07675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
563	13033		2.75	6.0E-01	5602869	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (GLA20), mRNA
1364	14398	27389	1.92	6.0E-01	AF065283.1	NT	Human respiratory syncytial virus strain CH103-53b attachment protein (G) gene, complete cds
3828	16968	29770	0.9	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicaemia virus N. P. M. G. Nv. L genes, French strain 07-71

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4217	17246		1.61	6.0E-01	AF068985.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
4279	17308	30187	0.99	6.0E-01	AB028319.1	NT	Yaba monkey tumor virus DNA, BamH1 restriction fragment E, M and partial C, partial and complete cds
5353	18468	31327	2.14	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5514	18914	31547	2.22	6.0E-01	AW139713.1	EST_HUMAN	U1-H1-aab-a-10-0.U1 a1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619.3
6889	19746	33022	2.68	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6818	19872	33161	0.87	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
6988	20211	33539	0.78	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6988	20211	33540	0.78	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7577	20539	33698	5.61	6.0E-01	AJ277691.1	NT	Homo sapiens partial LMOT gene for LIM domain only 1 protein, exon 1
8461	21430	34847	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8461	21430	34848	4.55	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10182	23107	36589	1.84	6.0E-01	AB008183.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10836	23558		1.66	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-3)
10749	23671		0.48	6.0E-01	BE637779.1	EST_HUMAN	RC2-FN0094-180700-017-408 FN0094 Homo sapiens cDNA
11878	24760	38345	2.79	6.0E-01	AI420623.1	EST_HUMAN	U0807.X1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:2095621.3
12638	25322	31788	1.87	6.0E-01	11421863	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12731	25384		2.78	6.0E-01	AA706087.1	EST_HUMAN	Z99055.1 Soares fetal liver spleen, 1NF.LS_S1 Homo sapiens cDNA clone IMAGE:462776.3
12918	25777	31522	4.71	6.0E-01	9055303	EST_HUMAN	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12947	25715		3.4	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1002	14053	27005	0.87	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3283	16337	29256	4.95	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
3283	16337	29287	4.95	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4250	17276		4.08	5.9E-01	AF182768.1	NT	Rattus norvegicus catenax 2 mRNA, partial cds
6809	19887	32943	1.45	5.9E-01	AF085440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7481	20447	33903	2.44	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
8332	21301	34716	0.46	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8985	21951	34375	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
8901	22853	38314	0.89	5.9E-01	AF083204.2	NT	Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10273	23198		0.66	5.9E-01	P06483	SWISSPROT	IE6 PROTEIN
10548	23470	39065	1.19	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
11031	23995	37523	2.46	5.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (OTMP KINASE)
11037	24001	37526	49.8	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein kinase phosphatase delta (XPTP-D) mRNA, complete cds
11309	24258	37795	2.749	5.9E-01	AF197944.1	EST_HUMAN	P4M-DT0041-190100-002-003 DT0041 Homo sapiens cDNA
11526	24407	39021	1.53	5.9E-01	AF064626.1	NT	Mus epididymal SPRET/TEI CD48 antigen (Cd48) gene, partial cds
12297	25108	31838	2.43	5.9E-01	L42320.1	NT	Aspergillus nidulans alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12541	25284		2.86	5.9E-01	AB017705.1	NT	Oryzopsis oryzae pTG gene for orcidine-5-phosphate decarboxylase, complete cds
12740	25390		0.24	5.9E-01	P34628	SWISSPROT	MYOCELLULOSE-ASSOCIATED PROTEIN 1A (CONTAINS: MAP1 LIGHT CHAIN LC2)
1924	14948	27944	1.28	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
2571	15573	28592	1	5.9E-01	7305230	NT	Mus musculus low density lipoprotein B (Ldlb), mRNA
4009	17048	29854	1	5.9E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4542	17868	30452	4.23	5.9E-01	AB003077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
5448	18550		0.84	5.9E-01	AE002152.1	NT	Ureaplasma urealyticum section 93 of 99 of the complete genome
5909	18705	31862	0.75	5.9E-01	Q10669	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6308	18378	32618	1.82	5.9E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-500E06 5'
8445	19510	32760	0.73	5.9E-01	D50801.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
8985	20208		2.55	5.9E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8219	21188		2.63	5.9E-01	H41571.1	EST_HUMAN	Yn18103.s1 Soares adult brain N2654B557 Homo sapiens cDNA clone IMAGE:176767 3' similar to gb:578187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8423	21392	34803	0.39	5.9E-01	AJ280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8532	21500	34916	2.57	5.9E-01	P14328	SWISSPROT	qh85d10.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8532	21500	34917	2.57	5.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
9243	22289	39540	9.71	5.9E-01	AJ270774.1	NT	Homo sapiens partial TOF-4 gene for T-cell transcription factor-4, exons 6-11
9323	22288	35718	1.02	5.9E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9324	22288	35719	0.46	5.9E-01	Q22471	SWISSPROT	PUTATIVE CASEIN KINASE I F4B2.2 IN CHROMOSOME X
9954	22881		0.81	5.9E-01	BF031608.1	EST_HUMAN	601557747F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11334	24284	37808	6.8	5.9E-01	AJ243213.1	NT	Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5
11373	24320		2.69	5.9E-01	BF700062.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11476	24419		1.61	5.9E-01	BF700062.1	EST_HUMAN	602127677F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
1492	14625	27496	1.11	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1492	14625	27497	1.11	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
3056	16113		0.77	6.7E-01	6755253	NT	Mus musculus plasminogen variant translocation 1 (Pvt1), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3237	19292	28214	1.38	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOV01A)
3516	16661		2.78	5.7E-01	AB033503.1	NT	Populus euphratica pices-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3922	19692	29876	1.05	5.7E-01	AF011591.1	NT	Homo sapiens T cell receptor beta chain (BV6S72-BJ1S1) mRNA, partial cds
5213	18222	31097	11.22	5.7E-01	4505050	NT	Homo sapiens lymphocyte antigen 8 complex, locus H (LY8H) mRNA
6490	19556	32806	4.36	5.7E-01	BF035413.1	EST_HUMAN	601484962.F11 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858560 5'
6869	19522	33218	0.82	5.7E-01	AA184201.1	EST_HUMAN	z338cd06.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:685674 5'
7042	18374	31282	1.3	5.7E-01	AL111440.1	NT	Betula cinnerea strain 14 cDNA library under conditions of nitrogen deprivation
8041	20078	34374	2.13	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8903	21272		0.61	5.7E-01	AJ251635.1	NT	Mus musculus Kcnq1, Lipe5, Mash2, Toga-1, Tesc4 and Tesc8 genes, alternative transcripts
8723	21691		0.52	5.7E-01	AJ050061.1	EST_HUMAN	HA0885 Human fetal liver cDNA library Homo sapiens cDNA
10159	23084	36560	1.22	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10169	23084	36561	1.22	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10940	23660	37376	0.75	5.7E-01	BF540952.1	EST_HUMAN	602067712.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
12262	26078		1.49	5.7E-01	BE716051.1	EST_HUMAN	NR3-HT0736-183700-003-a02 HT0736 Homo sapiens cDNA
1889	14914	27607	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
1899	14914	27608	1.6	5.6E-01	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
3376	16426	29351	1.53	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3378	16426	29352	1.63	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4268	18237	30174	0.71	5.6E-01	DB8135.1	NT	Chicken TBP gene, exon8, complete cds
5205	17297	31089	0.93	5.6E-01	BF032377.1	EST_HUMAN	601452855.F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3856717 5'
9155	22121	35550	14.66	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKG Homo sapiens cDNA clone GKCFSF05 5'
9155	22121	35551	14.66	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKG Homo sapiens cDNA clone GKCFSF05 5'
9730	22758	36211	1.23	5.6E-01	AB038762.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12163	25011		3.4	5.6E-01	BE886280.1	EST_HUMAN	601514007.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915487 5'
12270	25092	36176	1.73	5.6E-01	AA463435.1	EST_HUMAN	np76p10.e1 NCL_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:940674 similar to contains element P1R7 repetitive element1
12636	18341	31280	1.81	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12662	26540		3.06	5.6E-01	P60506	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13060	26596		4.66	5.6E-01	BF573829.1	EST_HUMAN	602132029.F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271834 5'
13110	26530		1.33	5.6E-01	AA683861.1	EST_HUMAN	ae74b04.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:998871 3'
1216	14254	27212	0.82	5.6E-01	8803912	NT	Rattus norvegicus Protophyll Coenzyme A carboxylase, beta polypeptide (Pcub) mRNA
2712	15706	28722	6.31	5.6E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	15706	28723	5.31	5.5E-01	P03341	SW/ISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12, CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2929	15997	28908	0.78	5.5E-01	6002085	NT	Homo sapiens superkiller virulicidic activity 2 (S. cerevisiae homolog) like (SKIVL2), mRNA
3079	16156		1.48	5.5E-01	H48218.1	EST_HUMAN	x018a10.01 Soares adult brain N265H5557 Homo sapiens cDNA clone IMAGE:178265 3'
3248	16303	29227	4.75	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3704	16747	29681	2.24	5.5E-01	P48755	SW/ISSPROT	POB-RELATED ANTIGEN-1
5203	18218	31094	1.08	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds
7467	20433	33789	0.58	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; CREB-RP, and tenascin X (TNX) genes, complete
7467	20433	33789	0.58	5.5E-01	AF030001.1	NT	Nolch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
7504	20469		0.87	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8702	21759	35181	0.66	5.5E-01	A1791769.1	EST_HUMAN	orb2c01.y6 NCI CGAP Jutb Homo sapiens cDNA clone IMAGE:1602336 5'
10125	23051		0.89	5.5E-01	U98416.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10743	23665	37160	0.87	5.5E-01	T05047.1	EST_HUMAN	EST02835 Fetal brain; Stralogene (ccl#336206) Homo sapiens cDNA clone HFB0035
148	13249	26178	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
148	13249	26179	9.02	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
587	13655	26566	1.34	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
587	13655	26570	1.34	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsA (gsA) genes, complete cds; and unknown genes
1278	14311	27272	2.93	5.4E-01	AW85087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2116	15133		2.81	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2265	15279	28304	2.28	5.4E-01	AJ276582.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5740	16934	32014	0.91	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c70 CN0030 Homo sapiens cDNA
6315	19386	32628	0.8	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIST1, complete cds
7228	20248	33582	0.77	5.4E-01	BE96592.2	EST_HUMAN	601660276R1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3906090 3'
7558	20521	33877	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7558	20521	33878	0.76	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) (INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE)
7560	20523	33381	1.78	5.4E-01	Q64428	SWISSPROT	602076545F1 NIH MG. 92 Homo sapiens cDNA clone IMAGE:4243690.5'
10349	23273		1.93	5.4E-01	BF572338.1	EST_HUMAN	
11414	24359	37893	2.19	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NAD(P)H] (NR)
11552	24589	38159	1.82	5.4E-01	AW373694.1	EST_HUMAN	QV4-BT0636-271289-089-H04 BT0636 Homo sapiens cDNA
11941	24821	38416	3.29	5.4E-01	Q60975	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11941	24821	38417	3.29	5.4E-01	Q60975	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
12215	25054		3.88	5.4E-01	A185398.1	EST_HUMAN	W37604.X1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126.3' similar to gb:U13452 LAMIN A (HUMAN);
517	13588	26508	1.86	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21- hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Sf), and complement component C2 (C2) genes >
2150	15168	28162	0.97	5.3E-01	AF13919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2160	15168	28183	0.97	5.3E-01	AF13919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2794	15786	28903	8.92	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2794	15786	28904	8.92	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3257	16311	20232	3.25	5.3E-01	AF087868.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4239	17268		1.33	5.3E-01	U39687.1	NT	Myoplasma genitalium section 9 of 51 of the complete genome
5633	18631	31569	2.06	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711.5'
5633	18631	31570	2.06	5.3E-01	A1820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:740711.5'
5633	18729	31890	0.76	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112.5'
5633	18729	31891	0.76	5.3E-01	AA193672.1	EST_HUMAN	zu42g09.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112.5'
5729	18823	32003	2	5.3E-01	BE645620.1	EST_HUMAN	7673c12.x1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:3288118.3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5729	18823	32004	2	5.3E-01	BE645620.1	EST_HUMAN	7673c12.x1 NCL_CGAP_P228 Homo sapiens cDNA clone IMAGE:3288118.3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9255	22221		1.94	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for repetitive element;
9307	22272	35703	0.76	5.3E-01	BF433968.1	EST_HUMAN	7671c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element;
9307	22272	35704	0.76	5.3E-01	BF433968.1	EST_HUMAN	7671c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10572	23494	36986	0.74	5.3E-01	A1654210.1	EST_HUMAN	wg4402.x1 NCI_CGAP_Met15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA, HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
10977	23697	37410	0.7	5.3E-01	11428833	EST_HUMAN	Homo sapiens nucleoporin 214KD (NUP214), mRNA
11888	24877	38354	6.19	5.3E-01	BE566261.1	EST_HUMAN	B01339887.F1 NIH_JMGC_33 Homo sapiens cDNA clone IMAGE:3882168 5'
12144	26776		4.97	5.3E-01	AA916053.1	EST_HUMAN	og30605.s1 NCI_CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb-J02611
817	13875	26822	16.24	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1168	14209	27163	7.88	5.2E-01	Q9WV30	SW/SSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-A15)
1195	14235	27190	3.01	5.2E-01	AF224492.1	NT	(NUEL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1003	14927		3.19	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2156	15172	28191	2.36	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3136	15193	29102	1.57	5.2E-01	U06942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3251	16306		1.14	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii tcd gene for isocitrate dehydrogenase, complete cds
3419	18464		1.39	5.2E-01	AL116780.1	NT	Batryllus cinereus strain T4 cDNA library under conditions of nitrogen deprivation
3458	16504	29424	2.72	5.2E-01	AA594165.1	EST_HUMAN	am77q05.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3848	16891		1	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mrh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5180	18189		1.04	5.2E-01	AL163291.2	NT	Homo sapiens chromosome 21 segment HS21C081
5736	18330	32008	1.02	5.2E-01	AA384261.1	EST_HUMAN	zc44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
10058	25700	36480	0.84	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10088	25700	36460	0.84	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10282	23217	36701	0.52	5.2E-01	AA194518.1	EST_HUMAN	zq06009.r1 Stratiogene nucleic acid 337209 Homo sapiens cDNA clone IMAGE:628783 5'
10367	23309	36787	1.76	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13031	25678		6.82	5.2E-01	P18516	SW/SSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
818	13694	26602	2.34	5.1E-01	M88609.1	NT	Human adrenocortical reductase gene, exons 3 to 12
849	13715	26536	3.53	5.1E-01	AL233944.1	NT	Polyglutamine vitellin (strain PI vt1) 16S rRNA gene
849	13715	26537	3.53	5.1E-01	AL233944.1	NT	Polyglutamine vitellin (strain PI vt1) 16S rRNA gene
1660	14692		1.26	5.1E-01	X87885.1	EST_HUMAN	R.norvegicus mRNA for mammalian fusca protein
4103	17137	30032	4.81	5.1E-01	AU58495.1	EST_HUMAN	w39b12.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2427263 3'
4216	17245	30130	2.99	5.1E-01	P96380	SW/SSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6348	19417	32658	0.57	5.1E-01	BES41088.1	EST_HUMAN	B0103606.F1 NIH_JMGC_10 Homo sapiens cDNA clone IMAGE:346000 5'
6407	19475		0.83	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAU07 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7102	22036	33339	1.52	5.1E-01	R80873.1	EST_HUMAN	Y94a03.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8918	21884	36309	0.82	5.1E-01	AW809881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8918	21884	36310	0.62	5.1E-01	AW809881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
10043	22870	36437	4.3	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
10046	22973	36440	3.2	5.1E-01	W22302.1	EST_HUMAN	6951 Human retina cDNA 17sp01-cleaved sublibrary Homo sapiens cDNA not directional
10521	23443	36941	0.89	5.1E-01	M94578.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12264	25088	38174	2.09	5.1E-01	BF40777.1	EST_HUMAN	602007471F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069744 5'
12368	25709		2.47	5.1E-01	BF030207.1	EST_HUMAN	601568683F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828767 5'
12811	25310		3.92	5.1E-01	BF436982.1	EST_HUMAN	nae0110.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to containe element
2144	15161	28176	0.97	5.0E-01	4885552	NT	TAR1 repetitive element
2144	15161	28177	0.87	5.0E-01	4885552	NT	Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmitotic segregation increased 2-like 9 (PMS2L9), mRNA
2154	15170	28187	2.39	5.0E-01	AF08210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL DNA biosynthesis initiating protein (dnaA), ATP operon (epiCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2154	15170	28188	2.39	5.0E-01	AF08210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL DNA biosynthesis initiating protein (dnaA), ATP operon (epiCDGAHFE), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2172	15188		0.91	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3761	16802	29714	0.8	5.0E-01	U56574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3842	16882	29786	1	5.0E-01	U38483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3887	16927	29835	2.74	5.0E-01	AB033910.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6801	19055		0.94	5.0E-01	BF576199.1	EST_HUMAN	602132842F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271593 5'
7928	20869	34256	0.66	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7928	20869	34257	0.66	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8875	21842		1.87	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8918	21884	35404	0.59	5.0E-01	BF107848.1	EST_HUMAN	60182350R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4043485 3'
9813	21136	34638	3.16	5.0E-01	BF417212.1	EST_HUMAN	601608971F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4156632 5'
9683	22910		1.31	5.0E-01	P35573	SW/ISSPROT	GLYCOSYL DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLYCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9683	22910	36376	1.31	5.0E-01	P35573	SW/ISSPROT	GLYCOSYL DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLYCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10766	23678		1.38	5.0E-01	BE869218.1	EST_HUMAN	601446024F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3849438 5'
12302	25113		6.28	5.0E-01	AF028215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13004	25658		2.21	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13011	25693		5.6	5.0E-01	O13661	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
780	13349	28768	2.03	4.8E-01	BF571462.1	EST_HUMAN	002076849F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243880 5'
1668	14700	27676	2.37	4.8E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1821	14849	27941	0.89	4.8E-01	Q01654	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
5480	18580	31491	1.43	4.8E-01	Q01554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6153	19228	32467	2.97	4.8E-01	AF020391.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6153	19228	32459	2.67	4.8E-01	AF020391.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7885	20543	34007	1.89	4.8E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7972	20911	34301	0.7	4.8E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYL-TRANSFERASE
7972	20911	34302	0.7	4.8E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYL-TRANSFERASE
9341	22006		1.77	4.8E-01	BF207871.1	EST_HUMAN	601874964F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4102503 5'
9542	22505	35954				EST_HUMAN	h50c002.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714
9651	26009		0.99	4.8E-01	AW339905.1	EST_HUMAN	O68714 HERC2
10851	26033		2.64	4.8E-01	10648803	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10881	26033	37097	0.96	4.8E-01	AF053580.1	NT	Mus musculus ednrm1 cyclase 1 (Adyrl) cDNA, partial cds
10888	26039	37314	0.57	4.8E-01	X90000.1	NT	H. sapiens DNA for BCL7A gene and BCL7A/IGH locus fusion
12186	25041		1.41	4.8E-01	AF176912.1	EST_HUMAN	Homo sapiens neurotrophin-1B-cell stimulating factor-3 gene, complete cds
12997	25693		6.43	4.8E-01	AA613562.1	EST_HUMAN	ng22a11.st NCI_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1144652 3'
							Secchiaromyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5585	18081	31649	8.83	4.8E-01	J02987.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
6936	19899	33184	0.69	4.8E-01	U92862.1	EST_HUMAN	nu8509.st NCI_CGAP_AYT Homo sapiens cDNA clone IMAGE:1217813
6946	19899		3.82	4.8E-01	AA658878.1	EST_HUMAN	Homo sapiens reproduction 8 (D8S2298E) mRNA
7538	20501		1.99	4.8E-01	5031650	NT	Homo sapiens chromosome 21 segment HS21C009
7929	20872	34281	0.78	4.8E-01	AL163209.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8037	20874	34366	3.96	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8037	20874	34370	3.96	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
							MERS repetitive element
8237	21206	34611	0.98	4.8E-01	AJ820744.1	EST_HUMAN	PM1410350-201298-004-304 HT0350 Homo sapiens cDNA
9800	22304		0.97	4.8E-01	BE155149.1	EST_HUMAN	PM1410350-201298-004-304 HT0350 Homo sapiens cDNA
10368	23291		0.56	4.8E-01	BF968633.1	EST_HUMAN	002184287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
11081	24043		1.75	4.8E-01	X83502.1	NT	S. cerevisiae ORFs from chromosome X

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12277	25096		1.65	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12503	25737		3.32	4.8E-01	AF227555.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
13083	25768		1.49	4.8E-01	AJ132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6564	19721	32866	8.88	4.7E-01	BF27173.1	EST_HUMAN	60188360F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:406387.5'
7241	19976	33273	0.92	4.7E-01	AI204374.1	EST_HUMAN	q172a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:175544.3'
8197	21107	34577	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811.5'end
8197	21167	34578	0.59	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811.5'end
9430	22394	35634	0.57	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11193	24146		4.78	4.7E-01	AF102873.1	NT	Influenza A virus isolate h61597 hemagglutinin (HA) gene, partial cds
11422	24366	37801	1.78	4.7E-01	U41069.1	NT	Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 16, and partial cds
11613	24551	38111	1.74	4.7E-01	BF62958.1	EST_HUMAN	60204388F1 NCI_CGAP_Bln7 Homo sapiens cDNA clone IMAGE:4181303.5'
11704	24669	38246	1.49	4.7E-01	AW839448.1	EST_HUMAN	RC8-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12929	25173		1.93	4.7E-01	BE87763.1	EST_HUMAN	60151333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912465.5'
12929	25173		1.38	4.7E-01	BF676515.1	EST_HUMAN	602163926F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4294974.5'
3759	18798	29709	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481.5'
3759	18798	29710	1.53	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481.5'
5180	18109		0.93	4.6E-01	M11267.1	NT	Bovine stacid 21-hydroxylase gene (P-450-c21) gene, complete cds
5463	18593	31503	1	4.6E-01	BF313593.1	EST_HUMAN	60160234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472.5'
5483	18593	31504	1	4.6E-01	BF313593.1	EST_HUMAN	60160234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472.5'
5548	18545	31586	3.33	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5548	18545	31587	3.33	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5923	19721	31880	1.95	4.6E-01	BE734761.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637.5'
5923	19721	31880	1.95	4.6E-01	BE734761.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637.5'
5939	18735	31897	3.12	4.6E-01	AI247679.1	EST_HUMAN	q159102.x1 Soares_testis_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011.3' similar to
5939	18735	31898	3.12	4.6E-01	AI247679.1	EST_HUMAN	q159102.x1 Soares_testis_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849011.3' similar to
5947	18743	31906	1.46	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5730	18824		0.85	4.6E-01	AF212124.1	NT	Anolis schwartzii cytochrome b gene, partial cds; mitochondrial product
5921	18811		0.78	4.6E-01	BE817247.1	EST_HUMAN	Pfmo-BN0290-120600-001-F07 BN0260 Homo sapiens cDNA
6002	19085	32285	0.51	4.6E-01	D26215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6002	19085	32285	0.51	4.6E-01	D26215.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6386	19454	32699	0.92	4.6E-01	AE000894.1	NT	complete genome
6881	19833	33231	0.52	4.6E-01	AF115340.1	NT	Bacillus subtilis Bbm (ubm) gene, complete cds

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6032	20156	33474	1.43	4.8E-01	U62332.1	NT	Emricella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6032	20156	33475	1.43	4.8E-01	U62332.1	NT	Emricella nidulans NEMPA (nempa) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7441	25981	33759	0.83	4.8E-01	L07320.1	NT	Murine cytochrome b5 gene, complete cds
8001	20840	34333	0.78	4.8E-01	AA493577.1	EST_HUMAN	h04h05 st NCI CGAP Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8093	21029	34333	0.63	4.8E-01	AEC04031.1	NT	Xyella fastidiosa, section 177 of 229 of the complete genome
8063	21631	36062	13.26	4.8E-01	BF607399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4267628.5
9099	22065	35490	0.47	4.8E-01	AA932237.1	EST_HUMAN	0676008 st NCI CGAP Kds Homo sapiens cDNA clone IMAGE:1572087.3 similar to gb:M36341 ADP.
9099	22065	35491	0.47	4.8E-01	AA932237.1	EST_HUMAN	0676008 st NCI CGAP Kds Homo sapiens cDNA clone IMAGE:1572087.3 similar to gb:M36341 ADP.
9056	22599	36048	0.99	4.8E-01	P55202	SW/ISSPROT	RIBOSYLATION FACTOR 4 (HUMAN);
9056	22599	36049	0.96	4.8E-01	P55202	SW/ISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10024	22851	36418	0.99	4.8E-01	AF162283.1	NT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
10024	22851	36419	0.99	4.8E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10335	23259	36736	1.52	4.8E-01	AB115634.1	EST_HUMAN	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10335	23259	36737	1.62	4.8E-01	AB115634.1	EST_HUMAN	wg73a12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766.3
11335	24285	37618	2.28	4.8E-01	P96163	SW/ISSPROT	wg73a12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766.3
11343	24293	37618	4.94	4.8E-01	BE185449.1	EST_HUMAN	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
11445	24388	37618	3.98	4.8E-01	BE27325.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11769	23954	37476	4.41	4.8E-01	BE27325.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11769	23954	37477	4.41	4.8E-01	AF019399.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12449	25208	37477	1.69	4.8E-01	D53316.1	EST_HUMAN	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
1718	14748	27949	0.92	4.8E-01	BE311420.1	EST_HUMAN	HUMT06F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN:105F03
1926	14950	27949	1.34	4.8E-01	AE001831.1	NT	5'
1926	14950	27947	1.34	4.8E-01	AE001831.1	NT	601142705F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505993.5
							Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
							Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2881	15940	28857	5.38	4.9E-01	AA677088.1	EST_HUMAN	255d02.e1 Soares, fetal_liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3328	16379	29300	3.85	4.9E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3369	16438	26364	1.62	4.9E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4060	17098		1.23	4.9E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4101	17135	30030	1.12	4.9E-01	AI708908.1	EST_HUMAN	aa9609.xt Barstead acra HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4205	18325	4205	4.08	4.9E-01	AW873485.1	EST_HUMAN	h06002.xt Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4890	17595	30984	1.09	4.9E-01	BE893445.2	EST_HUMAN	6016572591 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866023 3'
5828	18724	31885	1.3	4.9E-01	AW608314.1	EST_HUMAN	QV24.PT0012-140100-031-c09 P10012 Homo sapiens cDNA
6760	19814		1.74	4.9E-01	Q00098	SWISSPROT	COAT PROTEIN
7844	20804	33699	0.93	4.9E-01	M37036.1	NT	Rat nuclear protein B23.1 and B23.2
7887	20811	34188	2.64	4.9E-01	AI858849.1	EST_HUMAN	w32e02.xt NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
7991	20320	34325	0.51	4.9E-01	P60070	SWISSPROT	SWISNF COMPLEX 170 KDA SUBUNIT ;
8950	21618		0.87	4.9E-01	M32661.1	NT	DNA PRIMASE
8746	21714	35137	3.86	4.9E-01	AI848596.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
							t255g11.xt NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
8905	21871	35297	0.74	4.9E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
9133	22099		1.72	4.9E-01	11444786	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9351	22316	35742	0.78	4.9E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
10300	23225		0.89	4.9E-01	9630816	NT	Homo sapiens hypothetical protein DKFZp547G7183 (DKFZp547G7183), mRNA
10661	23781	37281	29.2	4.9E-01	M86006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10861	23781	37282	26.2	4.9E-01	M86006.1	EST_HUMAN	Bombay mori nuclear poly(hydroxy) virus, complete genome
11212	24165	37695	2.3	4.9E-01	AW591271.1	EST_HUMAN	EST02551 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
12165	25955		5.3	4.9E-01	BE871461.1	EST_HUMAN	EST02551 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
12349	25744		1.48	4.9E-01	O18838	SWISSPROT	xe1401.xt NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:270385 3' similar to SW:INT8_MOUSE
12462	26211		1.64	4.9E-01	AI132045.1	NT	Q64282 VIRAL INTEGRATION SITE PROTEIN INT-6 [1];
12891	25478		8.22	4.9E-01	11422099	NT	Q64282 VIRAL INTEGRATION SITE PROTEIN INT-6 [1];
2052	15071		2.23	4.9E-01	6630503	NT	OUT AT FIRST PROTEIN
							Thelazia errulata ahaT2 gene
							Homo sapiens testis-specific kinase 2 (TESK2), mRNA
							Mus musculus integral membrane-associated protein 1 (Imagp1), mRNA
2398	15405	28430	7.02	4.9E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)

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3326	16377	29298	1.96	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3326	16377	29299	1.96	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3330	16381	28302	1.8	4.4E-01	BF068726.1	EST_HUMAN	701d02.YT NCI CGAP Br18 Homo sapiens cDNA clone IMAGE:3393786 5'
4282	17281		1.75	4.4E-01	BE378707.1	EST_HUMAN	801231139.F1.NH.MGC.44 Homo sapiens cDNA clone IMAGE:3603693 5'
5494	18594	31505	1.63	4.4E-01	PO4828	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5494	18594	31506	1.63	4.4E-01	PO4828	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5772	18864	32045	1.71	4.4E-01	SG65019.1	NT	muslin [rat, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 360 nt]
5790	18882	32064	1.82	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLC05G12 5'
6094	19145	32356	1.42	4.4E-01	A1198413.1	EST_HUMAN	q62h11.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6094	19145	32357	1.42	4.4E-01	A1198413.1	EST_HUMAN	UNKNOWN PROTEIN ;
6388	19436	32680	1.9	4.4E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN ;
6462	19527		1.17	4.4E-01	AA776132.1	EST_HUMAN	ae55d11.at Stratagene kinase brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
7627	20487	33950	0.85	4.4E-01	AE000571.1	NT	TYROSINE-PROTEIN KINASE LYN (HUMAN);
8173	21443		12.88	4.4E-01	Z11879.1	NT	Helicobacter pylori 26695 strain 49 of 134 of the complete genome
8173	21443		12.88	4.4E-01	Z11879.1	NT	S. tuberosum mRNA for induced a100n tip protein (partial)
9116	22081	35609	0.74	4.4E-01	AA058427.1	EST_HUMAN	3168a03.s1 Stratagene colon (4637204) Homo sapiens cDNA clone IMAGE:509836 3'
9506	22469	35913	0.72	4.4E-01	AF112540.1	NT	HIV-1 isolate 081076 from USA, envelope glycoprotein (env) gene, partial cds
9538	22501	35949	0.68	4.4E-01	AW612578.1	EST_HUMAN	h105c08.x1 NCI CGAP_Kdr11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:M5SH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9845	22559	36038	1.21	4.4E-01	OB2839	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10321	23245	36725	2.1	4.4E-01	A126850.1	EST_HUMAN	qs9709.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910821 3'
10322	23246		3.91	4.4E-01	P28622	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10457	23379	36972	5.07	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10740	23562	37155	1.27	4.4E-01	S76404.1	NT	beta-HKA-H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10740	23562	37157	1.27	4.4E-01	S76404.1	NT	beta-HKA-H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
12432	25198	31624	5.78	4.4E-01	6877874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12687	25535	31727	2.83	4.4E-01	9627742	NT	Autographa californica nucleopolydnavirus, complete genome
12687	25535		1.45	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
411	13484	26419	2.49	4.3E-01	AF156218.1	NT	Callinectes jactans MW/LW opsin gene, upstream flanking region
411	13484	26420	2.49	4.3E-01	AF156218.1	NT	Callinectes jactans MW/LW opsin gene, upstream flanking region
1607	14639	27816	0.96	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-B01 SN0024 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2883	15942		1.83	4.3E-01	AW935268.1	EST_HUMAN	GM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3073	16130	28042	0.94	4.3E-01	AW698477.1	EST_HUMAN	MFO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4178	17209	30093	1.32	4.3E-01	U00308.1	NT	Human conotoxin 1 gene and flanks
4435	13484	28419	1.53	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4435	13484	28420	1.63	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5154	18164		1.17	4.3E-01	8635250	NT	Xestia c-nigrum granulovirus, complete genome
5291	18298	31157	1.16	4.3E-01	BE780182.1	EST_HUMAN	801468030F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3871255 5'
5438	18540	31449	0.88	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BATZ (HLA-B-ASSOCIATED TRANSCRIPT 2)
5438	18540	31450	0.89	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BATZ (HLA-B-ASSOCIATED TRANSCRIPT 2)
5990	19075	32273	1.5	4.3E-01	BE181855.1	EST_HUMAN	QV1-HT0638-070500-191-408 HT0638 Homo sapiens cDNA
6010	19093	32293	1.83	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6866	19919	33214	4	4.3E-01	AJ001678.1	NT	Columba columba japonica lncg gene
7049	20071		0.85	4.3E-01	Q33567	SWISSPROT	DNA GYRASE SUBUNIT B
7652	20622		1.83	4.3E-01	BF346001.1	EST_HUMAN	802023134FT NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158295 5'
8116	21053		0.62	4.3E-01	M58843.1	NT	Human lipoprotein associated coagulation inhibitor (LACI) gene, exon 2
8770	21737		2.69	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flac-fla) genes, complete cds
9810	22814	35068	1.04	4.3E-01	Y14904.1	NT	Erwinia amylovora rcaV gene
10084	23011	36463	1.88	4.3E-01	AW693048.1	EST_HUMAN	h74010.Y1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:268554 5'
10084	23011	36484	1.68	4.3E-01	AW693048.1	EST_HUMAN	h74010.Y1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:268554 5'
10589	23511	37005	0.85	4.3E-01	AW170559.1	EST_HUMAN	trf6305.x1 Soares_NHOCc cervical tumor Homo sapiens cDNA clone IMAGE:2688400 3' similar to
10879	23789	37301	0.48	4.3E-01	H65292.1	EST_HUMAN	trf6305.x1 Soares_fetal liver spleen TNFHS Homo sapiens cDNA clone IMAGE:208203 3'
11277	24180	35503	1.95	4.3E-01	AF075628.1	NT	Equus caballus microsatellite LEX027
11539	24748	39031	1.77	4.3E-01	AW693658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
11539	24748	39032	1.77	4.3E-01	AW693658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
13035	25592		2.24	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1360	15855	27365	1.77	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3623	16886	29680	1.43	4.2E-01	AE03047.1	NT	XJella testidosa, section 53 of 229 of the complete genome
3651	19894	29809	1.04	4.2E-01	AI280338.1	EST_HUMAN	q9b401.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879045 3'
3724	18324		1.22	4.2E-01	N81203.1	EST_HUMAN	789E1 fetal brain cDNA Homo sapiens cDNA clone 789E1-K similar to R07879, Z40498
3833	16933	29843	0.60	4.2E-01	AW693527.1	EST_HUMAN	QVQ-LT0015-180200-127-R01 LT0015 Homo sapiens cDNA
4007	17046	29953	1.72	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4726	17746	30637	4.9	4.2E-01	AA534093.1	EST_HUMAN	h98h01.s1 NCL CGAP_P10 Homo sapiens cDNA clone IMAGE:95777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4820	17837	30735	3.62	4.2E-01	R13487.1	EST_HUMAN	Y77601.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5801	18893	32076	1.38	4.2E-01	BF242035.1	EST_HUMAN	601879721F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4108493 5'
5876	18955	32166	1.23	4.2E-01	AW954162.1	EST_HUMAN	RC3-C10254-060400-029-g04 C10254 Homo sapiens cDNA
6329	19398	32841	0.91	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS210247
7139	20116	33428	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7139	20115	33428	9.39	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7201	25871	33563	5.51	4.2E-01	S82304.1	NT	Breast-invasive cancer gene (rat, WF, spleen, Genomic, 419 nt, segment 2 of 2)
7300	20272	33807	5.9	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7822	20770	34146	0.52	4.2E-01	AL165282.2	NT	Homo sapiens chromosome 21 segment HS210052
8325	21294	34706	2.56	4.2E-01	AW957448.1	EST_HUMAN	EST3369413 MAGE resequences, MAGE Homo sapiens cDNA
8325	21294	34709	2.56	4.2E-01	AW957448.1	EST_HUMAN	EST3369413 MAGE resequences, MAGE Homo sapiens cDNA
8548	21516	34834	0.49	4.2E-01	4758038	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
10329	23253		0.72	4.2E-01	AA705007.1	EST_HUMAN	Z95901.s1 Soares fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10541	23463	36958	0.43	4.2E-01	AF181854.1	NT	Lessa virus strain 603213 glycoprotein precursor and nucleoprotein genes, complete cds
10862	23782	37283	1.53	4.2E-01	AW863695.1	EST_HUMAN	MR3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
11382	24329	37569	2.39	4.2E-01	AB023489.1	NT	Oryzias latipes OIGCT mRNA for membrane guanylyl cyclase, complete cds
11723	24609	38186	1.77	4.2E-01	BE066485.2	EST_HUMAN	60166035R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806085 3'
13090	25618		1.4	4.2E-01	AI392837.1	EST_HUMAN	g10055.x1 NCL CGAP, CLT1 Homo sapiens cDNA clone IMAGE:2108360 3'
1105	14149	27090	1.96	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210188-142 BT091 Homo sapiens cDNA clone
1096	14140	27096	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1105	14149	27100	1.33	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2722	15716	28734	1.43	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2951	16008	28832	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
2951	16008	28933	2.07	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3314	16367	29287	0.69	4.1E-01	AA900344.1	EST_HUMAN	g164508.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4303	17322	30212	2.54	4.1E-01	AI242027.1	NT	Rhodococcus sp. AD45 isoA, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ



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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9445	22409	35846	1.45	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Slpeo-pending), mRNA
9923	22807		0.58	4.1E-01	AF160597.1	NT	Voelvo gymnocaudus Vgym590 cytochrome b (cytb) gene, complete cds; mitochondrial gene for
10628	23548		1.18	4.1E-01	AF138078.2	NT	mitochondrial product
10776	23696	37184	1.1	4.1E-01	AF849578.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome, segment 3/6
10873	23793	37294	0.61	4.1E-01	P18584	SWISSPROT	AV849578 GUC Homo sapiens cDNA clone GLC8VD12.3
10873	23793	37295	0.61	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK559)
10943	23883		2.1	4.1E-01	BF346382.1	EST_HUMAN	GL2-HT10137-200593-010-e08 HT10137 Homo sapiens cDNA
11188	24144	37877	39.55	4.1E-01	X58700.1	NT	Zea mays ZMPSNS2 gene for 16 KDa zein protein
12751	25831		3	4.1E-01	D87875.1	NT	Homo sapiens DNA for anyold precursor protein, complete cds
142	15833		0.65	4.0E-01	AW84723.1	EST_HUMAN	RG2-CT0201-280588-012-d10 CT0201 Homo sapiens cDNA
1040	14085	27036	0.71	4.0E-01	8404656	NT	Lequeus rubellus mitochondrion, complete genome
1342	14377	27346	1.17	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm) mRNA, complete cds
1481	14514		5.11	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2022	15883	28054	1.12	4.0E-01	Z69933.1	NT	Aerobolus immersus msc2 gene
2167	15183	28203	1.09	4.0E-01	AE001931.1	NT	Aerobolus immersus msc2 gene
2167	15183	28204	1.09	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2816	13246	28176	1.27	4.0E-01	6679460	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2878	16537	28959	1.34	4.0E-01	AL163280.2	NT	Mus musculus ubiquitin-protein ligase e3 component h-recogin (Ubr1), mRNA
2979	16037	28960	1.34	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C090
							Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide transferase (murA) genes, complete cds
3709	16752	28968	2.32	4.0E-01	AF068903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3840	16880	29783	3.28	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3840	16880	29784	3.28	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4655	17872		9.36	4.0E-01	Q31849	SWISSPROT	EST382681 IMAGE sequences, MAGK Homo sapiens cDNA
8015	18068	32289	1.14	4.0E-01	AW870810.1	EST_HUMAN	801877853FT NIH_MGC 565 Homo sapiens cDNA clone IMAGE4106221 5'
6226	18300	32533	0.51	4.0E-01	BF243741.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE (P130) (CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 8 KD PEPTIDE)
6578	18658	32904	0.92	4.0E-01	P27285	SWISSPROT	Homo sapiens OCTN2 gene, complete cds
8345	21314	34729	0.8	4.0E-01	AB016625.1	NT	EST128068 Carabellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
9360	22325	35753	0.98	4.0E-01	AA323289.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11895	24776		2	4.0E-01	BF030282.1	EST_HUMAN	601568288FT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12030	24906		1.75	4.0E-01	L76030.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12448	25793		3.03	4.0E-01	AL153300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12968	26538		1.6	4.0E-01	P59049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STES INTERGENIC REGION
1378	14412	27383	1.65	3.9E-01	AF206518.1	NT	Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2850	15847	28970	3.62	3.9E-01	AB033018.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2716	15710	28726	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2718	15710	28727	4.26	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3113	18170	29050	4.95	3.9E-01	AJ225866.1	NT	Simulium mellid egl, syB2, cys3 genes and orf3
4106	17140	30035	1.25	3.9E-01	BF592011.1	EST_HUMAN	781d01.xt NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339189 3'
5027	18041	30024	1.74	3.9E-01	BE728697.1	EST_HUMAN	601563948FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6042	19124	32329	5.95	3.9E-01	BF203038.1	EST_HUMAN	601862362FT NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6411	19478	32726	0.66	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8286	21265	34064	0.8	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase I (DPP-I) gene, complete cds
9213	22179	35610	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM3-GT0105-170899-004-D08 GT0105 Homo sapiens cDNA
9222	22188		0.68	3.9E-01	BF346534.1	EST_HUMAN	602018944FT NCI_CGAP_Br67 Homo sapiens cDNA clone IMAGE:4155322 5'
9390	22552	36003	1.41	3.9E-01	AW195888.1	EST_HUMAN	chr6p04.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701951 3' similar to TR-094821
9803	22855	39316	1.83	3.9E-01	A1937337.1	EST_HUMAN	094821 KIAA0713 PROTEIN;
10237	23162	36550	2.69	3.9E-01	M19679.1	NT	wp76a02.x1 NCI_CGAP_Br25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW-REF5_HUMAN P48382 BINDING REGULATORY FACTOR.1
10305	23230		0.46	3.9E-01	11485620	NT	Human cladinin 27 gene, exons 10 and 11, and L1 and Alu repeats
10365	23249	36947	0.82	3.9E-01	D68722.1	NT	Porphyra purpurea mitochondrion, complete genome
10527	23449	37397	0.48	3.9E-01	M18440.1	NT	Nicotiana glauca mRNA for TATA binding protein (TBP), complete cds
10985	23865		0.48	3.9E-01	M18440.1	NT	Human beta-82-crystallin (B2-1) gene, exon 4, partial cds
12219	25868		4.08	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
12344	28142		2.01	3.9E-01	Q161670	SWISSPROT	HOMEOBOX PROTEIN HLX1
12840	25452		1.49	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10588 (FLJ10588) mRNA
161	13284		9.02	3.8E-01	7019488	NT	Homo sapiens protein kinase PKXbeta (pkxbeta), mRNA
506	13577		0.8	3.8E-01	AB026291.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
1888	14911		1.19	3.8E-01	AE003870.1	NT	Xyella fastidiosa, section 16 of 229 of the complete genome
2465	15459	28493	1.24	3.8E-01	U41846.1	NT	Ceanothus bignoniifolius brignase acetylcholinesterase (ace-1) gene, complete cds
2577	15578	28597	2.26	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB9R-3) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2840	15900	28692	4.89	3.8E-01	6678002	NT	Mus musculus salivary carrier family 1, member 6 (Sicr6b), mRNA
3015	16073		0.89	3.8E-01	AL251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3081	18118	28033	2.11	3.8E-01	AF043933.1	NT	Plasmodium falciparum aminopeptidase N (ampN) gene, partial cds
3495	16542	29466	8.24	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3549	16566		0.75	3.8E-01	AB07219.1	EST_HUMAN	W38812.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357655 3'
3568	16595		0.87	3.8E-01	AB07219.1	EST_HUMAN	W38812.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357655 3'
3709	16811	29720	0.99	3.8E-01	BE154090.1	EST_HUMAN	PMD-HT0339-200405-010-G01 HT0339 Homo sapiens cDNA
5691	18786	31667	1.08	3.8E-01	Q04889	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6473	19538		0.6	3.8E-01	S46825.1	NT	p10n protein [mink, Genomic, 24-48 nt]
6779	19834	33117	5.49	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271295-049-602 BT0537 Homo sapiens cDNA
6924	20148	33468	4.76	3.8E-01	AB374601.1	EST_HUMAN	Y54711.X1 Soares_total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7128	20059	33565	1.24	3.8E-01	AL161513.2	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7743	20697	34063	0.67	3.8E-01	AA626274.1	EST_HUMAN	Zu86035.s1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:745064 3'
7759	20712		4.27	3.8E-01	X81607.1	NT	M.musculus gene for kallikrein-binding protein
7693	20937	34331	0.49	3.8E-01	V00693.1	NT	Yeast mitochondrial gene for A1'Pase (genes oli-2 and oli-4)
8640	21608	35031	0.45	3.8E-01	N81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8903	21869	35294	2.04	3.8E-01	AB048851.1	NT	Homo sapiens mRNA for KIAA1831 protein, partial cds
8972	21938	35363	0.79	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9159	22135	35561	1.47	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9919	22740		6.02	3.8E-01	T05413.1	EST_HUMAN	Y64305.r1 Soares fetal liver spleen 'NFLS' Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTRS repetitive element ;
11882	24744		3.41	3.8E-01	BE176219.1	EST_HUMAN	RCQ-HT0841-040900-532.b12 HT0841 Homo sapiens cDNA
12000	24877	39473	2.61	3.8E-01	R42560.1	EST_HUMAN	Y62H11.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:30289 3'
12000	24877	39474	2.61	3.8E-01	R42560.1	EST_HUMAN	Y62H11.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:30289 3'
12433	25199		4.23	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12557	25898		2.63	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12667	25343		2.84	3.8E-01	BE826256.1	EST_HUMAN	QV3-ET0093-160700-271-405 ET0093 Homo sapiens cDNA
13056	25954		2.03	3.8E-01	AF281463.1	NT	Mus musculus vomeronasal receptor V1R44 (V1r44) gene, complete cds
13063	25995	31422	1.4	3.8E-01	T54787.1	EST_HUMAN	Y642011.s1 Striatagene fetal spleen (H937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:AO69177 SERUM ALBUMIN PRECURSOR (HUMAN)
13080	26611	31660	1.57	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2490	15403	28518	12.56	3.7E-01	AB037631.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3474	16520	29442	11.71	3.7E-01	AF056396.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3884	18824	29833	0.7	3.7E-01	AA316482.1	EST_HUMAN	EST12115 Adrenal gland tumor Homo sapiens cDNA 5' end
4257	17259	30168	0.92	3.7E-01	AI218707.1	EST_HUMAN	Q69607.X1 Soares_NSF_Fg_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510180 3'
4348	17375	30255	1.84	3.7E-01	AW878037.1	EST_HUMAN	MF3-OT007-090300-104-b02 OT007 Homo sapiens cDNA
4416	17443	30334	3	3.7E-01	AE002408.1	NT	Nelasetra meningioidis serogroup B strain MC58 section 50 of 208 of the complete genome
5857	18947	32132	1.18	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (IX1) gene, complete cds
6080	19141	32353	1.35	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6550	19716	32993	0.66	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6580	19737		0.77	3.7E-01	L10353.1	NT	Mus aedocia haploglobin mRNA, complete cds
7350	20320	33567	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA
7658	20618	33683	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:388652 5'
7658	20618	33884	0.65	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:388652 5'
8089	21006	34404	0.71	3.7E-01	T66802.1	EST_HUMAN	ye50607.r3 Soares fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:68324 5'
8872	21840	35084	1.83	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4) mRNA
8872	21840	35085	1.83	3.7E-01	11438739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4) mRNA
8708	21978	35101	0.69	3.7E-01	AA902912.1	EST_HUMAN	dk43011.s1 NCL_CGAP_La2 Homo sapiens cDNA clone IMAGE:1516791 3'
8558	22518		3.78	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15-dioxygenase (BCDO gene)
10530	23452		0.52	3.7E-01	K00691.1	NT	mouse Ig germline alpha membrane exon region
10570	23482	36984	3.69	3.7E-01	AI33441.1	EST_HUMAN	ql4607.X1 Soares_fetal_lung_NbH1L19W Homo sapiens cDNA clone IMAGE:1950997 3'
11205	24150	37889	1.9	3.7E-01	X05558.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11369	24316	37842	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11369	24316	37843	2.81	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11794	23949	37470	2.34	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12014	24891		1.53	3.7E-01	AA973540.1	EST_HUMAN	bc46403.s1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1569221 3' similar to gbM77698
12050	24933		3.22	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12136	25501		2.6	3.7E-01	J04082.1	NT	Mus musculus retinoblastoma 1 (Rb1) mRNA
12309	25117		4.23	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle A1P1ADP translocator (ANT1) gene, complete cds
12764	25406		1.86	3.7E-01	AL121154.1	EST_HUMAN	Chlamydomonas pallidus partial omp1 gene for outer membrane protein 1
12829	25447	31722	2.71	3.7E-01	Y16000.1	NT	DNF20762K075.r1 762 (synonym: hmb2) Homo sapiens cDNA clone DKFZ762K075 5'
	987		11.35	3.6E-01	U86241.1	NT	Homo sapiens NF2 gene
1317	14048		997	3.6E-01	U86241.1	NT	Human mltp gene, partial cds
1317	14352	27320	2.66	3.6E-01	T80255.1	EST_HUMAN	yc03065.r1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:24443 5'
1317	14352	27321	2.66	3.6E-01	T80255.1	EST_HUMAN	yc03065.r1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:24443 5'
1931	14955	27951	6.09	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1931	14955	27952	6.09	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1968	14989	27692	6.4	3.6E-01	AF216207.1	NT	Mus musculus fibronectin protein S18 (Rps19) gene, complete cds
2399	15408		3.56	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2463	15487	28510	1.29	3.6E-01	U05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2483	15487	28511	1.29	3.6E-01	U05435.1	NT	Rattus norvegicus synaptic vesicle protein (SV2) mRNA, complete cds
2495	16498	28524	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0177-181059-011-q07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2688	16637	28660	1.23	3.6E-01	P24206	SWISSPROT	ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE
2910	18322		5.89	3.6E-01	AF189485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3483	16529	29453	2.01	3.6E-01	X76755.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3483	16529	29454	2.01	3.6E-01	X76755.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4436	17462	30351	1.14	3.6E-01	BE707883.1	EST_HUMAN	RC1-H10545-150600-014-b12 H10545 Homo sapiens cDNA
4787	17805	30697	0.72	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5046	18058	30937	2.81	3.6E-01	AW339393.1	EST_HUMAN	had2gpa.x1 MCL CGAP LU24 Homo sapiens cDNA clone IMAGE:2872566 3'
5130	18145	31025	0.65	3.6E-01	BE067699.1	EST_HUMAN	MR4-B10358-270300-006-c10 B10358 Homo sapiens cDNA
5274	18280	31143	0.81	3.6E-01	AF087969.1	NT	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds
5274	18280	31144	0.81	3.6E-01	AF087969.1	NT	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds
6456	18558	31469	0.71	3.6E-01	AJ006965.1	NT	Homo sapiens lipo gene intron 5
							FORMATO HYDROGENLYASE SUBUNIT 8 PRECURSOR (PHL SUBUNIT 6) (HYDROGENASE-3 COMPONENT E)
6205	19279	32512	1.1	3.6E-01	P18431	SWISSPROT	Homo sapiens PHX gene
6623	19881	32958	1.8	3.6E-01	Y10156.1	NT	Homo sapiens PHX gene
7355	20325		3.63	3.6E-01	R94060.1	EST_HUMAN	X74608.r1 Soares fetal liver spleen 1NF1S3 Homo sapiens cDNA clone IMAGE:275987 5'
7600	20486	33828	1.86	3.6E-01	AW027174.1	EST_HUMAN	WT2010.x1 Soares_thymus_NHFT8 Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR-O18117
8506	21534	34954	0.64	3.6E-01	P88167	SWISSPROT	O15117 FYN BINDING PROTEIN [1]
8622	21590	35008	14.06	3.6E-01	AL161583.2	NT	SCO-SPONDIN
							Arabidopsis thaliana DNA chromosome 4, config fragment No. 79
9330	22295	35724	0.53	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Roctel gene, and sodium phosphate transporter (NPT3) gene, complete cds
9330	22295	35725	0.53	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Roctel gene, and sodium phosphate transporter (NPT3) gene, complete cds
9355	22320	35746	2.84	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

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9355	22320	35747	2.84	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9547	22510	35969	1.12	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9764	22885	36151	0.93	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9764	22885	36152	0.93	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9824	22673	36182	0.64	3.6E-01	X62825.1	NT	C. parvulus p16 gene for phospholipase C upstream region containing bent DNA fragment
10222	23147	36936	18.66	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4T5
10352	23276	36760	0.48	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211098-002-b10 CT0222 Homo sapiens cDNA
10352	23276	36751	0.48	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211098-002-b10 CT0222 Homo sapiens cDNA
11282	24242	37769	3.04	3.6E-01	BE002390.1	EST_HUMAN	301676418FT NIH_MGC: 21 Homo sapiens cDNA clone IMAGE:3958997 5'
11442	24385	37925	3.26	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11772	23827	37448	5.63	3.6E-01	AE000055.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12174	26868		2.05	3.6E-01	Y18210.1	NT	Homo sapiens hhr5 gene for hair keratin, exons 1 to 9
12247	25076		1.42	3.6E-01	D90901.1	NT	Synschoyella sp. PCC9803 complete genome, 3127, 271600-402289
12257	25083		6.35	3.6E-01	AE000395.1	NT	Escherichia coli K-12 MG1685 section 225 of 400 of the complete genome
12417	23187		6.26	3.6E-01	U69888.1	NT	Mus musculus Emr1 mRNA, complete cds
12770	25410		1.97	3.6E-01	11432568	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11h9ex) (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13033	25934		3.33	3.6E-01	AW190229.1	EST_HUMAN	X60e11.X1 NCI CGAP Part1 Homo sapiens cDNA clone IMAGE:2879116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
115	13226	26160	1.42	3.6E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
210	13311	26238	3.29	3.6E-01	6878933	NT	Mus musculus mannose receptor G type 2 (Mrc2), mRNA
728	13787	26722	1.48	3.6E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
728	13787	26723	1.48	3.6E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
790	13940	26765	4.95	3.6E-01	BF126795.1	EST_HUMAN	801811050FT NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4053951 3'
1623	14658	27634	0.96	3.6E-01	BF310688.1	EST_HUMAN	801894653F2 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4124244 5'
1648	14678	27651	2.67	3.6E-01	U36776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2291	15303	28328	1.28	3.6E-01	P06768	SWISSPROT	HOMEOBOX PROTEIN HOX-44 (HOX-1.4) (MH-3)
2613	15889	28638	1.13	3.6E-01	AA223252.1	EST_HUMAN	z08a09.s1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:660872 3'
3818	16856		7.27	3.6E-01	AA642138.1	EST_HUMAN	m66003.61 NCI CGAP Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4291	17320	30189	2.18	3.6E-01	AF071253.1	NT	Danio rerio homeobox protein (hox5b) gene, complete cds

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4922	17939	30831	0.7	3.5E-01	N81203.1	EST_HUMAN	789E1 total brain cDNA Homo sapiens cDNA clone 789E1-K similar to R078/9, Z60496
4699	17884	30874	6.46	3.5E-01	N18349.1	NT	Rat leukocyte common antigen (LCA) gene, exons 1 through 5
5407	18510	31387	0.84	3.5E-01	Q66687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5407	18510	31388	0.84	3.5E-01	Q66687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
6529	18226	31888	1.36	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6365	18434		0.77	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-at11 SN0012 Homo sapiens cDNA
6548	19809	32871	0.62	3.5E-01	AA431833.1	EST_HUMAN	zw7903.1.t Soares, testis, NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR-G1066035
6593	19653	32625	0.68	3.5E-01	U37160.1	NT	Bos laurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6821	19875	33184	0.92	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7257	19902		3.65	3.5E-01	X69505.1	NT	S. cerevisiae mRNA for CD31 protein (PECAM-1)
7769	20742	34115	0.81	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7769	20742	34116	0.81	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8023	20980	34358	0.77	3.5E-01	X06091.1	NT	E. coli L-arabinose transport operon with genes araF, araG and araH
8406	21375	34784	2.17	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8409	21378		0.87	3.5E-01	BF358871.1	EST_HUMAN	RC4-E70024-280600-014-807 ET0024 Homo sapiens cDNA
8810	21777		0.68	3.5E-01	AF061581.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9279	22248	35874	1.14	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10093	23018	36494	6.94	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL II) (BII)
10248	23171	36660	5.51	3.5E-01	Z26825.1	NT	X. laevis gene for albumin including HP1 enhancer
10326	23250	36728	1.01	3.5E-01	BE174794.1	EST_HUMAN	QV2-HT0677-090400-128-c07 HT0577 Homo sapiens cDNA
11088	24047	37069	2.48	3.5E-01	X67084.1	NT	C. gubeus rhodopsin gene for opsin protein
11362	24311	37838	1.68	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11362	24311	37839	1.68	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11919	24800	38361	1.67	3.5E-01	N71597.1	EST_HUMAN	Y290112.t Soares, multiple sclerosis, ZNBMHSP Homo sapiens cDNA clone IMAGE:280375 5'
11940	24820		1.77	3.5E-01	M82885.1	NT	Drosophila melanogaster dual bar protein (BarH2) gene, exon 1
11981	24868	38463	1.6	3.5E-01	L05145.1	NT	Human glucosylase (GCK) gene, repeat polymorphism
12269	25911		1.8	3.5E-01	AF287488.1	NT	Schistosoma mansoni strain NMR1 chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12341	25139		1.31	3.5E-01	X64685.1	NT	B.aurus apa1 gene for F0(F1) ATP synthase alpha-subunit
12501	28240		2.58	3.5E-01	AE001774.1	NT	Thermotoga maritima section 88 of 138 of the complete genome
13085	25842	31430	3.37	3.5E-01	H08014.1	EST_HUMAN	y64411.t Soares, retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
13085	25842	31431	3.37	3.5E-01	H08014.1	EST_HUMAN	y64411.t Soares, retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13106	25627		1.57	3.5E-01	4758297	NT	Homo sapiens v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neurofiblioblastoma derived oncogene homolog) (ERBB2), mRNA
708	13770		1.87	3.4E-01	AL242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
977	14028	26882	9.08	3.4E-01	Y08788.2	NT	Pseudomonas fluorescens coR, coS genes, orf222 and partial inaA gene
1329	14384	27332	2.76	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifH gene for NifA protein (positive regulatory element)
2410	15417	28441	2.01	3.4E-01	D90609.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3014	16072	28992	0.86	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3014	16072	28993	0.86	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3176	16230	29146	6.02	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3354	19405	29329	0.84	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3542	19588	29512	3.42	3.4E-01	AF108835.1	NT	Methylovorus sp. strain SS1 putative GpE (gpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3804	19844		1.78	3.4E-01	BF446010.1	EST_HUMAN	7b94d01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ15
4082	17116		1.48	3.4E-01	AA584189.1	EST_HUMAN	Q9UJ18 DU18C9.1 ;
4674	17695	30582	1.72	3.4E-01	BE06912.1	EST_HUMAN	nc11b10.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4889	18004		4.71	3.4E-01	AI240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5768	18860	32040	2.74	3.4E-01	AL161584.2	NT	q195.05.x1 NCL_CGAP_K103 Homo sapiens cDNA clone IMAGE:1667208 3' similar to contains Alu repetitive element
5909	18895		5.14	3.4E-01	AA085313.1	EST_HUMAN	Arabisopsis italiana DNA chromosome 4, contig fragment No. 90
6122	19200		1.74	3.4E-01	L02971.1	NT	zn12d11.s1 Stratagene RNT neuron (#837233) Homo sapiens cDNA clone IMAGE:347221 3'
6146	19221	32451	0.8	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 14B, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
9229	19303	32535	1.91	3.4E-01	AW204506.1	EST_HUMAN	00167161T1T1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:363628 3'
6392	19431	32674	1.78	3.4E-01	AL120544.1	EST_HUMAN	UHH-BH1-aal-e-12-Q-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6807	19959		1.19	3.4E-01	NG6225.1	EST_HUMAN	DKFZp761A249_11 T81 (synonym: hammy2) Homo sapiens cDNA clone DKFZp761A249 5'
7135	20111	33424	1.14	3.4E-01	AI468082.1	EST_HUMAN	zab3912.s1 Soares, fetal lung, NIHHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7281	19986	33283	0.81	3.4E-01	BF878702.1	EST_HUMAN	hm6305.x1 NCL_CGAP_Brr25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:537431
8238	21207		0.54	3.4E-01	AE000463.1	NT	LAMININ RECEPTOR (HUMAN);
8579	21547	34866	0.56	3.4E-01	Y14830.1	EST_HUMAN	002052829T1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248365 5'
8832	21769		1.8	3.4E-01	AA337083.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 393 of 400 of the complete genome
						NT	Homo sapiens TCRAV28 gene, allele A4, partial
						EST_HUMAN	EST41766 Endometrial tumor Homo sapiens cDNA 5' end



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
8909	21875	35301	0.64	3.4E-01	L04690.1	NT	Citabellus gileus cholesterol 7-alpha-hydroxylase gene, complete cds
9204	22170	35600	1.89	3.4E-01	9633624	NT	Bovine enarlovirus strain K2377, complete genome
9587	22529	35978	4.43	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9587	22529	35978	4.43	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9776	22717		0.49	3.4E-01	AB017510.1	NT	Ephydella fluviatilis mRNA for PLC-gamma8, complete cds
9801	21124	34527	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9801	21124	34528	6.03	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9845	22791	36243	0.43	3.4E-01	AF163857.1	NT	Dicystosellum discoideum putative GMP receptor CMFR1 mRNA, complete cds
10054	22881	36449	1.09	3.4E-01	U87763.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10249	23174	36654	2.14	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10843	23763		0.68	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11357	24307		3.51	3.4E-01	AE000981.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11393	24339	37869	4.96	3.4E-01	P09225	SWISSPROT	PROBABLE E4 PROTEIN
11427	24371	37909	1.87	3.4E-01	AF046981.1	NT	Rutillus arcuelli cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11828	24711	38295	1.66	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerol-3-phosphate dehydrogenase, complete cds
11866	24738	38323	3.3	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12098	24970	38557	1.9	3.4E-01	A155988.1	EST_HUMAN	ig7p05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2214874, 3' similar to contains L1.b1 L1
12149	25008		2.08	3.4E-01	U93504.1	NT	repetitive element ;
12281	25095		1.59	3.4E-01	Z21621.1	NT	Citrus variegation virus putative replicase gene, partial cds
12485	26231		13.04	3.4E-01	L26339.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12512	25761		3.88	3.4E-01	BE218652.1	EST_HUMAN	Human autoantigen mRNA, complete cds
12567	25895		2.19	3.4E-01	9833381	NT	hwa2108.x1 NCI_CGAP_U124 Homo sapiens cDNA clone IMAGE:3176127, 3' similar to contains PTR5.13
12673	25345	31763	3.49	3.4E-01	AJ287131.1	NT	beta vulgaris mitochondrion, complete genome
12972	25538		1.94	3.4E-01	AF019413.1	NT	Mus musculus S1L, MAP_17, CYP_1, SCL & CYP_1 genes
15	13195	26033	10.37	3.3E-01	X07980.1	NT	Homo sapiens HLA class III region containing unasci X (terasci-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKL2W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
106	13136	26033	4.34	3.3E-01	X07980.1	NT	Rhizobium leguminosarum syn plasmid pRL5.J1 nodX gene
448	13521	26454	1.3	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum syn plasmid pRL5.J1 nodX gene
534	13700	26621	2.28	3.3E-01	7662465	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
							Homo sapiens KIAA1100 protein (KIAA1100), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1205	14244	27203	3.29	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1310	14349	27312	2.44	3.3E-01	BF669890.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1610	14842	27618	1.55	3.3E-01	6733885	NT	Mus musculus disintegrin 5 (Dgn5), mRNA
1752	14781		1.13	3.3E-01	A432734.1	EST_HUMAN	EST5739722 Embryo, 8 week Homo sapiens cDNA 5' end
2043	15062		1.01	3.3E-01	AF031148.1	NT	Neurospora crassa capsularis strain Bain outer membrane protein MopB (mopB) gene, complete cds
2414	15421		4.45	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotidine phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2960	16018	28045	1.76	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
3028	16089		0.8	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P38)
3068	16125	29038	0.91	3.3E-01	AJ007832.2	NT	Streptomyces argillaceus mitramycin biosynthetic genes
3506	16553	29476	1.27	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3822	16862	29766	2.16	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3832	16872	29773	0.8	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3989	17029	29839	1.54	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4026	17084	29865	2.02	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4395	17423		1.51	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for resequencing, partial cds
4715	17735		1.41	3.3E-01	AI59914.1	EST_HUMAN	178b12.x1 NCL CGAP_U93 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gp.X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4875	17892	30781	1.33	3.3E-01	D64003.1	NT	Synectochytrid sp. FOC9803 complete genome, 22/27, 2755703-2668766
5397	18500	31377	2.48	3.3E-01	X88819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5397	18500	31378	2.48	3.3E-01	X88819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5664	18759	31928	0.55	3.3E-01	P36055	SWISSPROT	DYNAMIN
5664	18759	31929	0.55	3.3E-01	P36055	SWISSPROT	DYNAMIN
5894	18973	32166	0.61	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6056	19137	32247	1.75	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6056	19137	32248	1.75	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6154	19229	32459	0.82	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZONTE PROTEIN (CS)
6680	20165	33506	0.63	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6680	20165	33509	0.63	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7073	20095	33404	4.16	3.3E-01	AB28131.1	EST_HUMAN	164hd01.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285609 3' similar to contains Alu repetitive element/contains element L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7073	20095	33405	4.16	3.3E-01	AB28131.1	EST_HUMAN	364h01.x1 NCL CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2285609 3' similar to contains Alu repetitive element contains element L1 repetitive element;
8092	20090	34395	1.81	3.3E-01	N85148.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8098	21074	36300	22.63	3.3E-01	BF683954.1	EST_HUMAN	602140372F7F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
9080	22046	35469	0.66	3.3E-01	BF210322.1	EST_HUMAN	301873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9469	22433	35871				SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE KINASE 1) (MEK KINASE 1) (MEKK 1)
9733	22761	36215	0.98	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9733	22761	36218	0.98	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9889	22805	36258	2.8	3.3E-01	N69886.1	EST_HUMAN	Zet7101.s1 Soares_1661 Lung_NbHL19W Homo sapiens cDNA clone IMAGE:267849 3'
9910	22731	36186	2.61	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10350	23274		2.12	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
11076	24038	37561	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11076	24038	37562	2.85	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11365	24313		2.16	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCL CGAP_Bn604 Homo sapiens cDNA clone IMAGE:4213585 5'
11565	24505	38082	8.16	3.3E-01	BE219351.1	EST_HUMAN	hsv1g02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11673	24639	38218				SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (GBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP39)
12027	24903		3.19	3.3E-01	P47683	EST_HUMAN	hsv1g02.x1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12044	13135	26033	1.87	3.3E-01	AA908621.1	EST_HUMAN	Rhizobium leguminosarum sym plasmid pRL511 nodX gene
12246	25075	38170	1.94	3.3E-01	6598318	NT	Homo sapiens aldehyde oxidase 1 (AOX1) mRNA
12658	25530		4.82	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 267001-544000 nt. position (2/7)
13113	25932	31621	1.69	3.3E-01	BE312820.1	EST_HUMAN	301146730F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162000 5'
467	13530		2.08	3.3E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
719	13781		0.76	3.2E-01	AL181651.2	NT	Arabidopsis thaliana DNA chromosome 1, contig fragment No. 61
1168	14207	27161	10.6	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1287	14322	27885	1.77	3.2E-01	Z50202.1	NT	P.guillarzi acc-5.4 gene
1391	14425	27394	6.66	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1639	14671		0.9	3.2E-01	AF029730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1769	14818	27603	1.5	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1769	14828	27615	5.47	3.2E-01	AW657194.1	EST_HUMAN	EST1369284 IMAGE resequences, MAGD Homo sapiens cDNA
1789	14828	27616	5.47	3.2E-01	AW657194.1	EST_HUMAN	EST1369284 IMAGE resequences, MAGD Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1860	14886	27682	1.03	3.2E-01	AL111655.1	NT	Batrachia chereza strain T4 cDNA library under conditions of nitrogen deprivation
2168	16184	28205	2.33	3.2E-01	BF203877.1	EST_HUMAN	001688804FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:411612 5'
2948	15549		2.3	3.2E-01	7710079	NT	Mus musculus F304/ncp101 1 homeobox (Pbox1), mRNA
2720	15714	28732	1.56	3.2E-01	AF060568.1	NT	Homo sapiens promyelocyte leukemia zinc finger protein (PLZF) gene, complete cds
3822	16865		0.79	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4367	17594	30273	0.93	3.2E-01	4750195	NT	Homo sapiens synplekin (SYM) mRNA
4422	17449	30340	1.92	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4626	17551	30439	1.3	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 81 70 PROTEIN C13G7.04G IN CHROMOSOME 1 PRECURSOR
4767	17787		8.32	3.2E-01	BF693677.1	EST_HUMAN	602061872FT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4915	17932	30823	0.99	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5250	18258	31127	0.96	3.2E-01	A1008847.1	NT	Homo sapiens Interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5280	18286		4.18	3.2E-01	A1869472.1	EST_HUMAN	w25006.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2498195 3' similar to contains Alu repetitive element contains element PTK7 repetitive element
5344	18449	31320	2.71	3.2E-01	BE173964.1	EST_HUMAN	CNV0-HT0665-060300-266-f10 HT0669 Homo sapiens cDNA
6058	18749	32361	1.36	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6436	18502	32753				NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P56), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6749	18903	33084	0.81	3.2E-01	AF1718037.1	EST_HUMAN	AV1719377 FHTA Homo sapiens cDNA clone FHTAABH01 5'
6997	19049		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8189	21159	34689	0.44	3.2E-01	AJ277691.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8512	21480	34894	1.43	3.2E-01	M60286.1	NT	Rat ISO-alpha/nucleic factor gene, complete cds
8609	21577	34993	0.46	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12Wox1
8710	21678	35103	19.12	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit; exons 8, 9 and 3' flanking region
8713	21681	35108	17.12	3.2E-01	BF311635.1	EST_HUMAN	001897107FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8805	21772		1.54	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8845	21812	35231	1.13	3.2E-01	BF246771.1	EST_HUMAN	601855800FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8845	21812	35232	1.13	3.2E-01	BF246771.1	EST_HUMAN	601855800FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8919	21885	35311	2.13	3.2E-01	AE002015.1	NT	Drosophila melanogaster R1 section 152 of 220 of the complete chromosome 1
9019	21895	35405	0.63	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-42) gene, partial cds
9019	21895	35406	0.63	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-42) gene, partial cds

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Table 4

### Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9422	22387	35825	0.49	3.2E-01	AL183204.2	NT	Homo sapiens chromosome 21 segment H521G004
9432	22386		2.28	3.2E-01	M86511.1	NT	Human monocytic antigen CD14 (CD14) mRNA, complete cds
9505	22468	35911	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphoribute-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9505	22468	35912	0.45	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphoribute-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10353	23277	36752	3.37	3.2E-01	U44014.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10559	23461	36976	0.5	3.2E-01	BE326220.1	EST_HUMAN	h68705.x1 NCL CGAP L1024 Homo sapiens cDNA clone IMAGE:3181569 3'
10674	23586		3.71	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11028	23992	37519	3.03	3.2E-01	T06813.1	EST_HUMAN	EST104702 Fetal brain, Stratagene (differential display) Homo sapiens cDNA clone HFB0221
12286	25590	25590	3.07	3.2E-01	T07283.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12674	25543		1.39	3.2E-01	BE868946.1	EST_HUMAN	G01507620.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909532 5'
12804	25431		4.84	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12890	25719		1.48	3.2E-01	AF157625.1	NT	Bos taurus insulin 1,4,5-bisphosphatase receptor type 1 mRNA, complete cds
12836	25516		1.57	3.2E-01	L39874.1	EST_HUMAN	Homo sapiens deoxydicytadylate deaminase gene, complete cds
13001	25525	31306	1.33	3.2E-01	BE385778.1	NT	G01275409.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
13108	25528	31646	1.38	3.2E-01	A1745111.1	EST_HUMAN	I721c08.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2218954 3' similar to contains MER10.11 MER10 regulatory element 1
2679	15675	28596	3.02	3.1E-01	R148051.1	EST_HUMAN	y680b06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gblM64241 QM PROTEIN (HUMAN);
2708	15628	28717	4.64	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2708	15628	28718	4.64	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2809	15629		1.63	3.1E-01	AW620036.1	EST_HUMAN	h48908.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3188	16243		4.03	3.1E-01	AB025008.1	NT	Mus musculus gene for Ser/Thr kinase KIAIARE, exon 6
3927	16367	29880	0.93	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4959	18014	30801	1.25	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5239	18247	31119	0.79	3.1E-01	AF103070.1	NT	Rattus norvegicus MEN1 tumor suppressor (Men1) mRNA, alternative splice product, complete cds
18320	18320	31162	2.59	3.1E-01	AF16203.2	NT	Homo sapiens chromosome 21 segment H521G003
5555	18652	31595	9.78	3.1E-01	AF178111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3a) gene, exon 1
5681	18776	31943	0.65	3.1E-01	P24132	SWISSPROT	HYPOPHOSPHATE PROTEIN HIT236
5982	18777	31949	0.87	3.1E-01	Z14883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5953	18798		1.01	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polysein
5956	18955	32142	2.3	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6416	29680	32732	0.61	3.1E-01	R64322.1	EST_HUMAN	yc41704.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:189387 5'
6810	19898	32844	2.69	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-004 HN0001 Homo sapiens cDNA
6863	19740	33016	0.85	3.1E-01	AI284458.1	EST_HUMAN	q35401.x1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1874699 3'
6840	19893	33188	0.88	3.1E-01	X71887.1	NT	H sapiens gene for Immunoglobulin kappa light chain variable region A8 and A9
6930	20154		0.7	3.1E-01	AW377354.1	EST_HUMAN	MR2-CT10222-281099-005-H05 CT10222 Homo sapiens cDNA
7162	25634	31238	2.55	3.1E-01	BE137392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7942	20894	34275	0.88	3.1E-01	4895390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8038	20875	34371	0.49	3.1E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6p6) gene, complete cds; and Nai3 gene, exons 2-9 and 11-16
8168	21104	34502	0.64	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8168	21104	34503	0.64	3.1E-01	AW850168.1	EST_HUMAN	IL3-CT0219-271099-022-E03 CT0219 Homo sapiens cDNA
8695	21081	35386	0.83	3.1E-01	R45318.1	EST_HUMAN	y94601.s1 Scores Infant brain.1N1B Homo sapiens cDNA clone IMAGE:35639 3'
8968	21081	35386	0.83	3.1E-01	R45318.1	EST_HUMAN	y94601.s1 Scores Infant brain.1N1B Homo sapiens cDNA clone IMAGE:35639 3'
10262	23187	36671	0.52	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10427	23349	36833	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10427	23349	36834	1	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10488	23410	36907	1.73	3.1E-01	A1244001.1	EST_HUMAN	q18761.1x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1893980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COALYLASE PRECURSOR (HUMAN);
10655	23588		0.56	3.1E-01	T56325.1	EST_HUMAN	y47706.s1 Strabegens fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar to gb:U01038_rna22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11155	24142	37675	2.35	3.1E-01	BF216171.1	EST_HUMAN	6017833592F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4095814 5'
11884	24748	38328	2.3	3.1E-01	7662281	NT	Homo sapiens KIAA0784 gene product (KIAA0784), mRNA
12133	26002	38908	1.88	3.1E-01	AFO48683.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12133	25002	39009	1.88	3.1E-01	AFO48683.1	NT	Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
12415	25186		1.57	3.1E-01	AF294308.1	NT	Anolis opalinus isolate OS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12491	25210		4.64	3.1E-01	AF304162.1	NT	Silvestrodon vitreum 403 ribosomal protein S11 mRNA, partial cds
12592	25296		4.19	3.1E-01	AF196953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12944	25523		3.39	3.1E-01	AF196778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel alpha
73	15608	28112	1.78	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkcepsilon), mRNA
254	13351	26277	8.99	3.0E-01	AJ217135.1	NT	Homo sapiens Xa pseudouridine synthase, segment 1/2
1227	14265	27222	2.16	3.0E-01	AW300400.1	EST_HUMAN	xs03108.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1508	14541	27512	5.98	3.0E-01	AJ1006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2146	16192	28176	1.13	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3226	16280		1.26	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 <i>alyG</i> gene for polyglutamate lyase, complete cds
3879	16918	29827	1.46	3.0E-01	AW817785.1	EST_HUMAN	PfM-ST0282-261199-001-gp1 ST0282 Homo sapiens cDNA
3988	17037	29944	1.02	3.0E-01	AJ271736.1	NT	Homo sapiens Xa pseudocatalase gene, segment 2/2
4541	17564	30451	2.17	3.0E-01	AJ006756.1	NT	Balanophora physalis gene encoding atrial natriuretic peptide
5425	18528	31407	5.19	3.0E-01	BE741629.1	EST_HUMAN	60159460F NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5508	18608	31536	0.68	3.0E-01	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5510	18610	31541	0.76	3.0E-01	AF229247.1	NT	Centigalo orthopoxvirus hemagglutinin gene, complete cds
5582	18678	31641	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-ad3 BT0333 Homo sapiens cDNA
5582	18678	31642	3.81	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-ad3 BT0333 Homo sapiens cDNA
5619	18716	31874	4.05	3.0E-01	U01247.1	NT	Mus musculus 1281av Clara cell 10 kd protein (mCC10) gene, complete cds
7005	20131	33446	2.88	3.0E-01	D16313.1	NT	Mouse cycloratin 15 gene, complete cds
7041	18373	31281	0.71	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 3467 kDa laminin-binding protein mRNA, partial cds
7111	20045	33347	0.96	3.0E-01	AF259247.1	NT	Centigalo orthopoxvirus hemagglutinin gene, complete cds
7195	20219	33551	0.59	3.0E-01	X63941.1	NT	S. cerevisiae GAG1
7328	20269	33643	0.82	3.0E-01	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7549	20512	33870	4.68	3.0E-01	106477007	NT	Mus musculus midbrain (Mbr-pending), mRNA
7744	20598	34064	1.33	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8259	21228	34638	1.28	3.0E-01	AE001755.1	NT	Thermoplasma acidophilum section 67 of 136 of the complete genome
8716	21684		4.13	3.0E-01	9810161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9b), mRNA
8819	21786	35210	1.34	3.0E-01	BE696083.1	EST_HUMAN	001338078F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
9181	22147	35574	0.74	3.0E-01	AF141678.1	NT	Streptomyces sulfonolactone isopropyl N synthase (psbC) gene, partial cds
9223	22189		0.71	3.0E-01	7691085	NT	Homo sapiens DKFZP666M0122 protein (DKFZP666M0122), mRNA
9573	22535	35986	0.95	3.0E-01	AF225507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9532	22589	36320	0.51	3.0E-01	P76389	SWISSPROT	HYPOPHOSPHATE 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
10327	23251	36730	0.73	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288338 6'
10501	23423	36922	0.47	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetomycetans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10501	23423	36923	0.47	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetomycetans Tada (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10760	23681	37177	0.85	3.0E-01	AW116111.1	EST_HUMAN	bc03410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10762	23683	37179	2.14	3.0E-01	AB030231.1	NT	Aspergillus oryzae btpA gene for ER chaperone BIP, complete cds
10762	23703	37201	0.82	3.0E-01	BF683841.1	EST_HUMAN	602140733FT NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
10762	23703	37202	0.82	3.0E-01	BF683841.1	EST_HUMAN	602140733FT NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
12061	24634	38529	2.5	3.0E-01	H51028.1	EST_HUMAN	3p4410.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
12061	24634	38530	2.5	3.0E-01	H51029.1	EST_HUMAN	3p4410.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
12696	25875	38530	1.57	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12979	25917		2.92	3.0E-01	6677756	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
1747	14776		0.92	2.0E-01	AJ249895.1	NT	Mus musculus meta proto-oncogene and lgf2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
2039	15058	28077	1.19	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2260	15274	28266	1.2	2.9E-01	AF222718.1	NT	Chrysocodium syntrophus mitochondrion, complete genome
3255	16319	29240	1.92	2.9E-01	AW754235.1	EST_HUMAN	FW1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3255	16319	29241	1.92	2.9E-01	AW754235.1	EST_HUMAN	FW1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3912	16952	29853	1.03	2.9E-01	AI670836.1	EST_HUMAN	5q21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D16050 NIL-2-A ZINC FINGER PROTEIN [HUMAN]; contains element L1 repetitive element ;
3955	15595	29811	0.81	2.9E-01	AI759472.1	EST_HUMAN	W14410.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F5.7 CE15676 ;
4112	17148		0.7	2.9E-01	AW002902.1	EST_HUMAN	W02707.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2480395 3'
4511	17538	30420	1.24	2.9E-01	AA284468.1	EST_HUMAN	zs57412.x1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Aliu repetitive element;
4710	17731		1.5	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5156	18168		1.25	2.9E-01	AI870899.1	EST_HUMAN	W06103.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297509 3' similar to contains L1.2 L1 repetitive element ;
5275	18281	31145	3.3	2.9E-01	AJ131017.1	NT	Mus musculus SCA gene locus
5277	18283	31146	1.12	2.9E-01	BE741380.1	EST_HUMAN	601594241FT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948178 5'
5330	18438		1.49	2.9E-01	IK37485.1	EST_HUMAN	X77e12.s1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:28291 3'
5469	20065	33372	0.75	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthase 2 mRNA, complete cds
5858	18948	32133	5.1	2.9E-01	X56098.1	NT	B subtilis levanase operon lveA, lveV, lveG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, P18, P28, P30 and levanase
5858	18948	32134	5.1	2.9E-01	X56098.1	NT	B subtilis levanase operon lveA, lveV, lveG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, P18, P28, P30 and levanase
5871	18963	32149	6.12	2.9E-01	6879662	NT	Mus musculus Epi receptor A8 (Epha8), mRNA
6174	19249	32482	1.35	2.9E-01	AA418145.1	EST_HUMAN	2p67b12.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:787711 5'



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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8412	19480	32727	1.05	2.9E-01	U1797128.1	EST_HUMAN	wc27c05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312.3' similar to contains L1.H L1 repetitive element:
8459	19524	32775	2.3	2.9E-01	AU3420.1	NT	Bos taurus myosin I mRNA, complete cds
6559	19659	32831	0.8	2.9E-01	R08194.1	EST_HUMAN	y89008.t1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:141615.5'
6559	19659	32932	0.8	2.9E-01	R09194.1	EST_HUMAN	y89008.t1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:141615.5'
6883	19935		0.84	2.9E-01	Z50156.1	NT	D1discoidum gene for 34 kD actin binding protein
7043	20065	33372	0.58	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S adenosylmethionine synthetase 2 mRNA, complete cds
7179	18410	31211	1.67	2.9E-01	AF142326.1	NT	Mus musculus Filth protein (Flth) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7303	20274	33610	2.99	2.9E-01	Q04939	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7387	20337	33687	1.68	2.9E-01	AF100958.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Blnr1 (BING1), lapasin (lapasin), RelGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1, 3-galactosyl tr
8252	21221	34630	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287.5'
8262	21221	34631	1.67	2.9E-01	BE540422.1	EST_HUMAN	601065830.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287.5'
8489	21457	34874	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat3a gene, exons 5-19
8489	21457	34875	0.49	2.9E-01	AJ237937.1	NT	Bos taurus partial stat3a gene, exons 5-19
8502	21470		1.16	2.9E-01	BF21743.1	EST_HUMAN	601892570.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113.5'
8682	21650		0.45	2.9E-01	AF197458.1	NT	Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3- isopropylmalate dehydrogenase (leuS) gene, complete cds; and isopropylmalate dehydratase subunit (leuO) gene, partial cds
8942	21808	35333	0.77	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901.3'
9277	22243	36572	1.01	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9388	22353	35784	0.8	2.9E-01	M22462.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9501	22606	39053	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/8
9601	22609	39054	0.76	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/8
11240	24183	37711	1.7	2.9E-01	AF126943.1	NT	Typanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11467	24440	37689	1.86	2.9E-01	V01934.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11497	24440	37690	1.88	2.9E-01	V01934.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11913	24794	38385	2.95	2.9E-01	AL193078.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 5/6
12109	24976	39570	2.1	2.9E-01	AW234742.1	EST_HUMAN	UI-H-BW0-ann-F10-Q-U1 st NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2726694.3' wz8105.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2655921.3' similar to contains element
12651	25334	31760	1.47	2.9E-01	AW005871.1	EST_HUMAN	MER2B repetitive element:
12728	25381	31747	4	2.9E-01	AF092433.1	NT	Homo sapiens TNF- $\alpha$ -inducible RNA binding protein (TIRP) gene, complete cds
13025	25573	31694	1.35	2.9E-01	V08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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13025	25573	31695	1.35	2.9E-01	Y08937.1	NT	Olefinylmonas reinhardtii mRNA for nitrite reductase structural locus
570	13640		2.2	2.9E-01	U07136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
676	13644		1.41	2.9E-01	U28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1085	14129	27083	3.9	2.9E-01	AF16850.1	NT	Gaira guira oocyte maturation factor Mos (c-mos) gene, partial cds
1282	14317	27279	1.06	2.9E-01	BE313442.1	EST_HUMAN	601148733FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1282	14317	27280	1.06	2.9E-01	BE313442.1	EST_HUMAN	601148733FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1295	14330	27291	2.85	2.9E-01	D86560.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	14770	27756	2.22	2.9E-01	AW60020.1	EST_HUMAN	QV17CT0384-120200-065-305 CT0384 Homo sapiens cDNA
2028	16048	28062	2.08	2.9E-01	AL047620.1	EST_HUMAN	DKFZ558612321_11 586 (synonym: NUT1) Homo sapiens cDNA clone DKFZ558612321
2141	16156	28174	1.51	2.9E-01	AW611195.1	EST_HUMAN	hfd4b03.XT Source_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812333 3'
2479	15483	28507	2.18	2.9E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2554	15556	3.07	3.07	2.9E-01	AL161655.2	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2674	15671	28589	1.35	2.9E-01	AB020975.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2682	16040		1.48	2.9E-01	AF176480.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2683	16041	28963	2.57	2.9E-01	Z14037.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2993	16041	26994	2.57	2.9E-01	Z14037.1	NT	B. laurus microsatellite (ETH121)
3360	16439	29356	1.16	2.9E-01	AP000004.1	NT	B. laurus microsatellite (ETH121)
4021	17059	29690	1.72	2.9E-01	AE001180.1	NT	Pyococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7)
4150	17181		0.67	2.9E-01	AE004480.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4226	17265		2.41	2.9E-01	A050868.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 11 of 528 of the complete genome
4488	17513	30401	2.62	2.9E-01	P13915	SWISSPROT	ov44g10.x1 Scores, Islets, NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
4822	17939	30737	0.92	2.9E-01	D16050.1	NT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4822	17939	30738	0.92	2.9E-01	D16050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4866	17983	30771	2.71	2.9E-01	AF030154.1	NT	Human mRNA for transcription factor AREB6, complete cds
4887	17914	30804	1.37	2.9E-01	BF528188.1	EST_HUMAN	Bovine adenovirus 3 complete genome
4920	17937	30829	1.69	2.9E-01	AI272669.1	EST_HUMAN	60202603FT NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180129 5'
5394	25837	31362	23.73	2.9E-01	AA349937.1	EST_HUMAN	ql6sc11.X1 Scores, NHTMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element L TRS repetitive element;
5687	18782	31954	2.52	2.9E-01	AB010625.1	EST_HUMAN	EST15707/2 Infant brain Homo sapiens cDNA 5' end
5915	18001		1.04	2.9E-01	AW692583.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
6028	19111	32313	0.57	2.9E-01	AA765296.1	EST_HUMAN	CNH-BN0024-160200-118-912 BN0024 Homo sapiens cDNA
							ca01009.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gbM34559 FK508-BINDING PROTEIN (HUMAN);

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6048	19129		0.49	2.8E-01	AA004576.1	EST_HUMAN	z441601.1 Scores every tumor NBR0T Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6300	25094		0.78	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6343	19412	32653	2.02	2.8E-01	AF003124.1	NT	Measlesvirus hemagglutinin fructose-bisphosphate aldolase mRNA, complete cds
6343	19412	32654	2.02	2.8E-01	AF003124.1	NT	Measlesvirus hemagglutinin fructose-bisphosphate aldolase mRNA, complete cds
6395	18947	33244	8.31	2.8E-01	BF611216.1	EST_HUMAN	UI-H314-act-F04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7201	20225	33557	0.82	2.8E-01	U65300.1	NT	Orthomyx heterodys cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7678	20541	33900	0.51	2.8E-01	BE881455.1	EST_HUMAN	6074801.7F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3892142 5'
7675	20539		1.03	2.8E-01	U05933.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbL) gene, chloroplast gene encoding chloroplast protein, partial cds
7724	20580	34044	0.77	2.8E-01	X59880.1	NT	L-esculetum yd2 mRNA for GTP-binding protein
8429	21398	34808	1.12	2.8E-01	A1346128.1	EST_HUMAN	6074801.X1 NCI_CGAP_C88 Homo sapiens cDNA clone IMAGE:1928289 3' similar to gb-X065323_cds1
8429	21398	34809	1.12	2.8E-01	A1346128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8551	21519	34938	2.25	2.8E-01	U51088.1	NT	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8659	21826	35249	0.49	2.8E-01	AA011629.1	EST_HUMAN	6074801.X1 NCI_CGAP_C012 Homo sapiens cDNA clone IMAGE:1419983 3' similar to gb-X067789 IG
8936	21902		7.34	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
9821	22370	38127	0.91	2.8E-01	U17251.1	NT	60202387F1 NCI_CGAP_Bmi7 Homo sapiens cDNA clone IMAGE:4158525 5'
10069	22098		0.85	2.8E-01	L13654.1	NT	Neurospora crassa negative regulator sulfur controller-2 (econ-2) gene, complete cds
10248	23173	36682	0.83	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (econ-2) gene, complete cds
10248	23173	36683	0.83	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (econ-2) gene, complete cds
10310	23234	39716	0.6	2.8E-01	AF294393.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10420	23342	36628	4.08	2.8E-01	7708163	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
10878	23598		0.94	2.8E-01	9528134	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10878	23598		0.94	2.8E-01	9528134	NT	Homo sapiens hypothelial protein (LOC51319), mRNA
11085	24055	37133	0.44	2.8E-01	BE968727.2	EST_HUMAN	Fujinami sarcoma virus, complete genome
11085	24055	37178	1.9	2.8E-01	BF241092.1	EST_HUMAN	607168422R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839786 3'
11085	24055	37179	1.9	2.8E-01	BF241092.1	EST_HUMAN	6071680794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109560 5'
11125	24085	37612	2.86	2.8E-01	BF685070.1	EST_HUMAN	607185248F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4109350 5'
11608	24548		4.02	2.8E-01	BF674023.1	EST_HUMAN	607185248F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
12312	26120	31843	1.39	2.8E-01	AF269477.1	NT	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273859 5'

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12694	25351		23.64	2.8E-01	D83320.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12788	25420	31738	3.09	2.8E-01	BE176998.1	EST_HUMAN	PM4-HIT0506-030400-001-a07 HT0508 Homo sapiens cDNA
12817	25439	31742	1.37	2.8E-01	BE500116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955908 5'
12969	25879		3.15	2.8E-01	11433828	NT	Homo sapiens C/EBP-binding protein kinase beta (C/EBP-beta), mRNA
13097	25973		1.76	2.8E-01	AW025400.1	EST_HUMAN	wu68955.x1 NC1 CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2527928 3'
477	13549	26477	2.95	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
615	13660	26558	9.49	2.7E-01	AA450061.1	EST_HUMAN	z39p10.x1 Soares, total, fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1286	14301	27262	2.18	2.7E-01	AB004805.1	NT	Pomacea purpurus transposable element Tpr100 gene for transposase, complete cds
1826	14658		2.21	2.7E-01	X78815.1	NT	G. lamblia SR2 gene
1742	14772	27757	2.68	2.7E-01	W58067.1	EST_HUMAN	zid2h10.1 Soares, fetal, heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1781	14820	27805	2.49	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2145	15885		2.29	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monocamine transporter type 2, promoter region and exon 1
2376	15383	28405	9.36	2.7E-01	Y13668.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (V89), partial
2461	15465	28488	3.97	2.7E-01	A030888.1	EST_HUMAN	ta43c11.x2 NC1 CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
2809	15968	28691	1	2.7E-01	AF251276.1	NT	Mus musculus serine protease inhibitor 14 (Spi14) mRNA, complete cds
2907	16055		0.91	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
4038	17076	28976	1.74	2.7E-01	AUG28015.1	EST_HUMAN	w62a11.x1 NC1 CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2462828 3'
4053	17090	29885	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4053	17090	29888	0.76	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4081	17097	29891	2.33	2.7E-01	L77568.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4828	17945	30837	0.76	2.7E-01	L27516.1	NT	Trilicium aestivum (W ca66) gene, complete cds
5079	18088		4.11	2.7E-01	AW859131.1	EST_HUMAN	RC1-CT0286-200200-016-e03 CT0286 Homo sapiens cDNA
5339	18444	31187	2.13	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (CHOX-1.4)
5587	18664		1.11	2.7E-01	AB033171.1	NT	Astrepore myophthalma mitochondrial cyb gene for cytochrome b, partial cds
8478	19541	32787	0.51	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
8478	19541	32788	0.51	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
8765	19819	33100	1.06	2.7E-01	AEC01094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

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6765	19819	33101	1.06	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6946	20170	33494	2.1	2.7E-01	Q01354	SWISSPROT	FIBRILLIN 1 PRECURSOR
7283	19988	33901	0.84	2.7E-01	A1540070.1	EST_HUMAN	h08h08.x1 NC1_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7580	20542	33901	0.8	2.7E-01	Q11079	SWISSPROT	UTROPHIN 20.9 KD PROTEIN B0963.3 IN CHROMOSOME X
7811	20760	34135	0.86	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7811	20760	34136	0.86	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7862	20883	34285	1.9	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7952	20803	34285	1.6	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8012	20850	34343	0.83	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
8012	20850	34344	0.86	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to myosin-binding protein H
8084	21021	34421	0.83	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8196	21186	34578	0.86	2.7E-01	AA013147.1	EST_HUMAN	z635b11.s1 Scores refine N2b4HR Homo sapiens cDNA clone IMAGE:360667 3' similar to contains Alu repetitive element.
8360	21329		0.52	2.7E-01	AF048820.1	NT	Cerassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8475	21444	34861	0.43	2.7E-01	AW868503.1	EST_HUMAN	MRI-SN0082-100500-402-409 SN0082 Homo sapiens cDNA
8527	21495	34909	0.52	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:235111 3'
8534	21602	35025	0.74	2.7E-01	AL161562.2	NT	A. thaliana thaliana DNA chromosome 4, contig fragment No. 52
9172	22078	35035	0.52	2.7E-01	Q14764	SWISSPROT	MAJOR VAILT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9382	22347	35778	0.51	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Trs534
9680	22641	36088	11.09	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9688	22641	36099	11.09	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9691	22844		2.17	2.7E-01	P37928	SWISSPROT	FIMBRIN W PROTEIN
10180	23085	36562	0.64	2.7E-01	D69660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10471	23399	36953	0.85	2.7E-01	AF091648.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10477	23399	36956	2.83	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc1 isoform a (NF-ATc1) mRNA, complete cds
10511	23533	37029	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, Intron 9
10511	23533	37030	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, Intron 9
11163	24121	37648	4.87	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCD008 5'
11163	24121	37648	4.87	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCD008 5'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11171	24128	37668	2.31	2.7E-01	AJ133268.1	NT	Homo sapiens carotidin-1/2 locus, Contig1, DTS22, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12056	24839		2.08	2.7E-01	BE141035.1	EST_HUMAN	MRO-HT0067-201069-002-210 HT0067 Homo sapiens cDNA
12050	24861		1.52	2.7E-01	O14181	SWISSPROT	PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C
12509	25244	31802	1.39	2.7E-01	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
12757	25258		1.48	2.7E-01	A3008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12857	25460		1.83	2.7E-01	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
12948	25526		3.16	2.7E-01	AF217491.1	NT	Homo sapiens fragile 160 oxidoreductase (FOR) gene, exon 6
470	13841	26470	1.97	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
481	13654		1.5	2.6E-01	D18459.1	NT	Bos taurus mRNA for mb-1, complete cds
1394	14428	27937	1.68	2.6E-01	BE65087.1	EST_HUMAN	60151038F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE3912345 5'
1431	14465	27441	1.38	2.6E-01	AB013260.1	NT	Glycine max pseudogene for Bd 30K
1912	14638	27631	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1912	14638	27632	6.4	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:U38072 80S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2104	15121		7.48	2.6E-01	AW733152.1	EST_HUMAN	B. malitimus rbcL gene
2480	15484		0.99	2.6E-01	Y12896.1	NT	601128016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2880043 5'
2553	15555		8.24	2.6E-01	BE27240.1	EST_HUMAN	EST386935 MAGe sequences, MAGM Homo sapiens cDNA
3108	16165		1.02	2.6E-01	AW974631.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3594	16539	28559	1.02	2.6E-01	M22342.1	NT	
3857	16700	28616	2.11	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3982	17022	28932	0.77	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial rps8 gene for RNase P RNA subunit
3982	17022	28933	0.77	2.6E-01	AJ012174.2	NT	Chlamydomonas reinhardtii partial rps8 gene for RNase P RNA subunit
4181	17212	30100	17.99	2.6E-01	BE080598.1	EST_HUMAN	QY18170330-040400-132-403 B10630 Homo sapiens cDNA
4384	17412	30296	1.39	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4522	17547	30434	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4522	17547	30435	0.82	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4579	17601	30497	1.47	2.6E-01	AA457617.1	EST_HUMAN	aab907.r1 Stratiococcus felis reira 997202 Homo sapiens cDNA clone IMAGE:838477 5'
4677	17698	30585	2.31	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3.1) mRNA, complete cds
4745	17765	30559	1.45	2.6E-01	AF142703.1	NT	Ophiostoma radicans malurase-like protein (malK) gene, complete cds; chloroplast gene for chloroplast product

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	18021	30909	4.38	2.6E-01	H04959.1	EST_HUMAN	Y51c05.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5051	18091		0.78	2.6E-01	AA884623.1	EST_HUMAN	am33111.3.1 Scores_NFL_I_GGC_S1 Homo sapiens cDNA clone IMAGE:1469505 3'
5414	18517		1.06	2.6E-01	AB035972.1	NT	Parametrium caudatum gene for PAP, complete cds
5524	18623	31588	0.69	2.6E-01	M96050.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAax genes, complete cds
5561	18747		0.71	2.6E-01	AB62398.1	EST_HUMAN	1418603.r1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element
5659	18958	32146	0.68	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, plm-2 protooncogene homolog plm-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor: IGHM enhancer 3 genes, partial cds; and unknown gp
6189	25993		2.61	2.6E-01	AE001811.1	NT	Thermoplasma maritima section 123 of 136 of the complete genome
6325	19395	32637	1.81	2.6E-01	AI562557.1	EST_HUMAN	1602612.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6325	19395	32638	1.81	2.6E-01	AI562557.1	EST_HUMAN	1602612.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6552	19622	32887	1.01	2.6E-01	AL162767.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 8/7
6825	19876	33169	0.8	2.6E-01	BE792052.1	EST_HUMAN	601591754.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636156 5'
6825	19876	33170	0.6	2.6E-01	BE792052.1	EST_HUMAN	601591754.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3636156 5'
7238	20259	33563	0.75	2.6E-01	AB174380.1	EST_HUMAN	wd4804.x1 Scores_NFL_I_GGC_S1 Homo sapiens cDNA clone IMAGE:2331366 3' similar to gb:U57721
7920	20580	33944	0.72	2.6E-01	BE749961.1	EST_HUMAN	PEPTIDYL-GLYCINE ALPHAMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7953	20586		0.73	2.6E-01	AL139077.2	NT	CMO-H70245-031169-085-104 HT0245 Homo sapiens cDNA
7700	20658		0.61	2.6E-01	AA196149.1	EST_HUMAN	z992601.r1 Streptococcus Helia cell s3 937216 Homo sapiens cDNA clone IMAGE:627672 5'
8013	20951	34345	1.53	2.6E-01	RI0385.1	EST_HUMAN	y37403.r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:U12517.U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8071	21006	34406	0.65	2.6E-01	Q09855	SWISSPROT	HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN C28E6.01 IN CHROMOSOME 1
8152	21152	34550	1.13	2.6E-01	R02411.1	EST_HUMAN	y832607.r1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:124212 5'
8236	21205	34610	1.17	2.6E-01	BE14433.1	EST_HUMAN	MRO-H70169-181169-003-d12 HT0169 Homo sapiens cDNA
8480	21449	34656	0.82	2.6E-01	X62841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8480	21449	34887	0.62	2.6E-01	X62841.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8677	21645	35059	2.87	2.6E-01	BF343588.1	EST_HUMAN	S02014422.F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150399 5'
8753	21721	35143	1.92	2.6E-01	Q10189	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11G11.02 IN CHROMOSOME II

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Describer
9042	22008	35428	4.09	2.6E-01	BE830339.1	EST_HUMAN	RC3-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9042	22008	35428	4.09	2.6E-01	BE830339.1	EST_HUMAN	RC3-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9522	22671	38128	0.99	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
10096	23022		0.63	2.6E-01	AF037121.1	NT	Lontia caerulea cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10227	23162	36641	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFRH-G)
10227	23162	36642	1.08	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KFRH-G)
10550	23472		0.91	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10875	23795		0.91	2.6E-01	Y10198.1	NT	Homo sapiens PHOX gene
10876	23869		0.48	2.6E-01	Y16974.2	NT	Danio rerio mRNA for RPTP-alpha protein
11854	24736		32.27	2.6E-01	X51755.1	NT	Human lambda8-immunoglobulin constant region complex (germline)
12268	25091		2.77	2.6E-01	10160555	NT	Mus musculus jerky (Jrk), mRNA
12464	25693		3.3	2.6E-01	BE883491.1	EST_HUMAN	60151T052F1 NIH JMGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12528	25257	31806	4.42	2.6E-01	AF316996.1	NT	Homo sapiens NaK-ATPase gamma subunit (FYXD2) gene, complete cds, alternatively spliced
12846	25456		2.01	2.6E-01	D88425.1	NT	Gavia cobbaya mRNA for serine/threonine kinase, complete cds
12974	25558		1.74	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13010	25692		3.07	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
241	13340	26265	2.33	2.6E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	13340	26265	1.97	2.6E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
265	13362		4.93	2.6E-01	M28501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
833	13890	26844	1.87	2.6E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1123	14167	27116	0.8	2.6E-01	T88937.1	EST_HUMAN	Xa11g07.r1 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1522	14654	27525	1.95	2.6E-01	AL115624.1	NT	Babyle cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1741	14771		5.06	2.6E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1900	15880	27920	0.94	2.6E-01	BE66604.1	EST_HUMAN	PMA-C10400-310700-005-008 CT0400 Homo sapiens cDNA
1900	15880	27921	0.94	2.6E-01	BE66604.1	EST_HUMAN	PMA-C10400-310700-005-008 CT0400 Homo sapiens cDNA
2417	15424		13.96	2.6E-01	AA000875.1	NT	Aquifex mediterraneus section 7 of 109 of the complete genome
2503	15606		1.09	2.6E-01	AA251687.1	EST_HUMAN	2a11a12.11 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:684862 5'
2644	15641	28695	0.94	2.6E-01	X95310.1	NT	B. laurus mRNA for D-aspartate oxidase
3423	16471		2.93	2.6E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3545	16591	29516	0.87	2.5E-01	AF233872.1	NT	Danio rerio peptide YY precursor gene, complete cds
3560	16606	29526	7.04	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3691	18500	26803	1.15	2.5E-01	A1741483.1	EST_HUMAN	Wt1507.x1 Scars. NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:234780.3
3691	18500	26804	1.15	2.5E-01	A1741483.1	EST_HUMAN	Wt1507.x1 Scars. NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:234780.3
4098	17390	29223	1.76	2.5E-01	P23223	SWISSPROT	AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4348	17373		0.99	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4780	17800	30608	1.34	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4788	17808	30608	4.71	2.5E-01	A007768.1	NT	Charistoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4821	17838	30738	2.32	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4840	17857		3.69	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4870	17887	30775	0.64	2.5E-01	BE696785.1	EST_HUMAN	h02911.x1 Scars. NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3922600.5
5086	18066	30972	0.84	2.5E-01	AW873588.1	EST_HUMAN	WP:1717P8A_284.D CE22856 ;
5243	18251		0.96	2.5E-01	AA768359.1	EST_HUMAN	ca83a08.61 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319920.3 similar to contains Alu repetitive element;
5398	18502	31380	13.58	2.5E-01	S63390.1	NT	T3 receptor-associating collector-1 [human, fetal liver, mRNA, 2830 nt]
6070	19151	32363	0.84	2.5E-01	AJ005345.1	NT	Homo sapiens KVLDT1 gene
6071	19152		0.87	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6525	19588	32847	0.49	2.5E-01	P22219	SWISSPROT	PROTEIN KINASE VPS15
6780	18835	33118	0.86	2.5E-01	AJ251973.1	NT	Homo sapiens partial Slesfin-1 gene
7245	18980	33277	0.8	2.5E-01	8394138	NT	Rattus norvegicus rabin 3 (RABIN3), mRNA
7575	20637	33898	0.79	2.5E-01	U13992.1	NT	Feline calicivirus CF108 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds, and unknown gene
7604	20565		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7652	20798	34174	0.68	2.5E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7688	20841	34223	3.88	2.5E-01	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C082
8177	21147	34655	2.72	2.5E-01	BF109040.1	EST_HUMAN	7167a03.x1 Scars. NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3325389.3
8168	21156	34587	0.62	2.5E-01	BE960712.1	EST_HUMAN	60165393142 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828198.3
8568	21636	34956	2.02	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3862899.5
8740	21708	35131	0.67	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K)
8983	21948	35373	3.37	2.5E-01	H5326.1	EST_HUMAN	x8407.1 Scars fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202501.5
9227	22193	35623	0.81	2.5E-01	M88526.1	NT	Mouse taste-specific protein (TPX-1) gene, exon 10
9674	22827	36280	18.45	2.5E-01	U98951.2	NT	Homo sapiens matrix metalloproteinase MMP-1 gene, promoter region

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9874	22827	36281	16.46	2.5E-01	U89551.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9881	22814	36268	2.03	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9931	22814	36269	2.03	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10468	23330	36873	1.7	2.5E-01	AF581967.1	EST_HUMAN	RCS-ST0186-130100-018-407 ST0186 Homo sapiens cDNA
10707	23929	37124	0.44	2.5E-01	11465652	NT	Porphyra purpurea chloroplast, complete genome
10909	23829	37342	1.58	2.5E-01	AW152246.1	EST_HUMAN	x940c10.1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/consensus element MSR1 repetitive element;
10912	23832	37346	1.38	2.5E-01	X69491.1	NT	Mouset LTR LINE DNA
10992	23912	37427	0.45	2.5E-01	A0934721.1	EST_HUMAN	wp88a11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468876 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA;
10992	23912	37428	0.46	2.5E-01	A0934721.1	EST_HUMAN	wp88a11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468876 3' similar to SW:CEBD_HUMAN P49716 CCAAT/ENHANCER BINDING PROTEIN DELTA;
11473	24357	37892	4.47	2.5E-01	D50814.1	NT	Human mRNA for KIAA0724 gene, partial cds
12120	24990	38591	2.34	2.5E-01	AE000711.1	NT	Aquifex aeolicus section 43 of 109 of the complete genome
12204	25046	38925	4.55	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
12230	25059	38925	5.87	2.5E-01	AL161641.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
12691	25805	31627	1.64	2.5E-01	AF170072.1	NT	Spodoplera frugiperda CALNUG mRNA, complete cds
555	13625	28543	0.66	2.4E-01	AA698316.1	EST_HUMAN	on70604.a1 Soares_NFL1_OBC_S1 Homo sapiens cDNA clone IMAGE:1662023 3'
848	13905	28684	2.67	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1307	14343	27307	15.11	2.4E-01	AJ286880.1	NT	Homo sapiens KIAA0851 gene (partial), XT13 gene and LZTFL1 gene
1307	14343	27308	15.11	2.4E-01	AJ286880.1	NT	Homo sapiens KIAA0851 gene (partial), XT13 gene and LZTFL1 gene
1384	14418	27387	1.01	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1866	14683	27936	27.14	2.4E-01	AF257753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1916	14940	27936	1.21	2.4E-01	AF251705.1	NT	Zaocys dharmades fructose-1,6-bisphosphatase mRNA, complete cds
2146	15164	28180	0.97	2.4E-01	AF111168.2	NT	Homo sapiens saline pilinoly transferase, subunit II gene, complete cds; and unknown genes
2178	15163	28180	1.04	2.4E-01	AF45984	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (GA1 PROTEASE)
2271	15294	28310	2.23	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2391	15399	28424	1.65	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:3318807 3' similar to SW:PRSB_XENLA
2544	15546	28569	2.37	2.4E-01	Z56534.1	NT	O42586995 protease-1
2772	15764	28785	2.11	2.4E-01	X71783.1	NT	D. discoideum (A33-K) potA gene
2767	15759	28807	3.03	2.4E-01	AF030154.1	NT	S. pombe swd gene
						NT	Bovine adenovirus 3 complete genome
3149	18206		3.16	2.4E-01	U72725.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retroviral gag/pol genes, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	18219	29134	1.71	2.4E-01	X74209.1	NT	H sapiens AGT gene, PstI fragment of intron 4
3675	18718	29832	1	2.4E-01	AF169763.1	NT	Podaopara anethina HET-C protein (Het-C) gene, complete cds
3773	18915	29724	0.95	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4002	17098		0.87	2.4E-01	D28960.1	NT	Rattus norvegicus mRNA for alpha3 crystallin-related protein, complete cds
4974	17989		0.93	2.4E-01	AL161589.2	NT	Aedes albopictus thalassa DNA chromosome 4, contig fragment No. 85
5089	18069	30975	0.95	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5337	18374	31574	0.77	2.4E-01	A1925707.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457128 3'
5537	18634	31575	0.77	2.4E-01	A1825707.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457128 3'
5692	18659	31605	0.94	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5738	18632	32011	0.92	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5738	18632	32012	0.92	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5766	18958		0.85	2.4E-01	M83377.1	NT	Callus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
5991	25949		1.03	2.4E-01	AJ133936.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2) gene
5998	19082	32279	2.06	2.4E-01	BF592336.1	EST_HUMAN	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6098	19177	32395	2.07	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6209	19283	32815	2.02	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6264	19337	32570	0.84	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDADE11 5'
6323	19566	32844	0.89	2.4E-01	AA396572.1	EST_HUMAN	270402.s1 Soares, Jellis, NHT Homo sapiens cDNA clone IMAGE:27683 3'
6685	19742	33018	1.72	2.4E-01	AI698989.1	EST_HUMAN	wc2211.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:U03464
7247	19892	33279	0.84	2.4E-01	AF169863.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7598	20529	33988	7.93	2.4E-01	L43001.1	NT	Musclea vicia tyrosine aminotransferase gene, complete cds
7748	20701	34058	0.65	2.4E-01	N48732.1	EST_HUMAN	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7694	20933		0.51	2.4E-01	U05013.1	NT	395511.r1 Soares, multiple sclerosis_2/bbHMSIP Homo sapiens cDNA clone IMAGE:277460 5'
7899	20935	34329	0.97	2.4E-01	AF229644.1	NT	Rattus norvegicus Sprague-Dawley hemis oxygenase-2 non-reducing isoform gene, complete cds
8416	21385	34762	0.51	2.4E-01	X97262.1	NT	Mus musculus paf gene and promoter
8416	21385	34763	0.51	2.4E-01	X97262.1	NT	Mus musculus paf gene and promoter
8662	21660	35083	1.5	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8946	21912	35337	0.98	2.4E-01	BF242794.1	EST_HUMAN	60187679P1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106288 5'
9001	21907		0.57	2.4E-01	BF978275.1	EST_HUMAN	602036189P1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9487	22451	35891	0.51	2.4E-01	AL138077.2	NT	Campylobacter jejuni NCTC11169 complete genome, segment 4/6

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9487	22451	35892	0.51	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 4/6
9921	22742	36193	7.83	2.4E-01	AB63515.1	EST_HUMAN	w443002.v1 Scores_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:230906 3' similar to contains MER22.b1 TARK1 repetitive element
10082	22989	36457	0.57	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10082	22989	36458	0.57	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10805	23728	37227	1.69	2.4E-01	Q03982	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11118	24078	37003	2.68	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11185	24141	37875	1.77	2.4E-01	AF030189.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11534	24475		1.52	2.4E-01	Z21647.1	NT	P. asiatica mosaic virus genomic RNA
12096	24967	38564	4.80	2.4E-01	P08900	SWISSPROT	PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR
12160	25015	38617	2.5	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12294	25746		1.93	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12391	25150		2.1	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mcf protein (mcf7 gene)
12578	26734		2.27	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12782	26846		1.31	2.4E-01	BF229976.1	EST_HUMAN	RC3-CT0413-100900-023-b09 CT0413 Homo sapiens cDNA
13008	26569		8.49	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
369	13464	26394	0.98	2.3E-01	S75898.1	NT	acornclase [Drosophila guttata-zebra finches, ovary, mRNA, 3188 nt]
838	13704		5.85	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
668	13733	26558	21.34	2.3E-01	U07596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
834	13987	26937	4.19	2.3E-01	BE311833.1	EST_HUMAN	801142073F1 NIH_LMG_C 14 Homo sapiens cDNA clone IMAGE:3605816 5'
1511	14543	27514	1.33	2.3E-01	6677980	NT	Mus musculus reticular protein sorting 4b (yesc4b) mRNA
1588	14801		1.02	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1608	14840	27617	1.21	2.3E-01	AJ245480.1	NT	Braconia napus sig gene for S-locus glycoprotein, cultivar T2
1636	14658	27644	2.32	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2081	15079		1.33	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2452	15457	28478	2.76	2.3E-01	BE297718.1	EST_HUMAN	301175862F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3331013 5'
2650	15957	28876	1.27	2.3E-01	M11318.1	NT	Human erythropoietin gene, complete cds
2835	14422	27381	2.34	2.3E-01	AB015033.1	NT	Marmelaria agarovirans pV81 gene for DNA gyrase subunit B, partial cds, strain:FO 14957
2974	16032	28055	1.25	2.3E-01	A4801379.1	EST_HUMAN	not found at NCL_CGAP_Phof1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element/contains element 17H1 repetitive element
3100	16157		7.15	2.3E-01	R21732.1	EST_HUMAN	Y21D07.51 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3383	16432	29380	1.28	2.3E-01	H66836.1	EST_HUMAN	Y27H10.11 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:213283 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3854	16884	28768	1.06	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3956	16986		5.02	2.3E-01	7682133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4212	17241		0.82	2.3E-01	U03267.1	NT	Rat atrial natriuretic factor (ANF) gene, 5' end
4377	17405	30285	0.94	2.3E-01	R62282.1	EST_HUMAN	Y1701.1.1 Soares placentar NB24P Homo sapiens cDNA clone IMAGE:149017.6
4428	17455		2.24	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4479	17504	30392	1.07	2.3E-01	D00869.1	NT	Synechococcus sp. PCC6903 complete genome, 1/27, 1-133859
4515	17540	30426	1.8	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKMI3) mRNA, complete cds
4584	17608	30502	7.42	2.3E-01	5031684	NT	Homo sapiens nuclear transport factor 2 (p160nuc protein 15) (PP15) mRNA
5087	18097	30973	0.65	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5200	18209	31083	0.91	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter, (NP73) gene, complete cds
5377	18481	31358	2.19	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5503	18603	31532	2.51	2.3E-01	BF058381.1	EST_HUMAN	P03300.GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]; ;
5508	18704	31851	4.55	2.3E-01	X95587.1	NT	C-familial rami gene
5753	18827		1.07	2.3E-01	L39112.1	NT	Vitellogenin core small subunit ribosomal RNA gene
5846	18935	32119	0.81	2.3E-01	S90371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2865 nt]
6051	19132	32340	2.02	2.3E-01	A1708940.1	EST_HUMAN	as27612.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318448.3 similar to gb-X13238
6051	19132	32341	2.02	2.3E-01	A1708940.1	EST_HUMAN	CYTOKROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6812	19866	33154	0.76	2.3E-01	AF168089.1	NT	as27612.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318448.3 similar to gb-X13238
7051	20083	33591	5.28	2.3E-01	A1718148.1	EST_HUMAN	CYTOKROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7318	20289	33632	0.69	2.3E-01	B623323	NT	CYTOKROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7505	20470	33830	0.76	2.3E-01	AF000227.1	NT	mitochondrial product
7646	20606	33972	2.65	2.3E-01	AF175389.1	NT	as27612.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318448.3 similar to gb-X13238
7649	20609	33974	10.72	2.3E-01	A1719881.1	EST_HUMAN	CYTOKROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7649	20609	33975	10.72	2.3E-01	A1719881.1	EST_HUMAN	CYTOKROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7696	20810		3.39	2.3E-01	6754779	NT	myoglobin (Myo15), mRNA

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Probe SEQ ID NO	Exon SEQ ID NO	ORF SEQ ID NO	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	20815	34183	1.36	2.3E-01	BE688071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
8028	20885		2.69	2.3E-01	N80983.1	EST_HUMAN	zn720B.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:282358 5'
8073	21010	34408	0.63	2.3E-01	11416821	NT	Homo sapiens proteodactherin alpha cluster (LOC633950) mRNA
8073	21010	34409	0.63	2.3E-01	11416821	NT	Homo sapiens proteodactherin alpha cluster (LOC633950) mRNA
8184	21154	34582	0.6	2.3E-01	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8628	21295	34710	2.02	2.3E-01	M68931.1	NT	Oxyficha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8638	21805	35222	0.54	2.3E-01	U57969.1	NT	Mus musculus prosapopin (psap) (SGF-1) gene, complete cds
9125	22091	35510	0.48	2.3E-01	AW090541.1	EST_HUMAN	xc89d06.x1 NCI CGAP_Br35 Homo sapiens cDNA clone IMAGE:2591554 3'
9240	22208	35539	0.45	2.3E-01	AW984480.1	EST_HUMAN	EST376533 IMAGE resequences, MAGH Homo sapiens cDNA
9498	22460	35601	0.59	2.3E-01	AA372164.1	EST_HUMAN	EST184081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9498	22460	35601	0.59	2.3E-01	AA372164.1	EST_HUMAN	EST184081 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9940	22867	36329	0.63	2.3E-01	6676318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd) mRNA
10086	23013	36498	0.78	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2866739 5'
10141	23067	36543	0.59	2.3E-01	AW984480.1	EST_HUMAN	EST376533 IMAGE resequences, MAGH Homo sapiens cDNA
10191	23116	36600	1.36	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
10226	23151	36840	0.57	2.3E-01	AW364633.1	EST_HUMAN	PMSD1T00395-281269-001-104 DT0039 Homo sapiens cDNA
10294	23219	36702	2.8	2.3E-01	BE173060.1	EST_HUMAN	MRQ.H1T0558-240400-014-g11 H1T0558 Homo sapiens cDNA
10351	23275	36748	2.33	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10609	23730	37232	0.8	2.3E-01	AF201629.1	NT	Murine hepatitis virus strain 2, complete genome
10820	23741		6.12	2.3E-01	BF13377.1	EST_HUMAN	601164615R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
11355	24305	37832	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11355	24305	37833	1.49	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11522	24463	38015	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11622	24463	38016	1.69	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11679	24645	38222	2.81	2.3E-01	AEC02167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
12089	24689	38568	1.47	2.3E-01	AE004663.1	NT	Pseudomonas aeruginosa PAO1, section 229 of 829 of the complete genome
12279	25008		5.42	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2-B8 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25168		6.48	2.3E-01	T27231.1	EST_HUMAN	HCOE5T144T129M8 Homo sapiens cDNA clone HCC44 5'
12403	25176		2.24	2.3E-01	AW863940.1	EST_HUMAN	PMA-SN0012-030400-001-b08 SN0012 Homo sapiens cDNA
12460	25882	31417	2.82	2.3E-01	AW309823.1	EST_HUMAN	x121d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813775 3' similar to TR-OBZ175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2 : contains PTR5.b2 TAR1 repetitive element;

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12494	25937	31312	11.07	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:390889 5'
12544	25207		2.98	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4297719 5'
12591	25268		3.71	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gatel ion channel
12660	25348		2.12	2.3E-01	U46645.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12628	25511		1.49	2.3E-01	BF475911.1	EST_HUMAN	ncf38H12.X1 Lupacl, sciatic_nerve Homo sapiens cDNA clone IMAGE:336930 3' similar to contains element MEF38 repetitive element;
80	13206	26190	0.99	2.2E-01	AJ052190.1	EST_HUMAN	cc14a10.X1 Soares, fetal_liver, spleen -1NfLS, S1 Homo sapiens cDNA clone IMAGE:1875290 3' similar to
1597	14800	27578	2.33	2.2E-01	AF187850.1	NT	Homo sapiens PPAIR delta gene, promoter region
2100	15117	28139	2.22	2.2E-01	M34840.1	NT	Fresh-water sponge EnH1 alpha collagen (COLF1) gene
2412	15419	28443	6.18	2.2E-01	BF677833.1	EST_HUMAN	602065050F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249699 5'
2563	15594	28611	2.54	2.2E-01	BE581258.1	EST_HUMAN	601482629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3366190 5'
2593	15594	28612	2.54	2.2E-01	BE581258.1	EST_HUMAN	601482629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3366190 5'
2893	15592	28988	4.89	2.2E-01	BE156625.1	EST_HUMAN	PM2-H1T0353-281289-403-412 HT10353 Homo sapiens cDNA
2893	15592	28989	4.89	2.2E-01	BE156625.1	EST_HUMAN	PM2-H1T0353-281289-403-412 HT10353 Homo sapiens cDNA
2932	15990		1.29	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3403	16452		2.28	2.2E-01	AF181552.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 52
3827	16887		0.56	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4240	17269		1.2	2.2E-01	AF116102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4247	17276	30158	5.88	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Konk6) genes, complete cds
4292	17321	30200	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
4292	17321	30201	2.33	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
4383	17411	30294	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4383	17411	30295	1.21	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4456	17482	30370	23.17	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA
4853	17980		1.97	2.2E-01	D30804.1	NT	Human beta-cytoplasmic actin (ACTB) pseudogene
4858	17985	30773	1.88	2.2E-01	AA211216.1	EST_HUMAN	z887c05.r1 Stralagene hNT neuron (#8937233) Homo sapiens cDNA clone IMAGE:648988 5'
5082	18092		1.34	2.2E-01	L13289.1	NT	Mus musculus vinculin gene, exon 3
5160	18189	31048	1.22	2.2E-01	BE141035.1	EST_HUMAN	MR0-HT0087-201099-002-c10 HT0087 Homo sapiens cDNA
5181	18190	31066	1.51	2.2E-01	H06048.1	EST_HUMAN	V42H09.r1 Soares fetal_liver spleen -1NfLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb:Z14116.1_rnat CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
5282	18271		1.06	2.2E-01	AJ146320.2	NT	Homo sapiens chromosome 21 segment H521C006

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5938	19328	32112	2.18	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5849	18339		3.59	2.2E-01	D84000.1	NT	Synedryalis sp. PCC6803 complete genome, 10/27_2302729-2539099
6114	19192	32419	0.61	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Txt) mRNA, complete cds
6114	19192	32419	0.61	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Txt) mRNA, complete cds
6894	19917	33211	0.7	2.2E-01	AB039490.1	NT	Homo sapiens gene for fukutin, complete cds
6984	20189	33914	0.58	2.2E-01	AA490108.1	EST_HUMAN	ab02409.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:639659 3'
6984	20189	33915	0.68	2.2E-01	AA490108.1	EST_HUMAN	ab02409.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:639659 3'
7222	20244	33578	7.78	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMAPHC06 5'
7336	20307	33660	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpa) genes, complete cds, and unknown genes
7336	20307	33661	1.43	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpa) genes, complete cds, and unknown genes
7509	20474	33834	2.11	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7509	20474	33835	2.11	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7728	20584	34048	0.59	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7898	20905	34297	0.8	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8000	20939	34332	0.5	2.2E-01	AB024693.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8334	21323		2.61	2.2E-01	AF165143.1	NT	Mus musculus rrm23-MT gene, promoter region
8425	21394	34605	1	2.2E-01	Z48933.1	NT	E. coli sepA and sepB genes
8598	21882	35284	0.49	2.2E-01	AI132818.1	NT	Pan troglodytes Mecp2 gene 3'UTR
9234	22200	35629	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9234	22200	35630	0.51	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9247	22213	35643	4.12	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 139 of the complete genome
9297	22293	35663	0.47	2.2E-01	U09984.1	NT	Mus musculus CR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
9378	22341		3.69	2.2E-01	AW856039.1	EST_HUMAN	PI3-C10383-241295-009-b07 C10383 Homo sapiens cDNA
9470	22434	35872	1.4	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Defaf1), mRNA
9553	22515	35966	1.4	2.2E-01	BF376354.1	EST_HUMAN	IMR1-TN0045-110900-009-c02 TN0045 Homo sapiens cDNA
9644	22568	36037	1.3	2.2E-01	W02988.1	EST_HUMAN	IMR1-TN0045-110900-009-c02 TN0045 Homo sapiens cDNA
9682	22819	36274	15.89	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9707	22960	36716	0.66	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinase-like protein 3 (xldp3)
9718	22746	36197	0.78	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9731	22759	36212	4.38	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) genes, complete cds



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9979	22006	36371	0.5	2.2E-01	Q60980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10174	23086	36579	3.74	2.2E-01	AF197841.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPaHSP21) mRNA, complete cds;
10313	23237	36719	1.78	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for ethnoplasm product
10337	23459	36958	1	2.2E-01	982587.1	NT	601869724.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100188 5'
10687	23619	37113	0.52	2.2E-01	T69472.1	EST_HUMAN	Human herpesvirus 6, complete genome
10697	23619	37114	0.52	2.2E-01	T69472.1	EST_HUMAN	1A634308.11 Stratiotes ovary (4637217) Homo sapiens cDNA clone IMAGE:75535 5'
10735	23657	37150	0.51	2.2E-01	AF068264.1	NT	1A634308.11 Stratiotes ovary (4637217) Homo sapiens cDNA clone IMAGE:75535 5'
10810	23731	37274	0.86	2.2E-01	AF071001.1	NT	Pseudomonas aeruginosa quinolone ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthase A (exaD) genes, complete cds; and pyrroloquin-
10856	23776	37275	0.87	2.2E-01	AE001562.1	NT	Mus musculus PTHR1 (Pthr1) gene, partial cds
11751	24034	38215	3.77	2.2E-01	X01818.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11759	23944	37466	3.41	2.2E-01	T708215	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
12317	25950		2.32	2.2E-01	U82871.2	NT	Drosophila 68C glue gene cluster
12406	25179		3.38	2.2E-01	AF188943.1	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12513	17482	30370	6.82	2.2E-01	AW361088.1	EST_HUMAN	Homo sapiens chromosome Xp28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cellfalin (GALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12514	25248		1.7	2.2E-01	AW661922.1	EST_HUMAN	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
13111	25948		1.38	2.2E-01	AF271285.1	NT	RC1-CT0249-141159-021-g04 CT0249 Homo sapiens cDNA
872	14024	26978	1.58	2.1E-01	AA560286.1	EST_HUMAN	H17502.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2872823 3'
975	14025	26980	1.03	2.1E-01	AL161504.2	NT	Phidopus surculus uncoupling protein 3 mRNA, partial cds
1128	14169		2.38	2.1E-01	AE002314.2	NT	nm3161.1 at NCI CGAP Lip2 Homo sapiens cDNA clone IMAGE:1081804
1203	14242	27169	0.88	2.1E-01	6754289	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
1203	14242	27200	0.88	2.1E-01	6754289	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1512	14544	27515	1.05	2.1E-01	AJ249885.1	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2) mRNA
1929	14953	27949	1.94	2.1E-01	AA008824.1	EST_HUMAN	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2) mRNA
2165	15181	28201	3.26	2.1E-01	BF695073.1	EST_HUMAN	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Aurl76 pseudogenes
2489	15895	28516	2.16	2.1E-01	HT39683.1	EST_HUMAN	6k73a02.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gbkK02765
							COMPLEMENT C3 PRECURSOR (HUMAN);
							602083128.F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
							iy04407.s1 Soares fetal liver spleen TNLFS Homo sapiens cDNA clone IMAGE:232837 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15895	28517	2.18	2.1E-01	H73988.1	EST_HUMAN	W0407.s1 Soares fetal liver spleen 1NF13 Homo sapiens cDNA clone IMAGE:232837 3'
2836	15994	28914	2	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3461	16507	29428	0.92	2.1E-01	AAG3482.1	EST_HUMAN	nc90b10.s1 NCI CGAP_C98 Homo sapiens cDNA clone IMAGE:1159579 3'
3819	16859		6.5	2.1E-01	6838861	NT	Beta vulgaris mitochondrion, complete genome
4045	17083		1.16	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4084	17118	30013	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4084	17118	30014	1.48	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4403	17431		1.62	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4807	17628	30520	1.75	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
5063	18073	30653	5.08	2.1E-01	D13567.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5110	18120	30984	1.13	2.1E-01	Q01339	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)
5216	18225	31089	0.92	2.1E-01	AE001528.1	NT	Helicobacter pylori strain J99 section 87 of 132 of the complete genome
5374	18479	31352	5.48	2.1E-01	BF672695.1	EST_HUMAN	602152001.F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
7071	20093	33403	1.16	2.1E-01	AJ223392.1	NT	Dodo fragile mitochondrion 16S rRNA gene, partial cds
7083	20017	33320	1.32	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7636	20596	33969	0.78	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7636	20596	33960	0.78	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7848	20608		2.34	2.1E-01	AE000972.1	NT	Achoetobolus litoralis section 135 of 172 of the complete genome
7973	20912	34303	1.77	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT19) gene, complete cds
8027	20994	34359	1.08	2.1E-01	AF066867.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8027	20994	34390	1.08	2.1E-01	AF066867.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8086	21022		0.61	2.1E-01	T87354.1	EST_HUMAN	yB301.r1 Soares fetal liver spleen 1NF15 Homo sapiens cDNA clone IMAGE:114763 5'
8407	21376		1.04	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8847	21814	35234	5.05	2.1E-01	U68389.1	NT	Haemophilus influenzae hmdC, putative haemochrom processing protein (hmcC), and haemochrom protein (hmcC) genes, complete cds
9149	22115	35540	0.84	2.1E-01	AL040637.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
9149	22115	35541	0.84	2.1E-01	AL040637.1	EST_HUMAN	DKFZp434H0614_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0614 5'
9302	22357	35787	6.08	2.1E-01	Z35788.1	NT	Saccharibae chromosome 1 reading frame ORF YBL025w
9662	22798	36251	0.59	2.1E-01	N42536.1	EST_HUMAN	yJ71e10.r1 Soares melanocyte 2NHFM Homo sapiens cDNA clone IMAGE:270954 5'
9662	22798	36252	0.59	2.1E-01	N42536.1	EST_HUMAN	yJ71e10.r1 Soares melanocyte 2NHFM Homo sapiens cDNA clone IMAGE:270954 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9871	22824	36277	2.77	2.1E-01	X97378.1	NT	Althaliana mRNA for ARABBP1b protein
9876	22603	36387	1.28	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10692	23614	37109	1.13	2.1E-01	Z87057.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10725	23647	37140	2.89	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAK KINASE DELTA)
10731	22653	37146	0.93	2.1E-01	BF674254.1	EST_HUMAN	(80 KD) DIACYLGLYCEROL KINASE
11009	23874	37498	3.89	2.1E-01	AF294298.1	NT	Anolis lineatus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11890	24771		2.16	2.1E-01	11036847	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11905	24786	38376	1.61	2.1E-01	BE180422.1	EST_HUMAN	RC3-H10622-040500-013-b11 HT0622 Homo sapiens cDNA
12137	25502		1.38	2.1E-01	X57624.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12560	25339		1.94	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12860	25960		1.8	2.1E-01	LC2598.1	NT	Human granulosa gene
12914	25493		2	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
13045	25586	31682	1.62	2.1E-01	BE672330.1	EST_HUMAN	7A59602.XT NCI_CGAP_GCC8 Homo sapiens cDNA clone IMAGE:3228034 3'
201	13302	26231	1.32	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
535	13806		1.92	2.0E-01	7705601	NT	Homo sapiens CG-18 protein (LOC51008), mRNA
700	13792	26694	1.25	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allele type Vha2
811	13869	28818	1.66	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1013	14061	27012	0.72	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7127, 781449-920915
1127	14170	27121	2.93	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1259	14294	27258	1.42	2.0E-01	AJ132695.5	NT	Homo sapiens rect gene
1311	14347	27313	2.04	2.0E-01	AW384937.1	EST_HUMAN	PW1-HT0422-291239-002-c08 HT0422 Homo sapiens cDNA
1454	14487		1.39	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1483	14516	27490	15.27	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1555	14587	27569	2.13	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1560	14592	27665	1.52	2.0E-01	AF260700.1	NT	Homo sapiens sodiumiodide symporter mRNA, partial cds
1708	14736	27718	1.36	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (Bradyb1) gene, complete cds
1730	14760		2.09	2.0E-01	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1772	14801		3.8	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1907	14931	27826	0.94	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1907	14931	27927	0.94	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2335	15364		1.88	2.0E-01	X82877.1	NT	H. sapiens Nar-D-glucose cotransport regulator gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3469	16546	26472	0.74	2.0E-01	P46807.	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3582	16627		0.82	2.0E-01	AW238005.1	EST_HUMAN	XP15002.x1 NC1 CGAP_H19g Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3720	16763	26874	0.79	2.0E-01	P34641	SWISSPROT	MER21 repetitive element;
3855	16896	26799	1.14	2.0E-01	AL163204.2	NT	
3977	17017	26931	0.7	2.0E-01	Z46806.1	EST_HUMAN	Sue scrofa
4597	17618		10.26	2.0E-01	BE826165.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
5078	18088	30968	7.08	2.0E-01	8922080	NT	
5144	18163	31033	0.97	2.0E-01	Y19216.1	EST_HUMAN	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5298	18302	31163	0.93	2.0E-01	BE439491.1	EST_HUMAN	Homo sapiens putative palHBD pseudogene for hair keratin, exons 1 to 9
5520	18619	31553	2.31	2.0E-01	X56900.1	NT	HTM1-122F1 HTMT Homo sapiens cDNA
5831	18921	32104	1.89	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5840	19028	32220	0.99	2.0E-01	X97650.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6178	19253	32488	5.47	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valyl-RNA synthetase
6298	19370		0.79	2.0E-01	M76967.1	NT	Saccharomyces cerevisiae Halp3 (HAL3) mRNA, complete cds
6417	19484	32733	0.56	2.0E-01	P02467	SWISSPROT	Human hepatocyte growth factor gene, exon 1
6569	19829	32805	3.08	2.0E-01	X81033.1	NT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6679	19758	33012	4.26	2.0E-01	AW360855.1	EST_HUMAN	M. aureus mu class glutathione transferase gene
7612	20471	33938	1.27	2.0E-01	AF260371.1	NT	PM1-CT0247-141009-001-g08 CT0247 Homo sapiens cDNA
7678	20637	33969	0.72	2.0E-01	P54422	SWISSPROT	Gua musculus phosphofructokinase-1 C isozyme (Pfc) gene, exons 3 through 7
8064	20991	34389	0.61	2.0E-01	V00726.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8285	21254		6.17	2.0E-01	AF028028.1	NT	Mouse germ line gene coding for beta-globin (Y2)
8542	21540	34927	3.1	2.0E-01	X91151.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
9074	22040		0.43	2.0E-01	BE562247.1	EST_HUMAN	M. musculus scp2 gene exon 14
9709	22659	36115	1.09	2.0E-01	U82511.1	NT	601344648F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3677764 5'
9745	22696	36141	0.76	2.0E-01	U71122.1	NT	Dicystotellum discoidium random slug cDNA19 protein (rac19) mRNA, partial cds
9914	22795		8.23	2.0E-01	AE001278.1	NT	Arabidopsis thaliana pyruvate decarboxylase-2 (Pdc2) gene, complete cds
10103	23029	36508	0.62	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
10103	23029	36507	0.62	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10261	23178		1.94	2.0E-01	AF146992.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
10401	23323	36807	1.94	2.0E-01	AF086507.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10401	23323	36808	1.94	2.0E-01	AF086507.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10528	23450	36948	0.64	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23460	36949	0.94	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10575	23467		0.78	2.0E-01	X78388.1	NT	D melanogaster DNA mobile element (hoppe)
10770	23601	37188	0.97	2.0E-01	X97121.1	NT	R. norvegicus mRNA for NTR2 receptor
11188	24145	37578	2.24	2.0E-01	D80888.1	NT	Salvelinus plusius mRNA for transferrin, complete cds
11189	24145	37578	2.24	2.0E-01	D80888.1	NT	Salvelinus plusius mRNA for transferrin, complete cds
12841	26325		1.42	2.0E-01	AF206637.2	NT	Pinnaphalea promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12828	25779		1.96	2.0E-01	AF302773.1	NT	Homo sapiens ninhydrin-Lm isoform (ninhydrin) mRNA, complete cds
12837	25711	31609	1.34	2.0E-01	AW1975207.1	EST_HUMAN	EST1387405 VAGE sequences, MAGN Homo sapiens cDNA
12875	25508	31707	4.12	2.0E-01	U023562.1	EST_HUMAN	pe80410.a1 Soares_bellu_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12898	25483		2.98	2.0E-01	AF078164.2	NT	Homo sapiens Kirt70-binding protein (KUB3) mRNA, partial cds
110	13221		9.9	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlnt1), mRNA
352	13441	26365	8.09	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
657	13723	26647	2.66	1.9E-01	U32581.2	NT	Homo sapiens lamda10a protein kinase C-interacting protein mRNA, complete cds
657	13723	26648	2.66	1.9E-01	U32581.2	NT	Homo sapiens lamda10a protein kinase C-interacting protein mRNA, complete cds
664	13730	26655	8.69	1.9E-01	BE070801.1	EST_HUMAN	RC3-B170502-251199-011-d01 B170502 Homo sapiens cDNA
665	13730	26655	8.69	1.9E-01	BE070801.1	EST_HUMAN	RC3-B170502-251199-011-d01 B170502 Homo sapiens cDNA
888	14039		1.19	1.9E-01	7305160	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1106	14150	27101	9.83	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1372	14405	27376	2.9	1.9E-01	AF067282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1430	14464		3.22	1.9E-01	AF184623.1	NT	Pleurodon vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2390	15398	28423	3.99	1.9E-01	89223533	NT	Homo sapiens hypodermal protein FLJ10587 (FLJ10581), mRNA
2394	15692	28912	3.47	1.9E-01	U68066.1	NT	Sigmodon haplids p53 gene, partial cds
2349	16008		4.69	1.9E-01	J06922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3406	16455	29378	4	1.9E-01	D13187.1	NT	Mouse gene for immunoglobulin diversity region D1
3412	16639	29464	5.96	1.9E-01	R16467.1	EST_HUMAN	y42701.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:126547 5'
3817	16957	29763	0.87	1.9E-01	AF284071.1	NT	Rattus norvegicus arylamidase deacetylase gene, complete cds
3948	16988	29781	2.26	1.9E-01	P30788	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
4018	17057	29859	3.61	1.9E-01	AB006784.1	NT	Schistosoma japonicum bomb DNA for cytoplasmic dynein heavy chain, complete cds
4110	17144	30035	1.42	1.9E-01	AW0754106.1	EST_HUMAN	CM3-CT0315-271199-045-B11 CT0315 Homo sapiens cDNA
4259	17268	30169	1.24	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4468	17521	30408	0.83	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
5047	18050		1.15	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5231	18239		1.01	1.9E-01	AI631189.1	EST_HUMAN	rs59g12.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:U21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5685	18780		5.2	1.9E-01	AW130148.1	EST_HUMAN	x29a07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5728	18922	32002	8.11	1.9E-01	AF127857.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5839	18025	32219	0.71	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5987	18072		2.15	1.9E-01	AF0133116.1	EST_HUMAN	AU373116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6461	19528	32776	0.95	1.9E-01	AJ762391.1	EST_HUMAN	w54402.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
6527	19590	32850	0.88	1.9E-01	AW148452.1	EST_HUMAN	x14408.x1 NCI_CGAP_K18 Homo sapiens cDNA clone IMAGE:2818030 3' similar to gb:X03559 ATP
7164	18396	31240	1.46	1.9E-01	AF034920.1	EST_HUMAN	Yg09a12.ct Source infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7193	20217	33547	0.95	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7474	20440	33798	0.85	1.9E-01	U73846.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7709	20686	34033	0.76	1.9E-01	U69688.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7734	20689	34053	1.35	1.9E-01	U80922.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7784	20737	34109	2.64	1.9E-01	AF072724.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
8318	21287	34701	1.41	1.9E-01	AL161567.2	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
8034	22000	35421	12.88	1.9E-01	AB033024.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8287	22263	35692	1.32	1.9E-01	M14588.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9297	22263	35693	1.32	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10234	23159	36847	0.87	1.9E-01	AA912488.1	EST_HUMAN	Marsupial cat beta-globin gene mRNA, partial cds
10602	23524	37019	0.72	1.9E-01	BE830353.1	EST_HUMAN	085g10.ct NCI_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1637506 3' similar to contains Alu repetitive element;
10602	23524	37020	0.72	1.9E-01	BE830353.1	EST_HUMAN	RC6-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
11106	24066	37588	1.87	1.9E-01	AF223591.1	NT	RC5-ET0082-080700-022-A02 ET0082 Homo sapiens cDNA
11831	24714	38298	1.47	1.9E-01	M22253.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
12033	24909	38504	3.54	1.9E-01	AJ243213.1	NT	Rattus norvegicus sodium channel 1 mRNA, complete cds
12049	24922	38519	1.63	1.9E-01	L07344.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12975	25540		1.62	1.9E-01	AF036959.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5, 5' end
341	13154	28055	2.78	1.9E-01	U75200.1	NT	Rattus norvegicus nuclear serine/threonine protein kinase mRNA, complete cds
280	15837	26281	1.39	1.9E-01	AB022080.1	NT	Mus musculus p116lip mRNA, complete cds
							Mus musculus Ctg gene for chaperonin containing TCP-1 gamma subunit, partial cds

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370	13456	28386	1.91	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
883	14034	29898	0.89	1.8E-01	AI012212.1	EST_HUMAN	W07102.X1 NCL CGAP_LU24 Homo sapiens cDNA clone IMAGE:2337051 3'
1093	14136	27087	1.05	1.8E-01	AF000580.1	NT	Dichotylem discoidum miasm Dap5, complete genome
1293	14228	27280	9.43	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1503	14536	27907	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1503	14538	27508	1.17	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1864	14889		1.37	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1882	14807		1.47	1.8E-01	AI733708.1	EST_HUMAN	qg22410.x5 NCL CGAP_Kd3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR-075938 075938 GAMMA BUTYROBETAINE HYDROXYLASE
1930	14954	27950	1.69	1.8E-01	AB051897.1	NT	Mus musculus Soya8, Soya8, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Soya10 pseudogene, small inducible cytokine A5 precursor, complete cds
2702	15698		3.04	1.8E-01	AF184589.1	EST_HUMAN	QV3-DT0018-081200-036-g04 DT0018 Homo sapiens cDNA
2908	15697		1.85	1.8E-01	AF184589.1	NT	Jonopsidium aculea LEAFY protein (LEAFY2) gene, partial cds
2914	15872	28896	0.85	1.8E-01	AW162300.1	EST_HUMAN	X41a03.x1 Soares_NFL1_GBQ_S1 Homo sapiens cDNA clone IMAGE:2659755 3'
3141	16198	29108	1.35	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3378	16428	28564	0.82	1.8E-01	BF183582.1	EST_HUMAN	901809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3637	16880	28594	1.69	1.8E-01	H03389.1	EST_HUMAN	Y4F501.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3637	16880	28595	1.69	1.8E-01	H03389.1	EST_HUMAN	Y4F501.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4360	17387		0.75	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (B2A-DQB), complete cds
4586	17608	30503	6.42	1.8E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4806	17823	30718	2.5	1.8E-01	AB051897.1	NT	Mus musculus Soya8, Soya8, Soya16-ps, Soya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Soya10 pseudogene, small inducible cytokine A5 precursor, complete cds
5061	18003	30941	2.11	1.8E-01	X78794.1	NT	N. latum mRNA pNLA-35
5069	18094	30970	1.96	1.8E-01	AV1814270.1	EST_HUMAN	MR3-ST0203-151289-112-p06 ST0203 Homo sapiens cDNA
6084	18109	30982	0.93	1.8E-01	AT92382.1	EST_HUMAN	anc28p07.y5 Gessler Wilms Tumor Homo sapiens cDNA clone IMAGE:1700028 5'
6131	18140	31018	2.66	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-tetrocholate cotransporting polypeptide mRNA, partial cds
8214	18223		0.73	1.8E-01	U68150.1	NT	Coligo torosus TTA repeat microsatellite region Ltr4
8371	18476	31349	0.84	1.8E-01	BE082828.1	EST_HUMAN	RC9-BT0841-300300-011-H03 BT0841 Homo sapiens cDNA
8506	18892	32183	1.91	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90

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12901	25112	31840	1.88	1.8E-01	BF348623.1	EST_HUMAN	602015628F1.NC1.CGAP_Bme7 Homo sapiens cDNA clone IMAGE:4155318 5'
12752	25398		2.05	1.8E-01	Q60992	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12896	26469		1.65	1.8E-01	R24494.1	EST_HUMAN	YH48101.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12907	25469		1.90	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hxk1)
878	13648	28561	1.77	1.7E-01	BE385184.1	EST_HUMAN	601274604F1.NH.MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
509	13864	28614	2.22	1.7E-01	X53330.1	NT	P. dumeretii histone gene cluster for core histones H2A, H2B, H3 and H4
962	14015		1.83	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1998	15019		3.18	1.7E-01	AF255051.1	NT	Homo sapiens BINP3H (BINP3H) gene, complete cds; nuclear gene for mitochondrial product
2871	15931	28848	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpaR) gene, complete cds, and YRAL VIBCO gene, partial cds
2871	15931	28848	2.3	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpaR) gene, complete cds, and YRAL VIBCO gene, partial cds
2838	15996	28977	1.69	1.7E-01	AA336909.1	EST_HUMAN	EST141651 Endometrial tumor Homo sapiens cDNA 5' end
3010	16090	28968	1.22	1.7E-01	AJ238735.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3010	16090	28969	1.22	1.7E-01	AJ238735.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3122	16170	29089	1.68	1.7E-01	AF061514.1	NT	Toxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3378	16427	29333	0.82	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3462	16503	29429	1.48	1.7E-01	AJ268905.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3559	16989	29814	5.89	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4591	17612		1.9	1.7E-01	X62935.1	NT	Schistosoma gregaria alpha repetitive DNA
4876	17893	30782	1.21	1.7E-01	AJ247695.1	EST_HUMAN	q157c09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848806 3' similar to contains ORF.81 OFR repetitive element;
5165	18174		0.92	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ee) gene, complete cds
5210	18219	31095	0.74	1.7E-01	BF030010.1	EST_HUMAN	601557269F1.NH.MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5482	18582	31493	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.21 NC1.CGAP_Co3 Homo sapiens cDNA clone IMAGE:3810066 3' similar to gb:M17896 60S
5482	18582	31494	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.21 NC1.CGAP_Co3 Homo sapiens cDNA clone IMAGE:3810066 3' similar to gb:M17896 60S
5674	18769	31941	0.74	1.7E-01	U43599.1	NT	ADICIC RIBOSOMAL PROTEIN P1 (HUMAN);
6493	19528	32777	12.89	1.7E-01	H72115.1	EST_HUMAN	Brugia pahangi mitochondrial steady protein SHP3 (shp3) gene, complete cds
							ys02905.81 Soares fetal liver spliced 1NFLS Homo sapiens cDNA clone IMAGE:213688 3'



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6528	19589	32849	0.9	1.7E-01	AI370976.1	EST_HUMAN	h29c11.x1 Scores_fetal_lung_NHL16W Homo sapiens cDNA clone IMAGE:2045492 3'
6528	19589	32849	0.9	1.7E-01	AI370976.1	EST_HUMAN	h29c11.x1 Scores_fetal_lung_NHL16W Homo sapiens cDNA clone IMAGE:2045492 3'
7031	18963	31260	0.78	1.7E-01	BE300288.1	EST_HUMAN	000944057T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860248 3'
7033	20085		1.76	1.7E-01	AF028552.3	NT	Mesocricetus auratus orviductin precursor (OV) gene, complete cds
7198	20220		0.79	1.7E-01	Z92810.1	NT	Homo sapiens HFE gene
7430	20307	33749	1.68	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai/V72 prophage inserted region
7515	20480	33841	8.55	1.7E-01	BE734178.1	EST_HUMAN	80158022P2T1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7721	20678	34043	1.42	1.7E-01	P16724	SWISSPROT	COLLAGEN PROCESSING AND TRANSPORT PROTEIN UL56 (HLEF0 PROTEIN)
7739	25698	34057	0.71	1.7E-01	Q01965	SWISSPROT	PROBABLE ALPHA 3(V) CHAIN PRECURSOR
8194	21164	34573	1.24	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
8295	21265	34573	0.82	1.7E-01	AF150698.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8620	21688	35004	7.37	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8620	21688	35005	7.37	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
9045	22011	35433	0.6	1.7E-01	AW922873.1	EST_HUMAN	RC2-BN0032-120200-011-at10 BN0032 Homo sapiens cDNA
9079	22045	35468	3.22	1.7E-01	D00384.1	NT	Rat (SHR strain) Sx1 gene
9198	22162	35590	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neurologin 3 isoform gene, complete cds, alternatively spliced
9198	22162	35591	0.81	1.7E-01	AF217413.1	NT	Homo sapiens neurologin 3 isoform gene, complete cds, alternatively spliced
9349	22314	35739	0.44	1.7E-01	RT7002.1	EST_HUMAN	y99g02.r1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:144242 5'
9523	22486	35833	0.43	1.7E-01	BE253142.1	EST_HUMAN	801116672P2T1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9523	22486	35834	0.43	1.7E-01	BE253142.1	EST_HUMAN	801116672P2T1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9948	22875	36537	8.16	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/4
10056	22983	36451	0.47	1.7E-01	AW977458.1	EST_HUMAN	EST1388554 MAGIE resequences, MAGO Homo sapiens cDNA
10059	22983	36452	0.47	1.7E-01	AW977455.1	EST_HUMAN	EST1388554 MAGIE resequences, MAGO Homo sapiens cDNA
10073	23000	36470	1.83	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
10148	23074	36548	0.50	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10148	23074	36549	0.59	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10167	23092	36570	0.7	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-8), (sp8 gene)
10593	23515		2.43	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 C084
10759	23680	37176			11427203	NT	Homo sapiens soluble carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
10761	23682	37178	1.81	1.7E-01	AA627972.1	EST_HUMAN	hcg0007.s1 NCL_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gbL25081
10965	23866		0.42	1.7E-01	AL161542.2	NT	TRANSFORMING PROTEIN RHOC (HUMAN);
11040	24004	37530	8.17	1.7E-01	BE390835.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment NC_42

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11157	24115	37641	2.61	1.7E-01	AA814617.1	EST_HUMAN	d43a03.s1 NCI CGAP CNSI Homo sapiens cDNA clone IMAGE:1426924 3'
11447	24390	37633	8.03	1.7E-01	7106300	NT	Mus musculus adenomeliosis polyposis coli binding protein Eb1 (Eb1), mRNA
11447	24390	37634	8.03	1.7E-01	7106300	NT	Mus musculus adenomeliosis polyposis coli binding protein Eb1 (Eb1), mRNA
11703	24988	38246	1.6	1.7E-01	AA883375.1	EST_HUMAN	d4509a.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1400297 3'
12021	24998		1.66	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12141	25005	38616	1.74	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12273	25693		1.64	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12437	25736	31618	1.55	1.7E-01	AA847421.1	EST_HUMAN	ce18102.s1 NCI CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1380261
12555	25739					EST_HUMAN	b69g05.s1 NCI CGAP_U01 Homo sapiens cDNA clone IMAGE:2274872 3' similar to b6-M73776 RET[NOIC]
12833	25450	31723	1.69	1.7E-01	AI824404.1	EST_HUMAN	ACID RECEPTOR ALPHA-1 (HUMAN);
12833	25450	31723	14.15	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
126	13233	26162	2.02	1.8E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
680	15814	26670	1.56	1.8E-01	R37487.1	EST_HUMAN	X75512.t1 Soares placenta NbzHP Homo sapiens cDNA clone IMAGE:135559 5'
1504	14537	27509	1.4	1.8E-01	AA548663.1	EST_HUMAN	nc26n12.s1 NCI CGAP_Cot1 Homo sapiens cDNA clone IMAGE:1014839 3'
1525	14537	27528	4.54	1.8E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1941	14965	27682	1.79	1.8E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2001	15022		1	1.8E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2093	15992	28427	0.89	1.8E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2501	15504	29531	1.18	1.8E-01	AB037726.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2802	15961	28881	10.42	1.8E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2802	15961	28882	10.42	1.8E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3949	16592	29607	1.2	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3849	16592	29608	1.2	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol AB13 gene
3765	16527	29734	0.78	1.8E-01	AJ000982.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4025	17063		2.81	1.8E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4358	17383	30265	10.43	1.8E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4484	17509		3.1	1.8E-01	AW968601.1	EST_HUMAN	EST398077 IMAGE resources, MAGJ Homo sapiens cDNA
4491	17516		4.37	1.8E-01	8753318	NT	Mus musculus chaperonin subunit 3 (gamma) (Ccs3), mRNA
4916	17633	30524	1.43	1.8E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4916	17633	30525	1.43	1.8E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4952	17697	30885	4.38	1.8E-01	AA08843.1	EST_HUMAN	284h09.s1 Stralagene colon (#637204) Homo sapiens cDNA clone IMAGE:611361 3' similar to TR:E221955
5004	18018	30505	1.84	1.8E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
5004	18018	30506	1.84	1.8E-01	AJ006356.1	NT	Lycopodium esculentum Real fragment 2, satellite region
5004	18018	30506	1.84	1.8E-01	AJ006356.1	NT	Lycopodium esculentum Real fragment 2, satellite region

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5009	18079	30960	1.16	1.6E-01	BE018707.1	EST_HUMAN	bb3h08.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M67175 (TRYPTOPHAN-TRNA SYNTHETASE (HUMAN)); gb:X69657 M.musculus (MOUSE);
5461	18583	31475	0.87	1.0E-01	L45608.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5600	18596	31668	2.82	1.6E-01	AW197496.1	EST_HUMAN	xm4301.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2686989 3' similar to TR:O75984 O75984
5600	18596	31667	2.82	1.6E-01	AW197496.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN :
5912	18708	31865	2.31	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN :
8144	19219	32449	0.9	1.6E-01	AF0325803.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cbpε) gene, complete cds
8385	19453	32697	0.57	1.6E-01	BF183584.1	EST_HUMAN	RC3-NM0034370600-13-H01 BN0034 Homo sapiens cDNA
8395	19453	32698	0.57	1.6E-01	BF183584.1	EST_HUMAN	601809729R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6588	19628	32863	1.09	1.6E-01	AL161688.2	NT	001809729R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040335 3'
6588	19628	32864	1.09	1.6E-01	AL161688.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6950	20174	33498	0.95	1.6E-01	AA338047.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6950	20174	33519	0.66	1.6E-01	AB046786.1	NT	289004.r1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:728511 5'
7156	18398	31232	4.63	1.6E-01	AW291215.1	EST_HUMAN	Homo sapiens mRNA for KIAA1586 protein, partial cds
7518	20483	33844	0.61	1.6E-01	Z49832.1	NT	U144-B12-apt-b-05-Q1.st NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
8096	20993	34390	1.69	1.6E-01	AW246359.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR132w
8090	21026	34425	0.57	1.6E-01	6753237	NT	2822248.Spina NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8102	21038	34582	1.15	1.6E-01	AL136525.1	EST_HUMAN	Mus musculus Cdc22-dependent activator protein for secretion (Cdcps), mRNA
8201	21171	34582	1.26	1.6E-01	L49349.1	NT	U144-B12-apt-b-05-Q1.st NCI_CGAP_Sub4 Homo sapiens cDNA clone PLACE1004466 5'
8356	21328		0.51	1.6E-01	BE244087.1	EST_HUMAN	Gorilla gorilla androgen receptor gene, partial exon
8456	21425	34841	0.66	1.6E-01	U39243.1	NT	TCBPAP1E0697 Pedicella pro-B cell acute lymphoblastic leukaemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TOBAP0607
8676	21945	35399	0.85	1.6E-01	Z69119.1	NT	cDNA clone TOBAP0607
9178	22144	35571	0.71	1.6E-01	R13573.1	EST_HUMAN	Bacteroides vulgatus beta-lactamase (bta) gene, complete cds and mobilization protein (mobA) gene, complete cds
9285	22251		0.53	1.6E-01	L36861.1	NT	Bacillus subtilis complete genome (section 16 of 21), from 2997771 to 3213410
9322	22287	35717	1.9	1.6E-01	Z49801.1	NT	Y6808.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:28973 5'
9466	22430		0.63	1.6E-01	AF111167.2	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
10008	22636		2.08	1.6E-01	BF37571.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR001w
10012	22636	36404	2	1.6E-01	Z49801.1	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10048	22676		0.96	1.6E-01	BE155984.1	EST_HUMAN	RC3-ST0200-041199-011-H01 ST0200 Homo sapiens cDNA
							S.cerevisiae chromosome X reading frame ORF YJR001w
							PM2-HT0353-270100-004-111 HT0353 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11017	23982	37509	2.59	1.8E-01	AW950853.1	EST_HUMAN	IL3-CT0220-11189-028-007-CT0220 Homo sapiens cDNA
11122	24092	37607	1.82	1.8E-01	Z28073.1	NT	S.cervicollis chromosome XI reading frame ORF YKL073w
11122	24092	37608	1.82	1.8E-01	Z28073.1	NT	S.cervicollis chromosome XI reading frame ORF YKL073w
11344	24294	37820	1.51	1.8E-01	BE258649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11451	24394	384	3.84	1.8E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11740	24623	38204	6.59	1.8E-01	6671552	NT	Mus musculus adapter-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12155	25006		1.75	1.8E-01	6679468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pkg2), mRNA
12275	25095	38179	6.76	1.8E-01	AV719585.1	EST_HUMAN	AV719585 GLG Homo sapiens cDNA clone GLCEM07 5'
12608	25307		1.82	1.8E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12697	25721		22.15	1.8E-01	AB045310.1	NT	Cucumis sativus KS mRNA for anti-leukene synthase, complete cds
12856	25483		2.73	1.8E-01	AK024498.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12945	25524		2.55	1.8E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12971	25537	31719	2.24	1.8E-01	9208522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cargp5), mRNA
12978	25543		1.63	1.8E-01	BE267694.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
248	13345	28270	1.73	1.8E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	13345	28271	1.73	1.8E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
889	15813		2.4	1.8E-01	AV711698.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH06 5'
1094	14138	27089	1.51	1.8E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1099	14143	27083	2.55	1.8E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGS22 myosin heavy chain, 3'UTR
1115	14159		1.87	1.8E-01	AJ36123.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
1280	14315	27276	3.99	1.8E-01	D28535.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1280	14315	27277	3.99	1.8E-01	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1478	14511	27487	2.94	1.8E-01	AF117340.1	EST_HUMAN	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1923	14647	27943	1.65	1.8E-01	AW444451.1	EST_HUMAN	Mus musculus MAP kinase kinase 1 (Mokk1) mRNA, complete cds
2723	15717	28736	1.47	1.8E-01	BF695381.1	EST_HUMAN	U1H-B18-akb-b-09-01-NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2924	15982		1.1	1.8E-01	AW572518.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5'
3048	16105	29019	0.79	1.8E-01	MB1441.1	NT	aw56602.22 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb-X55072_nai
3363	18413	25538	5.55	1.8E-01	AA835049.1	EST_HUMAN	Boa tauasin factor V variant 2 (factor V) mRNA, complete cds
3391	18430	29357	0.74	1.8E-01	Z23104.1	NT	cod9408.at NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571397 3' similar to gb-M11433
3391	18430	29358	0.74	1.8E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
							Letagrelis mRNA for G protein-coupled receptor
							Letagrelis mRNA for G protein-coupled receptor

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3440	16487	29405	0.87	1.5E-01	AW612237.1	EST_HUMAN	rh29f02.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element:
3768	16810	29719	2.22	1.5E-01	U09894.1	NT	Mus musculus ICR/Swiss glyceraledehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3792	16823	29731	0.8	1.5E-01	71083358	NT	XYNA: Thermonaerobacterium: xynA: 4182 base-pairs
3795	16835	29740	0.66	1.5E-01	M97882.1	NT	U1005.x1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2961411 3'
3881	16920	29829	2.26	1.5E-01	AW65683.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
3896	16936	29846	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3896	16936	29847	0.71	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4080	17115	30011	2.63	1.5E-01	AW356550.1	EST_HUMAN	RC2-HT0149-191059-012-c03 HT0149 Homo sapiens cDNA
4273	17242	30127	0.83	1.5E-01	AL162284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4513	17538	30422	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583568F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838345 5'
4513	17538	30423	0.91	1.5E-01	BE791253.1	EST_HUMAN	601583568F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838345 5'
4756	17776	30872	1.88	1.5E-01	BF887695.1	EST_HUMAN	602087162F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4066223 5'
4763	17717	28735	2.86	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4247837 5'
4830	17847	30747	1	1.5E-01	BE173798.1	EST_HUMAN	CX0-HT0565-290200-245-b10 HT0565 Homo sapiens cDNA
4830	17847	30748	1	1.5E-01	BE173798.1	EST_HUMAN	CX0-HT0565-290200-245-b10 HT0565 Homo sapiens cDNA
5034	18048	30928	1.2	1.5E-01	AL161590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5134	18143	31023	1.07	1.5E-01	5579451	NT	Homo sapiens calbindin 1, (28KD)(CALB1), mRNA
5328	18434	31186	2.46	1.5E-01	P07598	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5357	18462	31331	1.03	1.5E-01	AF256652.1	NT	Calinin crocullus MHC class II beta chain (hclbeta) gene, complete cds
5401	18504		5.5	1.5E-01	P15166	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ASP)
5616	18712	31870	4.35	1.5E-01	AW650754.1	EST_HUMAN	IL3-C10219-160200-064-F10 C10219 Homo sapiens cDNA
5659	18755	31922	7.17	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5659	18755	31923	7.17	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
6012	19056	32295	0.79	1.5E-01	4506810	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA
6120	19168	32422	1.74	1.5E-01	6753559	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6120	19168	32423	1.74	1.5E-01	6753559	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6161	19238	32467	1.96	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6319	19390	32630	3.25	1.5E-01	BE77268.1	EST_HUMAN	601584322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19443		1.86	1.5E-01	4506398	NT	Homo sapiens RAD54 (S cerevisiae)-like (RAD54L) mRNA

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6478	18543	32791	1.7	1.5E-01	AF134007.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6651	25864	32985	1.8	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 88 of 172 of the complete genome
6681	19738	33013	4.83	1.5E-01	U147238	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3). mRNA
6692	19749	33026	1.8	1.5E-01	P49508	SWISSPROT	GLUTAMATE-CYSINE LIASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6740	10765	33075	2.35	1.5E-01	Q28462	SWISSPROT	ALMOGENIN
6842	19895	33189	0.85	1.5E-01	AA714786.1	EST_HUMAN	nc30d10.x1 NCL CGAP. GC80 Homo sapiens cDNA clone IMAGE:1241971.3
6871	19924	33220	1.8	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7171	18402	31247	5.15	1.5E-01	AW870285.1	EST_HUMAN	EST3382376 NCL CGAP. ressequences, MAGK Homo sapiens cDNA
7214	26878		0.71	1.5E-01	AA811545.1	EST_HUMAN	ob35022.1 NCL CGAP. GC81 Homo sapiens cDNA clone IMAGE:1337019.3 similar to contains element LTR2 repetitive element:
7424	20391		1.91	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7621	20581	33945	1.68	1.5E-01	AF731157.1	EST_HUMAN	wr520b.x1 NCL CGAP. U11 Homo sapiens cDNA clone IMAGE:2491310.3
7846	20783	34169	0.96	1.5E-01	AF289073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7846	20783	34170	0.86	1.5E-01	AF289073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7857	20802	34177	1.84	1.5E-01	AW500811.1	EST_HUMAN	U1-HF-BNO-alk-d-05-0-U1.11 NIH. MGC. 50 Homo sapiens cDNA clone IMAGE:3077409.5
7857	20802	34178	1.84	1.5E-01	AW500811.1	EST_HUMAN	U1-HF-BNO-alk-d-05-0-U1.11 NIH. MGC. 50 Homo sapiens cDNA clone IMAGE:3077409.5
8014	20952	34346	0.71	1.5E-01	U46590.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of bud-1.1 (SOL3) gene, complete cds
8393	21352	34769	1.21	1.5E-01	P21303	SWISSPROT	MEROZINTE RECEPTOR PK68 PRECURSOR (68 KD PROTECTIVE MINOR SURFACE ANTIGEN) INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8582	21530	34950	0.97	1.5E-01	AA970317.1	EST_HUMAN	od5912.x1 NCL CGAP. K1d5 Homo sapiens cDNA clone IMAGE:1572030.3 similar to gbM26062
8655	21623		1.01	1.5E-01	BE884769.1	EST_HUMAN	607150325F1 NIH. MGC. 71 Homo sapiens cDNA clone IMAGE:3912004.5
8743	21711		13.33	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human scita polyA+ mRNA (K6572) Homo sapiens cDNA clone GEN-529H09.5
8776	21743	35165	1.09	1.5E-01	L27695.1	NT	Pengasinodon gliae growth hormone (GH) mRNA, complete cds
8940	21908	35330	1.79	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds
8952	21928		0.74	1.5E-01	P43446	SWISSPROT	WNT-10A PROTEIN PRECURSOR
9190	22156	35895	1.31	1.5E-01	4501972	NT	Homo sapiens adipocyte-related protein complex 1, beta 1 subunit (ADTB1). mRNA
9490	22424	36882	3.06	1.5E-01	N74226.1	EST_HUMAN	za59606.x1 Soesies fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:268666.3 similar to
9548	22511	35960	1.03	1.5E-01	BF555465.1	EST_HUMAN	PIR344443 S44443 RAD23 protein homolog2 - human
9555	22517		2.73	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Poxvirus Differential Display Homo sapiens cDNA
9760	22701		0.87	1.5E-01	U130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAA-HB12.5
9808	21131	34634	6.92	1.5E-01	U00465.1	NT	AU130007 N72RP3 Homo sapiens cDNA clone NT2BP3000080.5
							Acipenser transmontanus Mielogenin mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10176	23101	36581	0.59	1.9E-01	M7144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10281	23208	36590	6.22	1.9E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10281	23208	36591	6.22	1.9E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10553	23483	36678	2.67	1.9E-01	X98562.1	NT	P. leucostictus mRNA for integrin beta subunit
10551	23573		0.32	1.9E-01	AB027750.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10671	23593	37089	2.49	1.9E-01	AB14046.1	EST_HUMAN	wk53h12.xt NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27608 BETA
10671	23593	37090	2.49	1.9E-01	AB14046.1	EST_HUMAN	wk53h12.xt NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27608 BETA
10753	23675	37172	2.19	1.9E-01	U40932.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10906	23626	37338	2.14	1.9E-01	AJ011964.1	NT	Danio rerio transcription factor Pax9p (Pax9) mRNA, complete cds
10906	23626	37339	2.14	1.9E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10906	23626	37339	2.14	1.9E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
11173	24130	37659	4.35	1.9E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11173	24130	37660	4.35	1.9E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11412	24358	37691	1.71	1.9E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11449	24392	37937	3.88	1.9E-01	AA425488.1	EST_HUMAN	zva6402.r1 Soares, fetal, fetus, No24F8, 9w Homo sapiens cDNA clone IMAGE:773091 5' similar to
11501	20581	33945	1.69	1.9E-01	AB973157.1	EST_HUMAN	contains element MER22 repetitive element;
12229	25769		11.17	1.9E-01	BF700582.1	EST_HUMAN	wr82608.xt NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
12607	25908		1.62	1.9E-01	AF030358.2	NT	602128753.F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4286549 5'
12607	25909		1.81	1.9E-01	AJ238332.1	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12698	25761		12.47	1.9E-01	R83077.1	EST_HUMAN	Mus musculus mRNA for death inducer-oligodendrocyte-1 (Dio-1)
12748	25814		2.45	1.9E-01	AV741272.1	EST_HUMAN	yv87604.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194430 5'
12855	25722	31613	7.87	1.9E-01	AL139074.2	NT	AV741272 CB Homo sapiens cDNA clone CBADAGD04 5'
13073	26006	31689	1.53	1.9E-01	AJ276242.1	NT	Campylobacter jejuni NCTC11168 complete genome, segment 1/6
288	13393		2.07	1.9E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
911	13666		3.95	1.9E-01	AF006683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV21S2A2 region
1264	14239		2.77	1.9E-01	DT1864.1	EST_HUMAN	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1793	14792		1.61	1.9E-01	6679990	NT	yv44601.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:112032 3'
1798	14795	27780	1.82	1.9E-01	AE001710.1	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
2002	15023		12.82	1.9E-01	AA720815.1	EST_HUMAN	Thermoplasma maritima strain 22 of 136 of the complete genome
2482	15466	28509	1.15	1.9E-01	P30709	SWISSPROT	hy72007.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2804	15768	28815	7.57	1.9E-01	AB335486.1	EST_HUMAN	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
							wnt74d01.xt NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3914	19554	29895	0.93	1.4E-01	R50232.1	EST_HUMAN	y937a03.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
3914	19554	29896	0.93	1.4E-01	R50232.1	EST_HUMAN	y937a03.r1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
4202	17233	30120	11.04	1.4E-01	AI89094.1	EST_HUMAN	b56502.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4202	17233	30121	11.04	1.4E-01	AI89094.1	EST_HUMAN	b56502.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4265	17294	30173	3.98	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z150b01.s1 Scores fetal liver spleen 1N1LS S1 Homo sapiens cDNA clone IMAGE:458973 3' similar to
							gb:201057_m01 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu
4440	17466		0.71	1.4E-01	AA776287.1	EST_HUMAN	repetitive element;
							Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila);homolog phosphodiesterase E2)
4703	17724	30518	0.69	1.4E-01	5453981	NT	(PDE4A), mRNA
4607	17824	30517	0.92	1.4E-01	AV680559.1	EST_HUMAN	AV680559 GKCC Homo sapiens cDNA clone GKCDUG09 5'
5379	18483	31398	4.72	1.4E-01	T90677.1	EST_HUMAN	y916c11.ct1 Stralagene lung (8937210) Homo sapiens cDNA clone IMAGE:117812 3'
5402	18505	31381	4.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5402	18505	31382	4.06	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6430	19496	32749	2.9	1.4E-01	BE326891.1	EST_HUMAN	h976c02.x1 NCI CGAP JKD11 Homo sapiens cDNA clone IMAGE:3133338 3'
6529	19687	32955	5.1	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000768 5'
6929	19687	32956	5.1	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000768 5'
6723	19779	33058	3.48	1.4E-01	AW082796.1	EST_HUMAN	x671d12.x1 Scores NFLC_T_GBC S1 Homo sapiens cDNA clone IMAGE:2551751 3'
6737	19793	33093	1.26	1.4E-01	SE266536.1	EST_HUMAN	60119523FT NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3537681 5'
6759	19813	33093	2.02	1.4E-01	BF376533.1	EST_HUMAN	QV14UM00305-08C0300-103-009 UN00038 Homo sapiens cDNA
7333	20304		0.74	1.4E-01	AI185683.1	EST_HUMAN	DKFZp761A0910.1 r1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A0910 5'
7615	20575		1.87	1.4E-01	AW015373.1	EST_HUMAN	UJH-BIO-aat-c-39-c-Ju.1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7841	20801	33965	0.61	1.4E-01	F08746.1	EST_HUMAN	HSC21D8011 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN
							w04f12.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN
7694	20852		0.61	1.4E-01	A1762827.1	EST_HUMAN	P49992 CASPASE-4 PRECURSOR:
7893	20927	34203	0.82	1.4E-01	U85645.1	NT	Oryctolagus cuniculus fructose 1,6 biphosphate aldolase (AldB) gene, complete cds
8029	20968	34361	1.24	1.4E-01	A1305192.1	EST_HUMAN	q96012.x1 Scores NHMPS1 Homo sapiens cDNA clone IMAGE:1876983 3'
8818	21785		1.24	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCSPH06 3'
							h92b12.x1 Scores NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
							TR:002710 002710 GAG POLYPROTEIN:
9136	22102		0.87	1.4E-01	A1635093.1	EST_HUMAN	IT1781912 Cx36 carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9264	22230	35581	4.68	1.4E-01	AA070703.1	EST_HUMAN	db8803.y1 Marfan Field Coochies Homo sapiens cDNA clone IMAGE:2487485 5'
9345	22310	35735	0.56	1.4E-01	AW023638.1	EST_HUMAN	y10h05.r1 Scores placenta N22HP Homo sapiens cDNA clone IMAGE:198973 5'
9478	22442	35983	0.94	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Scores placenta N22HP Homo sapiens cDNA clone IMAGE:198973 5'
9478	22442	35984	0.94	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Scores placenta N22HP Homo sapiens cDNA clone IMAGE:198973 5'



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9541	22904	35953	9.19	1.4E-01	BF10859.1	EST_HUMAN	501685465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9830	22574	36024	1.19	1.4E-01	W68411.1	EST_HUMAN	z64840.1 Scores_fetal_NH_H18W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element:
9702	22955	36109	0.43	1.4E-01	X73293.1	NT	M.xenodii genes rpoH, rpoB and rpoA
9702	22955	36110	0.43	1.4E-01	X73293.1	NT	M.xenodii genes rpoH, rpoB and rpoA
9713	22966	36123	1.44	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9713	22966	36124	1.44	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9805	21128	34532	2.06	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zeta finger protein (DNZ1) genes, complete cds
10164	23089	36597	0.55	1.4E-01	X66092.1	NT	C.perningens ORF for putative membrane transport protein
10346	23270	36747	1.12	1.4E-01	AF023813.1	NT	Macromitrium levalum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10448	23370	36961	0.57	1.4E-01	AW021908.1	EST_HUMAN	d29h08.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10448	23370	36962	0.57	1.4E-01	AW021908.1	EST_HUMAN	d29h08.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10619	23541	37039	0.67	1.4E-01	BF376285.1	EST_HUMAN	MR3-ST0218-211299-073-a08 ST0218 Homo sapiens cDNA
10619	23541	37040	0.67	1.4E-01	BF376286.1	EST_HUMAN	MR3-ST0218-211299-073-a08 ST0218 Homo sapiens cDNA
10829	23750	37395	0.56	1.4E-01	T84283.1	EST_HUMAN	y47403.1 Scores_fetal_liver spleen TNFSL Homo sapiens cDNA clone IMAGE:111365 5'
10829	23750	37396	0.71	1.4E-01	Z69117.1	NT	Bacillus subtilis complete genome (section 14 of 21), from Z594451 to 2812870
11191	24147	37680	2.69	1.4E-01	R63400.1	EST_HUMAN	376035.1 Scores_breast_2NH83 Homo sapiens cDNA clone IMAGE:154088 5'
11432	24376	37616	2.53	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11762	24637		1.59	1.4E-01	AL161466.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
11797	23952	37474	2.38	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11855	24737		1.55	1.4E-01	X52102.1	NT	M.musculus p18K gene for 18 kDa protein
12549	25272	31776	2.33	1.4E-01	X74773.1	NT	P.salina plastid gene ecoY
12562	25280		2.24	1.4E-01	11988117	NT	Rattus norvegicus desmin (Des), mRNA
12605	25964		2.35	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12702	25362	229	2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2869767-3002965
12778	25991		4.86	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12965	25792		3.72	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
13067	25601		2.63	1.4E-01	AW377698.1	EST_HUMAN	MR0-H10208-221299-204-c08 H10208 Homo sapiens cDNA
322	13414	26338	2.48	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 60 (GPR60) mRNA
322	13414	26339	2.48	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
630	13501	26519	2.91	1.3E-01	AB013138.1	NT	Homo sapiens gene for NBS1, complete cds
637	13703	26624	0.78	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
637	13703	26625	0.78	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
845	13901	26859	1.04	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
895	13960	26908	1.76	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1028	14074	27024	1.8	1.3E-01	AL117078.1	NT	Bovyla chinea strain T4 cDNA library under conditions of nitrogen deprivation
1129	14172	27215	2.88	1.3E-01	AL116285.1	NT	Bovyla chinea strain T4 cDNA library under conditions of nitrogen deprivation
1220	14258	27215	1.51	1.3E-01	AF1712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF03 5'
1438	14471	27699	0.93	1.3E-01	AF146277.1	NT	Homo sapiens adipsin protein CDS mRNA, complete cds
1976	14997	27699	2.07	1.3E-01	AL117078.1	NT	Bovyla chinea strain T4 cDNA library under conditions of nitrogen deprivation
2180	15195		1.69	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidiphila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2298	15310		0.96	1.3E-01	AW812104.1	EST_HUMAN	RC4-3T0173-191099-032-d12 ST0173 Homo sapiens cDNA
2389	15397		3.94	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2592	15593	28610	2.23	1.3E-01	N88918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3485	16511	29432	0.98	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyolipoyl transacylase mRNA, complete cds
3735	16777	29689	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3735	16777	29690	0.91	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3741	16783	29695	0.99	1.3E-01	AB032169.1	NT	Homo sapiens DDX gene for dihydrodialdehyde dehydrogenase 4 [AKR1C4], exon 2
3794	16777	29699	0.87	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3816	16868	29782	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4014	17053		1.48	1.3E-01	AL101581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4081	13703	26624	7.11	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
4081	13703	26625	7.11	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93UK
4163	17194		1.12	1.3E-01	AF020713.1	NT	Saccharophaga SPB22 complete genome
4185	17216		4.1	1.3E-01	AW354341.1	EST_HUMAN	QV3-DT0018-081298-036-403 DT0018 Homo sapiens cDNA
4194	17225	30114	2.47	1.3E-01	AF028605.1	NT	Schizosaccharomyces mansueti fructose biphosphate aldolase mRNA, complete cds
4215	17244	30129	20.19	1.3E-01	AW173741.1	EST_HUMAN	X02310.1 Soares_NFL1_T_OBC_S1 Homo sapiens cDNA clone IMAGE:281365 3'
4343	17370		1.49	1.3E-01	AL162280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17530	30414	0.8	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyoloyl transacylase mRNA, complete cds
4554	17587	30478	2.72	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
5014	18028		0.91	1.3E-01	AU136819.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone IMAGE:1004603 5'
5060	18070		0.83	1.3E-01	BF091680.1	EST_HUMAN	RC4-TN0077-188980-312-c05 TN0077 Homo sapiens cDNA
5308	18501	31379	0.76	1.3E-01	AW465988.1	EST_HUMAN	ha07606.x1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.51 L1 L1 repetitive element.
5436	18538	31446	1.98	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0033-100400-189-ac09 UM0033 Homo sapiens cDNA
5579	18675		0.91	1.3E-01	AF107793.1	NT	Emmella nidulans DNA-dependent RNA polymerase II RPB2 gene, partial cds
5655	18760		0.88	1.3E-01	AF056880.1	NT	Hepatitis C virus 88_C1.10 genome polyprotein gene, partial cds
5813	18803	32088	0.85	1.3E-01	BF210920.1	EST_HUMAN	60187456F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6089	19178	32386	0.58	1.3E-01	BF527261.1	EST_HUMAN	602038337F2 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6099	19178	32397	0.58	1.3E-01	BF527261.1	EST_HUMAN	602038337F2 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6630	19688	32987	17.29	1.3E-01	AB031326.1	NT	Schistosoma japonicum pombe gene for Alp41, complete cds
6720	19778	33055	2.08	1.3E-01	X88951.1	NT	C-jacchus thron 4 of visual pigment gene (red allele)
6840	20164	33487	0.64	1.3E-01	H73423.1	EST_HUMAN	yu0201.r1 Sources fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:232609 5'
6855	20180		0.92	1.3E-01	W25367.1	EST_HUMAN	2663 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7009	20135	33450	1.04	1.3E-01	BE782928.1	EST_HUMAN	60146565F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3899078 5'
7009	20135	33451	1.04	1.3E-01	BE782928.1	EST_HUMAN	60146565F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3899078 5'
7211	20234		0.72	1.3E-01	BF529560.1	EST_HUMAN	60204345F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7477	20443		2.15	1.3E-01	H48664.1	EST_HUMAN	y33402.r1 Sources fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:207076 5'
8292	21281		0.97	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
8308	21275	34688	1.59	1.3E-01		NT	Homo sapiens PRO081 protein (PRO081), mRNA
8339	21305	34720	1.18	1.3E-01	BF600522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8580	21548		0.95	1.3E-01	BE360228.1	EST_HUMAN	601335828F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8817	21685	35001	0.6	1.3E-01	11421536	NT	Homo sapiens TED protein (TED), mRNA
8888	21696		4.88	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YD1054c
8729	21697		4.2	1.3E-01	8823918	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8873	21840	35263	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
9300	22285	35694	0.55	1.3E-01	R11172.1	EST_HUMAN	y33q11.1 Sources fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP-R12B, RAT P23316 60S RIBOSOMAL PROTEIN ;
9300	22265	35695	0.65	1.3E-01	R11172.1	EST_HUMAN	y33q11.1 Sources fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:128284 5' similar to SP-R12B, RAT P23316 60S RIBOSOMAL PROTEIN ;
9574	22436	35587	0.65	1.3E-01	11069003	NT	Plutella xylostella granulovirus, complete genome
9574	22538	35588	0.65	1.3E-01	11069003	NT	Plutella xylostella granulovirus, complete genome

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9827	22876	36132	3.9	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
10129	23035		0.74	1.3E-01	N86348.1	EST_HUMAN	JR337F Human fetal heart, Lambda Zap Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 20
10411	23333		0.89	1.3E-01	8393940	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (P44), mRNA
10489	23411	36908	0.86	1.3E-01	AW851568.1	EST_HUMAN	MR2-G10222-001059-001-001 CT0222 Homo sapiens cDNA
10787	23702	37173	1.05	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
10891	23811	37318	0.66	1.3E-01	AL121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10938	23866	37372	0.45	1.3E-01	AW247836.1	EST_HUMAN	2820037 3prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2820637 3'
10996	23992		2.57	1.3E-01	BF330696.1	EST_HUMAN	MR4-BT0358-100700-010-N08 BT0358 Homo sapiens cDNA
11581	24519		3.66	1.3E-01	6671745	NT	Mus musculus collagen 2, muscle (COL2), mRNA
11670	24608	38182	1.77	1.3E-01	AW082338.1	EST_HUMAN	xc20709.xt NCI_CGAP_Cot8 Homo sapiens cDNA clone IMAGE:2884841 3'
11670	24608	38183	1.77	1.3E-01	AW082336.1	EST_HUMAN	xc20709.xt NCI_CGAP_Cot9 Homo sapiens cDNA clone IMAGE:2884841 3'
11922	24803	38396	2.33	1.3E-01	BE279449.1	EST_HUMAN	801156052F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3504804 5'
12397	25171	31817	1.83	1.3E-01	BE618346.1	EST_HUMAN	801482747F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3666003 5'
12535	25260		3.3	1.3E-01	AJ242780.1	NT	Gallus gallus scyl1 gene for lymphocytin, exons 1-3
12692	25357	31766	1.37	1.3E-01	BF572303.1	EST_HUMAN	802077752F1 NIH_MGC 92 Homo sapiens cDNA clone IMAGE:4252062 5'
12895	25475		1.48	1.3E-01	AB026826.1	NT	Ehrydalia fluviatilis mRNA for SALK 9, complete cds
12915	25494		2.52	1.3E-01	AW001114.1	EST_HUMAN	wk24089.xt Soares Dieckgraebe cdon NIHCD Homo sapiens cDNA clone IMAGE:2820977 3' similar to TR-Q16671
383	13496	26428	14.66	1.2E-01	AJ421744.1	EST_HUMAN	tr39602.xt NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gbU05760_mai1 ANNEXIN V (HUMAN);
424	13119		1.38	1.2E-01	U66912.1	NT	Dicystosellum discoidium ORF DG1016 gene, partial cds
549	13818		2.78	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1377	14411	27381	2.19	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1377	14411	27382	2.19	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1383	14417		4.89	1.2E-01	AV735249.1	EST_HUMAN	AU735249 cda Homo sapiens cDNA clone cdaAJ311 5'
1388	14421		0.92	1.2E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1507	14540		1.23	1.2E-01	AA897474.1	EST_HUMAN	q16671 Scars_NHL_T_CGC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR-Q16671
1635	14637	27643	1.62	1.2E-01	Q14934	SWISSPROT	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ;
1658	14680	27665	2.99	1.2E-01	AI285402.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-AT3)
1793	14812		18.68	1.2E-01	AG9211.1	NT	Hs960B.xt NCI_CGAP_Eco2 Homo sapiens cDNA clone IMAGE:1960563 3'
1834	14958		1.76	1.2E-01	AW449368.1	EST_HUMAN	Hs960B DNA for endogenous retroviral like element

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2193	18208	28227	1.65	1.2E-01	BF248490.1	EST_HUMAN	601821867F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4048224 6'
2294	15306	28329	1.21	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2395	15306	28814	2.05	1.2E-01	AW686556.1	EST_HUMAN	OV3-BN0046-220306-12b-f10 BN0046 Homo sapiens cDNA
2802	15602	28824	1.61	1.2E-01	BE216898.1	EST_HUMAN	hs55604.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3'
							1st8907.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1] contains element PTR5 repetitive element.
2738	15732	28748	37.59	1.2E-01	AI623388.1	EST_HUMAN	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2855	15915	28838	1.4	1.2E-01	U18018.1	NT	aa30cd3.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gpL05095
2913	16971	28895	2.03	1.2E-01	AI720470.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L30 (HUMAN);
2946	16004	28929	2.52	1.2E-01	MI6394.1	NT	Human creatine kinase-B mRNA, complete cds
3017	16075	28996	0.73	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3244	16209	29224	1.34	1.2E-01	AW370558.1	EST_HUMAN	OV1-BT0259-261059-021-c05 BT0259 Homo sapiens cDNA
3271	16325		0.82	1.2E-01	U07600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3533	16579	29302	0.86	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3533	16579	29503	0.86	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3620	16538		1.05	1.2E-01	Z69118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2796131 to 3013540
3780	16821		0.7	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4211	17240	30125	2.16	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4211	17240	30128	2.16	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4751	17771	30657	0.98	1.2E-01	Z48163.1	NT	L. esculentum mRNA for glycylase-1
5116	18126		1	1.2E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5150	18159	31038	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5150	18159	31039	0.91	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5164	18173	31052	1	1.2E-01	AL161618.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
5234	18242	31114	0.81	1.2E-01	BE974502.1	EST_HUMAN	601680469R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850711 3'
5322	18428	31178	0.75	1.2E-01	AA744389.1	EST_HUMAN	hs3504.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5373	18478	31351	0.91	1.2E-01	AF223391.1	NT	
5383	18487	31361	2.27	1.2E-01	W33033.1	EST_HUMAN	z080402.1 Soares_paritythroid_tumor_NHFA Homo sapiens cDNA clone IMAGE:321699 5'
5442	18544	31458	2.15	1.2E-01	Z69208.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5593	18979	31643	0.95	1.2E-01	Z48234.1	NT	M domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6324	19394	32630	2.66	1.2E-01	BE620943.1	EST_HUMAN	601469516F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6376	19444	32888	1.1	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6431	19497	32750	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL6-CTD031-221089-119-004 CT0301 Homo sapiens cDNA
6499	19503	32815	1.38	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6804	19858	33145	0.89	1.2E-01	BF347085.1	EST_HUMAN	602023112FT NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4195386 5'
6961	20180	33517	0.55	1.2E-01	AF295739.1	NT	JC virus agnoprotein, VP2, VP3, VP1, large T antigen, and small T antigen genes, complete cds
7210	20233	33557	0.67	1.2E-01	HA47769.1	EST_HUMAN	yp80104.1 Scores fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:193759 5'
7210	20233	33558	0.87	1.2E-01	HA47769.1	EST_HUMAN	yp80104.1 Scores fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:193759 5'
7854	20769	34175	0.82	1.2E-01	AJ217441.1	NT	Homo sapiens partial ILF3 gene for interleukin enhancer binding factor 3 (alternative transcripts drbp76, drbp76 gamma, drbp76 alpha and ILF3)
8063	21000	34598	0.9	1.2E-01	BF680613.1	EST_HUMAN	602155185FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296382 5'
8098	21034	34433	0.57	1.2E-01	D87495.1	NT	Human mRNA for KIAA0282 gene, partial cds
8098	21034	34434	0.57	1.2E-01	D87495.1	NT	Human mRNA for KIAA0282 gene, partial cds
8224	21193		1.24	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-109 BN0137 Homo sapiens cDNA
8295	21284	34675	3.1	1.2E-01	AJ913763.1	EST_HUMAN	yc99903.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8341	21310	34724	0.76	1.2E-01	Q02389	SWISSPROT	Q99739 MICROSMAL GLUTATHIONE S-TRANSFERASE II
8632	21620	35040	0.81	1.2E-01	AI832681.1	EST_HUMAN	NADH:UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX II-B22) (Cl-B22)
8739	21707		10.85	1.2E-01	AW083852.1	EST_HUMAN	at71b10.x1 Barleed cotton HPLR87 Homo sapiens cDNA clone IMAGE:2377435 3'
8739	21707						yc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587587 3' similar to gb:M13452 LAMIN A (HUMAN);
8750	21726		3.98	1.2E-01	AF03772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds, and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8768	21765	35187	0.89	1.2E-01	U03959.1	NT	N crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8768	21765	35188	0.89	1.2E-01	U03959.1	NT	N crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8848	21814		0.81	1.2E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
9037	22003		2.01	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 28 of 163 of the complete genome
9073	22039		0.64	1.2E-01	X16191.1	NT	M. musculus DNA fragment of Apolipoprotein B gene
9830	22813	36287	1.69	1.2E-01	X77691.1	NT	S. cerevisiae HXT5 gene
10385	23298	36765	1.64	1.2E-01	AV710857.1	EST_HUMAN	AY710857 Gu Homo sapiens cDNA clone GUAAKE08 5'
11282	24185		2.36	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11404	24348		2.55	1.2E-01	BE962324.2	EST_HUMAN	801855578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3946283 3'
11482	24425		1.57	1.2E-01	BF314481.1	EST_HUMAN	801800765FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11584	24522	38077	2.45	1.2E-01	AF190483.1	NT	Homo sapiens dynein intermediate chain DNAT1 (DNAT1) gene, exon 17
11738	24623	38201	1.6	1.2E-01	9994174	NT	Homo sapiens UDP-Gal:beta-GlcNAc beta 1,4-galactosyltransferase, polypeptide 4 (B4GALT4), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11836	24719		1.54	1.2E-01	M65108.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12162	25018		3.66	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone QLCF12 3'
12517	25246		2.78	1.2E-01	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
12593	25822	31304	6.17	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
12605	25432		2.66	1.2E-01	X53881.1	NT	R-norvegicus NF68 gene for 68kDa neurofilament
12847	25935	31310	1.58	1.2E-01	BE081418.1	EST_HUMAN	QV4-BT024-111199-031-g10 BT024.4 Homo sapiens cDNA
12889	25477	31731	9.62	1.2E-01	AI268003.1	EST_HUMAN	002005.X1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12971	25460		2.91	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12917	25902		9.28	1.2E-01	O68433	SWISSPROT	CYCLIN T
12846	25525	31712	1.76	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13032	16538		2.08	1.2E-01	296118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
13099	25823		1.5	1.2E-01	BF314481.1	EST_HUMAN	601800763FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
588	13636	26552	1.01	1.1E-01	AI651003.1	EST_HUMAN	Int663.X1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
617	13682	26559	1.84	1.1E-01	AA569006.1	EST_HUMAN	hmp89T1.s1 NCL CGAP_Cor10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gbX066985_Ina1
1057	14103	27054	1.55	1.1E-01	BF697308.1	EST_HUMAN	802129847FT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286771 5'
1087	14131		1.48	1.1E-01	AI181580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1163	19860	27158	4.8	1.1E-01	AW672158.1	EST_HUMAN	EST384T142 IMAGE resequences, IMAGE Homo sapiens cDNA
1284	14230	27255	2.03	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2888767-3002965
1524	14566	27627	2.48	1.1E-01	AU140383.1	EST_HUMAN	AI140383 PLACE2 Homo sapiens cDNA clone PLACE200403 5'
2322	15333		2.72	1.1E-01	6756215	NT	Mus musculus cdc T-cell antigen receptor alpha (Pctra) mRNA
2543	19828		0.93	1.1E-01	6976878	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1) mRNA
2574	15575		0.93	1.1E-01	AW821909.1	EST_HUMAN	RCQ-5T0379-2T0100-032-q04 ST0379 Homo sapiens cDNA
3046	16103	29017	0.95	1.1E-01	F03265.1	EST_HUMAN	HSC-TRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
3352	16403		1.66	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g) mRNA
3432	16430	28399	2.18	1.1E-01	BE393186.1	EST_HUMAN	601308678FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3466	16372	29433	1.3	1.1E-01	X62785.1	NT	C. reinhardtii nuclear gene on linkage group XIX
3599	16641	29560	0.8	1.1E-01	Y07695.1	NT	A. limnerus gene for transposase
3715	16756		0.86	1.1E-01	P67384	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3722	16765	29676	1.23	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4137	17109	30054	1.14	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-260100-026-q07 ST0280 Homo sapiens cDNA
4137	17198	30055	1.14	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-260100-026-q07 ST0280 Homo sapiens cDNA
4281	17310		9.36	1.1E-01	AF157066.1	NT	Drosophila melanogaster Karsch protein (kar) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4316	17345	30229	0.69	1.1E-01	AW802066.1	EST_HUMAN	IL5-UM0070-020500-068-a03 UM0070 Homo sapiens cDNA
4870	17691	30577	1.02	1.1E-01	S44957.1	NT	Tape-1 integral membrane protein TAPA-1 [pinea, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4889	17898	30774	0.98	1.1E-01	V07695.1	NT	A. lamarum gene for transposase
6056	17174		0.76	1.1E-01	AF030001.1	NT	Male testicular major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Nucle4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin-X (TNX) genes, complete>
5753	18847		1.36	1.1E-01	AA747216.1	EST_HUMAN	nc76d03.s1 NCL_CGAP_Esk1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5820	18919	32102	1.19	1.1E-01	AF020627.1	NT	8 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 8
5868	18957	32145	0.95	1.1E-01	AL110985.1	NT	Borly's chinese strain T4 cDNA library under conditions of nitrogen deprivation
5904	18990	32180	0.73	1.1E-01	BF330519.1	EST_HUMAN	602039176F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4186818 5'
5904	18990	32181	0.73	1.1E-01	BF330519.1	EST_HUMAN	602039176F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4186818 5'
5935	19021	32215	1.67	1.1E-01	X68851.1	NT	S. pombe ssb gene encoding protein kinase
5971	19036	32259	4.99	1.1E-01	M86533.1	NT	Providencia reitgeri penicillin G amidase gene
6142	19217	32446	1.63	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6184	19238	32470	1.54	1.1E-01	BE769162.1	EST_HUMAN	PK3-FT0024-130500-004-f12 FT0024 Homo sapiens cDNA
6184	19259	32493	8	1.1E-01	AW853699.1	EST_HUMAN	RC3-C10254-250099-011-e01 GT0254 Homo sapiens cDNA
6594	19624	32859	0.5	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6571	19631	32858	1.26	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6517	19675	32953	0.84	1.1E-01	AI216307.1	EST_HUMAN	3976006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6762	19816	33035	6.18	1.1E-01	O89635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6892	19915		2.81	1.1E-01	AF032822.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6992	20187	33512	2.23	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan class B (PIGB), mRNA
7249	19984	33291	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7249	19984	33282	0.65	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7393	20569		0.94	1.1E-01	BF332758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050853 5'
7523	20663	33860	1.59	1.1E-01	AF000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1486000 nt, position (617)
7781	20734	34105	7.69	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7791	20734	34108	7.69	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302019 5'
7639	20780	34108	0.54	1.1E-01	AA865008.1	EST_HUMAN	cu44903.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1629172 3'
7917	20860	34248	1.77	1.1E-01	PA1087	SWISSPROT	TRAB PROTEIN
7959	20900		0.79	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7861	20602	34294	2.99	1.1E-01	AA768784.1	EST_HUMAN	ah31068.s1 Soares_purithyroid_tumor_NHHPA Homo sapiens cDNA clone 1240403 3' similar to gbJ33483
8111	21048	34448	0.65	1.1E-01	BE782260.1	EST_HUMAN	CHROMOGRANIN A PRECURSOR (HUMAN);
8301	21270	34882	0.48	1.1E-01	U67482.1	NT	807470055FT NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3873229 5'
8550	21518	34938	1.61	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8550	21518	34937	1.61	1.1E-01	AA493574.1	EST_HUMAN	h04610.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8598	21698	34982	1.1	1.1E-01	X91233.1	NT	h04610.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8637	21605	34982	1.06	1.1E-01	AW817916.1	EST_HUMAN	H.sapiens LT16 gene
8637	21605	34982	1.06	1.1E-01	AW817916.1	EST_HUMAN	PM1-S10270-090200-001-009 S10270 Homo sapiens cDNA
8694	21662	35086	1.59	1.1E-01	AL134349.1	EST_HUMAN	DKFZ547P194_T1 547 (synonym: h6r1) Homo sapiens cDNA clone DKFZ547P194 5'
9170	22136	35562	1.82	1.1E-01	U02482.1	NT	Pedococcus acidilacti H plasmid pSMB74 pedocin ACP production (pap) gene cluster papA, papB, papC and papD genes, complete cds
9263	22228	35560	0.96	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9302	22327	35790	0.56	1.1E-01	AF050081.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9398	22383	35794	2.27	1.1E-01	AA192163.1	EST_HUMAN	Homo sapiens C16orf3 large protein mRNA, complete cds
9398	22383	35795	2.27	1.1E-01	AA192163.1	EST_HUMAN	zp93012.t1 Stratiogene muscia 837209 Homo sapiens cDNA clone IMAGE:927743 5'
9490	22454	35894	0.77	1.1E-01	Y12727.1	NT	zp93012.t1 Stratiogene muscia 837209 Homo sapiens cDNA clone IMAGE:927743 5'
9520	22483	35929	2.1	1.1E-01	T72875.1	EST_HUMAN	P.furiosus partial dph15 gene and argP gene
9548	22509	36029	0.62	1.1E-01	BE893260.1	EST_HUMAN	y41903.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9777	22718	36796	0.89	1.1E-01	BE142305.1	EST_HUMAN	gbM8181.S1 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9853	22789	36851	2.05	1.1E-01	BF085149.1	EST_HUMAN	601468972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922046 5'
10270	23195	37119	0.68	1.1E-01	AL161543.2	NT	CN3-HT0142-271059-026-g11 HT0142 Homo sapiens cDNA
10476	23398	37119	0.45	1.1E-01	BE319509.1	EST_HUMAN	MR2-GN0027-940800-005-a08 GN0027 Homo sapiens cDNA
10666	23488	37119	1.01	1.1E-01	R60590.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, centig fragment No. 43
10701	23623	37119	1.05	1.1E-01	U60528.1	NT	601140231F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049543 5'
11156	19103	26017	1.7	1.1E-01	F03295.1	EST_HUMAN	y4da08.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147084 3'
11267	24219	37119	3.13	1.1E-01	AF169092.1	NT	Ceratitis eplata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
11384	24331	37860	3.51	1.1E-01	R23708.1	EST_HUMAN	HSC1R1F022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
11392	24338	37868	1.54	1.1E-01	6981351	NT	Cerassius auratus activin beta A precursor mRNA, complete cds
11542	24483	38035	2.18	1.1E-01	Z11910.1	NT	y45612.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11542	24483	38035	2.18	1.1E-01	Z11910.1	NT	Rattus norvegicus Phosphotriesterase, liver, B-type (Pfk), mRNA
11642	24483	38035	2.18	1.1E-01	Z11910.1	NT	Z mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11636	24573	38137	3.66	1.1E-01	IP17437	SWISSPROT	Z mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12280	25084		2.03	1.1E-01	AA192153.1	EST_HUMAN	z93812.1 Stratiene muscle 637269 Homo sapiens cDNA clone IMAGE:627743 5'
12379	25181		3.68	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-03 NT0112 Homo sapiens cDNA
12626	26732		2.18	1.1E-01	BE974656.1	EST_HUMAN	80186051R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950804 3'
13038	28580	31689	1.89	1.1E-01	BF239753.1	EST_HUMAN	801906350F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134085 5'
13098	28912		1.32	1.1E-01	P14400	SWISSPROT	ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1
1206	14245		2.05	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) [LYSOSOMAL DNASE II]
12771	14312	27273					W68A01.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:249657 3' similar to contains MER7.8
12771	14312	27273	1.85	1.0E-01	AI985499.1	EST_HUMAN	NBT7 repetitive element 1
1363	14427	27398	2.25	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2497	19500	26528	1.16	1.0E-01	AW461365.1	EST_HUMAN	UHH-B18-alc-0-07-Q.U1 NCL CGAP_SuB8 Homo sapiens cDNA clone IMAGE:2736420 3'
3524	19570	29493	1.32	1.0E-01	BF033991.1	EST_HUMAN	801456301T1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3959849 5'
3732	16774	26686	0.69	1.0E-01	BF236918.1	EST_HUMAN	801905489F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134071 5'
3849	16889	29792	2.49	1.0E-01	AF287061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3978	17016	26930	2.69	1.0E-01	AF287061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4595	17607		0.86	1.0E-01	AF792349.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4741	17781	30655	1.32	1.0E-01	U50450.1	NT	an32c04.y5 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4957	17972	30883	2.34	1.0E-01	AW982344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5257	18274	31138	0.97	1.0E-01	AV721471.1	EST_HUMAN	EST364414 IMAGE: sequences, MAGB Homo sapiens cDNA
5273	18478		1.04	1.0E-01	AV763960.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBQE10 5'
5394	18497		8.1	1.0E-01	W86490.1	EST_HUMAN	AV763960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5462	18522		0.59	1.0E-01	X54015.1	NT	X62N04.s1 Scores_Tel1 Liver: spleen, TNF.LS, S1 Homo sapiens cDNA clone IMAGE:476993 3'
5980	19055		0.87	1.0E-01	AK024472.1	NT	Xcamptis genes for sensor and regulator protein
8140	19218	33445	12.15	1.0E-01	AF274875.1	NT	Homo sapiens mRNA for EL00055 protein, partial cds
6469	19534	32782	0.9	1.0E-01	AA481879.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
8463	19548	37697	0.65	1.0E-01	AA406039.1	EST_HUMAN	z941910.e1 Scores ovary tumor N9H0T Homo sapiens cDNA clone IMAGE:756258 3' similar to contains L1.43 L1 repetitive element 1
							z94702.1 Scores testis NHT Homo sapiens cDNA clone IMAGE:743002 3'
							y93408.1 Scores placenta Nt2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Aliu repetitive element
7220	20242		1.62	1.0E-01	R23821.1	EST_HUMAN	M.musculus with gene
8005	20947		2.16	1.0E-01	Y12498.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8108	21045	34444	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8108	21045	34445	0.65	1.0E-01	AJ011400.1	NT	Bos taurus mRNA for b17.2 subunit of NADH:ubiquinone oxidoreductase complex (complex I)
8265	21234	34645	0.63	1.0E-01	AA881091.1	EST_HUMAN	h032901.s1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:U34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8287	21268	34686	0.45	1.0E-01	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8287	21256	34666	0.45	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8506	21474		0.69	1.0E-01	47583365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8837	21604		0.94	1.0E-01	AW168797.1	EST_HUMAN	X06401.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2675680 3' similar to gb-X17208 40S
9540	22503	35952	1.19	1.0E-01	AF102855.2	NT	RIBOSOMAL PROTEIN S4 (HUMAN) contains TAR1, b. TAR1 repetitive element;
9852	22681	36241	0.54	1.0E-01	R44993.1	EST_HUMAN	Rattus norvegicus synapse SAPAP-interacting protein Synanon mRNA, complete cds
9865	22801		2.05	1.0E-01	M76729.1	NT	Homo sapiens infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9908	22728		2.65	1.0E-01	AE001591.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9922	22806	36259	0.51	1.0E-01	W01655.1	EST_HUMAN	Helicobacter pylori strain J98 section 62 of 132 of the complete genome
10180	23105	36596	1.63	1.0E-01	BF240154.1	EST_HUMAN	z26610.x1 Soares fetal heart UNHHT19W Homo sapiens cDNA clone IMAGE:327282 3'
10295	23220	36703	9.1	1.0E-01	AB046798.1	NT	601805661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10295	23220	36704	9.1	1.0E-01	AB046798.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10592	23424		0.95	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10597	23429	36928	0.55	1.0E-01	T51952.1	EST_HUMAN	EST569615 IMAGE: resequences, IMAGE Homo sapiens cDNA
10894	23616	37110	0.90	1.0E-01	BE792765.1	EST_HUMAN	y029406.x1 Striagene fetal spleen (H937205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
11018	23993		1.65	1.0E-01	AU159127.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
11370	24317	37844	2.25	1.0E-01	BF242946.1	EST_HUMAN	AU159127 THYROT1 Homo sapiens cDNA clone THYROT100895 3'
11370	24317	37845	2.28	1.0E-01	BF242946.1	EST_HUMAN	60187703F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4106089 5'
11729	24614	38191	3.16	1.0E-01	BE790543.1	EST_HUMAN	60187703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
12365	25491		4.11	1.0E-01	BE537718.1	EST_HUMAN	601892568F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
12538	25622		2.16	1.0E-01	7662166	NT	60106554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12904	25905		2.58	1.0E-01	X00654.1	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12798	25425		1.45	1.0E-01	AA737981.1	EST_HUMAN	Drosophila melanogaster fzf gene
12895	25481		4.47	1.0E-01	BE537718.1	EST_HUMAN	IK11603.x1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1255790 3'
12943	25522		1.32	1.0E-01	BE158905.1	EST_HUMAN	60106554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12959	25581		6.14	1.0E-01	U66534.1	NT	QV4-HT0401-211289-064-g03 HTD401 Homo sapiens cDNA
13016	25586		7.59	1.0E-01	AP001607.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
						NT	Bacillus thuringiensis genomic DNA, section 11/4
						NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pla-R1) mRNA, complete cds
2789	15781	28797	1.74	9.9E-02	AF274008.1	NT	
2798	15790	28808	1.71	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455385 5'
2798	15790	28809	1.71	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3455385 5'
3280	10334	28254	1.48	9.9E-02	AF099510.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3074	17014	29028	0.87	9.9E-02	A1821637.1	EST_HUMAN	24d5c03.x3 Soares ovary tumor NIH/OT Homo sapiens cDNA clone IMAGE:740932 3'
4707	17728	30622	1.02	9.9E-02	BE974249.1	EST_HUMAN	7d7f612.x1 NCI CGAP_L24 Homo sapiens cDNA clone IMAGE:3278998 3'
7044	20066	33373	2.59	9.9E-02	BE913498.1	EST_HUMAN	607504252F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906064 5'
7163	18394	31239	7.77	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blebsidin S deaminase, complete cds
8247	21216	34624	0.85	9.9E-02	AW103088.1	EST_HUMAN	x43c09.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
8247	21216	34626	0.85	9.9E-02	AW103088.1	EST_HUMAN	x43c09.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9812	22619	36068	1.23	9.9E-02	0755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
565	13635		1.88	9.8E-02	X56338.1	NT	O.saliva RAm3C gene for alpha-amyase
3160	16216	26130	4.26	9.8E-02	AF184274.1	NT	Daucus carota leucanthocyndin dioxygenase 2 (LDOX) mRNA, LDOX:2 allele, complete cds
4251	17280	30160	6.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4251	17280	30161	6.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7723	20579		0.94	9.8E-02	X54133.1	NT	Human HP7P delta mRNA for protein tyrosine phosphatase delta
9009	22613		1.21	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11788	23943	37466	1.83	9.8E-02	BF037421.1	EST_HUMAN	607460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
12330	25131		1.84	9.8E-02	8392761	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1352	14387	27357	1.75	9.7E-02	AB008008.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1589	14621		1.33	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2270	15283	28309	2.78	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-096-a04 HT0516 Homo sapiens cDNA
4008	17047		4.89	9.7E-02	Q89785	SWISSPROT	GELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5418	16621	31398	0.88	9.7E-02	AF099189.1	NT	Cardiobacter crescentius thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5418	16621	31398	0.88	9.7E-02	AF099189.1	NT	Cardiobacter crescentius thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6130	19207	32492	1.48	9.7E-02	AF064476.1	EST_HUMAN	EST37885406 MAGC resequences, MAGC Homo sapiens cDNA
7517	20482	33943	3.35	9.7E-02	AB99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
8315	21284	34697	1.09	9.7E-02	N22798.1	EST_HUMAN	hw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:264788 3'
8315	21284	34698	1.09	9.7E-02	N22798.1	EST_HUMAN	hw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:264788 3'
9201	22167	35597	1.52	9.7E-02	AI963984.1	EST_HUMAN	hw78006.x1 NCI CGAP_Ov48 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb-X92851_ma1
11629	24470		2.01	9.7E-02	U56337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2032	15051	28068	1.27	9.0E-02	AI080721.1	EST_HUMAN	Mus musculus ligatin (Ldlt) mRNA, partial cds
							0247d11.x1 Soares_NthMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2032	15051	28057	1.27	9.8E-02	AI080721.1	EST_HUMAN	0247d11.x1 Soares_NHNP-U_S1 Homo sapiens cDNA clone IMAGE:1878486 3'
4372	17359	30270	6.7	9.8E-02	Z32688.2	NT	Protein mirabilis fibrillar operon, strain Hf4320
5037	18050	30530	1.16	9.8E-02	AY089230.1	EST_HUMAN	EST375503 MAGE resequences, MAGE Homo sapiens cDNA
6225	19299		2.63	9.8E-02	BE910039.1	EST_HUMAN	60148088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8719	21857		0.65	9.8E-02	AI137084.1	EST_HUMAN	AUI137084 PLACET1 Homo sapiens cDNA clone PLACE1005740 5'
9902	22854	39315	1.35	9.8E-02	AV357898.1	EST_HUMAN	AV878988 GKC Homo sapiens cDNA clone GKCAAH02 5'
10231	23158		1.29	9.8E-02	BE694895.1	EST_HUMAN	601434030F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10359	23321	36805	1.27	9.8E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10399	23321	36809	1.27	9.8E-02	AJ243211.1	NT	602089789F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250669 5'
10479	23401	36898	0.44	9.8E-02	BF677270.1	EST_HUMAN	Anthrithum melius transposon Tam3 pseudogene for transposase (in S-5 copy)
10511	23433	36930	1.37	9.8E-02	AB013985.1	NT	Anthrithum melius transposon Tam3 pseudogene for transposase (in S-5 copy)
10511	23433	36931	1.37	9.8E-02	AB013985.1	NT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR (CD55)
10521	23543	37043	3.3	9.8E-02	P08174	SWISSPROT	Mycobacterium tuberculosis H37Rv complete genome, segment 102162
11094	24054	37577	5.31	9.8E-02	Z78702.1	EST_HUMAN	Zu191601.s1 Soares_NHT Homo sapiens cDNA clone IMAGE:745392 3'
12028	24904	38488	1.53	9.8E-02	AA625755.1	EST_HUMAN	ym18h03.s1 Soares Infant brain T1N18 Homo sapiens cDNA clone IMAGE:48653 3'
12933	25515		1.81	9.8E-02	H14589.1	EST_HUMAN	601563335F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932908 5'
12995	25553	31719	1.51	9.8E-02	BE728219.1	EST_HUMAN	CM2-BN0023-050/200-08/412 BN0023 Homo sapiens cDNA
4128	17161	30050	2.66	9.8E-02	AW692398.1	SWISSPROT	TRANSETOLASE 2 (TK-2) (TRANSETOLASE RELATED PROTEIN)
5748	18842	32025	0.81	9.8E-02	P51854	SWISSPROT	ac68609.s1 Straglene fetal retina 937202 Homo sapiens cDNA clone IMAGE:967736 3'
7294	20266	33501	0.51	9.8E-02	AA760728.1	EST_HUMAN	1Timesus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7522	20487	33549	4.14	9.8E-02	AB003473.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7818	20787	34144	7.16	9.8E-02	AL101538.2	NT	TRANSETOLASE 2 (TK-2) (TRANSETOLASE RELATED PROTEIN)
7863	18842	32025	0.89	9.8E-02	P51854	SWISSPROT	TRANSETOLASE 2 (TK-2) (TRANSETOLASE RELATED PROTEIN)
8212	21181	34591	2.85	9.8E-02	BF035861.1	EST_HUMAN	601435942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857245 5'
8212	21181	34592	2.85	9.8E-02	BF035861.1	EST_HUMAN	601435942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857245 5'
11039	24003	37528	2.31	9.8E-02	BF035861.1	EST_HUMAN	601435942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857245 5'
11039	24003	37529	2.31	9.8E-02	BF035861.1	EST_HUMAN	601435942F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857245 5'
1830	14876	27871	4.07	9.4E-02	BF671063.1	EST_HUMAN	60215082F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
3394	16934	29844	4.91	9.4E-02	Z33059.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102162
5240	18248		0.86	9.4E-02	X69105.1	NT	Lactobacillus bacteriophage phi19 complete genomic DNA
6450	19515	32768	1.21	9.4E-02	AF097363.1	NT	Trilium aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7851	20797	34173	0.54	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and lp135 gene, partial cds
8947	21913		2.5	9.4E-02	Z46963.1	NT	Aerobacter sp. cyd, cdc, socM, lysS, rubA, rubB, estB, oxyR, ppk, mltA, ORF2 and ORF3 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11280	20797	34173	2.22	9.4E-02	U78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and p53 gene, partial cds
12212	29528		10.73	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13087	25617	31692	1.37	9.4E-02	U27689.1	NT	Human pepBGT-1, belamine-GABA transporter mRNA, complete cds
3002	16060		1.71	9.3E-02	4809280	NT	Homo sapiens BA11-associated protein 3 (BAIAP3) mRNA
3041	16059		7.39	9.3E-02	6812525	NT	Homo sapiens nescientipryl epithelium specific protein 1 (NESG1), mRNA
3270	16324	29247	2.01	9.3E-02	BF76511.1	EST_HUMAN	602133086F NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288268 5'
4179	17210	30096	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286032F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4179	17210	30097	3.73	9.3E-02	BE391943.1	EST_HUMAN	601286032F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4768	17768		2.29	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAU08 5'
5745	18839		0.66	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8163	21091	34490	0.59	9.3E-02	AL163210.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210310
8591	21650	34075	0.6	9.3E-02	AW568007.1	EST_HUMAN	EST60 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9480	22444		0.42	9.3E-02	AL131178.1	NT	Bacillus cereus strain 14 cDNA library under conditions of nitrogen deprivation
10068	22995	36464	2.32	9.3E-02	BE962631.2	EST_HUMAN	60165588R1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855681 3'
10551	23473	36967	3.65	9.3E-02	Q19034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10551	23473	36968	3.65	9.3E-02	Q19034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10683	23603		3.49	9.3E-02	AW208117.1	EST_HUMAN	Phorbolacetum damselae subsp. damselae partial gylB gene for DNA gyrase B subunit
12482	25750		2.56	9.3E-02	AL249850.1	EST_HUMAN	h22812.21 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
12831	25778		9.12	9.3E-02	AW488850.1	EST_HUMAN	Mus musculus major histocompatibility locus class II region, Fas-binding protein Daxx (DAXX) gene, partial cds, Bmp1 (BMP1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), belar1, 3-galactosyl transferase (belar1, 3-galactosyl tr-)
13040	25824		2.24	9.3E-02	AF100566.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26252	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26253	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
231	13331	26254	7.81	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2236	15290		2.72	9.2E-02	RS4186.1	EST_HUMAN	Xp8907.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3194	16249	29167	3.72	9.2E-02	Q26831	SWISSPROT	MAJOR EPIDIDYMYAL-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3316	16569	29289	0.69	9.2E-02	AA634354.1	EST_HUMAN	h76801.1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:326136 3'
3959	16844		1.27	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
4286	17264		0.24	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4397	17361		1.04	9.2E-02	BE296722.1	EST_HUMAN	600944365F NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980176 5'
4665	17689		1.4	9.2E-02	X80402.1	NT	G.gallus Mia-CK gene
8342	21311	34725	1.87	9.2E-02	T49920.1	EST_HUMAN	yab9006r1 Straligene placenta (#637225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to pb-X66009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21485	34899	2.19	9.2E-02	X69256.1	NT	H.vulgaris x/yose isomerase gene
12002	24579	38475	1.74	9.2E-02	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
13019	25086		1.31	9.2E-02	11466872	NT	Podocypa anserina mitochondrion, complete genome
423	13118	26017	7.92	9.1E-02	X77665.1	NT	O. cuniculus K12 keratin gene
3684	16727		0.88	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-101286-001-002 BT0349 Homo sapiens cDNA
4610	17635	30419	1.5	9.1E-02	AL161564.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5304	18307		0.93	9.1E-02	AB010686.1	NT	Clona intestinalis endostyle-specific mRNA, complete cds
5819	18909	32093	1.27	9.1E-02	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLUC1, DDAH, G6b, G5b, G6c, G6d, G6e, G6f, BAT3, G5b, CSK2B, BAT14, GA, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7528	26000		0.52	9.1E-02	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7618	26576	33939	12.92	9.1E-02	AW150658.1	EST_HUMAN	ai74a05.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781958.5
7637	20879	34269	0.74	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 477
7677	20916	34307	0.87	9.1E-02	U38073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
9276	22242	39571	0.95	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10793	23714		1.94	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratiotes Homo sapiens cDNA clone FB19F10 3' end
10823	23744	37245	1.24	9.1E-02	S74059.1	NT	TG818=Cy actin [Tritoneustes graillassea urchins, embryos, Genomic, 5275 nt]
10852	23772	37271	0.8	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14887-5, G14587-6, and PRL1 genes
12151	25009		3.33	9.1E-02	9633464	NT	Bacteriophage Mu, complete genome
12393	25919		2.45	9.1E-02	AA170901.1	EST_HUMAN	z338h12.s1 Stratiotes muscic 937209 Homo sapiens cDNA clone IMAGE:811783 3' similar to SW-TRT3, HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12468	25217		1.82	9.1E-02	AF052895.1	NT	Rattus norvegicus cell cycle protein p56cdc gene, complete cds
12918	25771		1.78	9.1E-02	AJ291350.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
748	13807	28747	6.38	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MCV18) (KB CELLS FBP)
1840	14672	27645	6.7	9.0E-02	BE220482.1	EST_HUMAN	h3g910.x1 NCL_GCAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2815	15007	28626	6.5	9.0E-02	AF138522.1	NT	HIV-1 p6c095-06 from USA envelope glycoprotein (env) gene, partial cds
2815	15007	28627	6.5	9.0E-02	AF138522.1	NT	HIV-1 p6c095-06 from USA envelope glycoprotein (env) gene, partial cds
3347	16098	28621	1.11	9.0E-02	AF279135.1	NT	Dicystellum discoidium spore coat structural protein SP65 (cof5) gene, complete cds
4328	17356	30243	0.83	9.0E-02	S66757.1	NT	Corticosteroid-binding globulin [Simiit scireurus=squirrel monkeys, liver, mRNA, 1474 nt]
4328	17356	30244	0.83	9.0E-02	S66757.1	NT	Corticosteroid-binding globulin [Simiit scireurus=squirrel monkeys, liver, mRNA, 1474 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4448	17474	30383	1.26	9.0E-02	P56288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMNIN)
4895	17718	30811	2.37	9.0E-02	X69740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5281	18269	31137	0.93	9.0E-02	Q24587	SWISSPROT	REGULATORY PROTEIN ZESTIE
6110	18189	32409	14.12	9.0E-02	W56037.1	EST_HUMAN	z68a12.11 Soares fetal lung NblHL19W Homo sapiens cDNA clone IMAGE:287694 5' similar to PIR-S52171 S52171 small G protein - human;
6880	19832		1.14	9.0E-02	BF062851.1	EST_HUMAN	7f63d03.x1 NCL CGAP_Cort6 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element;
6931	20155	33473	0.93	9.0E-02	R62805.1	EST_HUMAN	y11508.01 Soares placenta N152-HP Homo sapiens cDNA clone IMAGE:138903 3'
12762	25404		2.03	9.0E-02	AF022286.1	NT	Escherichia coli strain E2348/89 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), OseD (oseD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrU (orU), >
1432	14465	27442	2.04	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1432	14465	27443	2.04	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2395	15403	28429	1.1	8.9E-02	BE153572.1	EST_HUMAN	PM0-HT0330-251196-003-301 HT0330 Homo sapiens cDNA
4227	17256		2	8.9E-02	AF280035.1	NT	Atrialium angustatum AtrialinF62 protein (AtrialinF62) gene, partial cds
5950	19036	32230	2.64	8.9E-02	AW482122.1	EST_HUMAN	UHH-B13-alc-f08-Q-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5950	19036	32231	2.64	8.9E-02	AW482122.1	EST_HUMAN	UHH-B13-alc-f08-Q-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5965	19051	32262	3.5	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7369	20367	33720	1.49	8.9E-02	P47289	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE]
7807	20757		2.02	8.9E-02	Z79021.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
8385	21354	34782	0.77	8.9E-02	P28475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS), TYPE I (NEURONAL NOS) (NNOS)
8468	21437	34655	0.7	8.9E-02	BF701685.1	EST_HUMAN	(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8468	21437	34655	0.7	8.9E-02	BF701685.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8945	21911	35336	5.01	8.9E-02	AA309319.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9978	22905	36369	0.62	8.9E-02	A1285827.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9978	22905	36369	0.62	8.9E-02	A1285827.1	EST_HUMAN	qu5505.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
9978	22905	36370	0.62	8.9E-02	A1285827.1	EST_HUMAN	MER10 repetitive element;
10090	23016	36492	0.87	8.9E-02	AA333356.1	EST_HUMAN	qu5505.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12150	25743		1.3	8.9E-02	P30143	SWISSPROT	EST14454 Fetal brain 1 Homo sapiens cDNA 5' end
12211	25758		1.91	8.9E-02	P18524	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
12387	25764		9.08	8.9E-02	BF996818.1	EST_HUMAN	MYOSIN-2 ISOFORM
12387	25764		9.08	8.9E-02	BF996818.1	EST_HUMAN	602129082F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12530	25253		1.81	8.9E-02	6890220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hatt1), mRNA
12571	25282		1.5	8.9E-02	U25605.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
1374	14408	27378	1.25	8.9E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3921	16087	26874	1.03	8.8E-02	AA356128.1	EST_HUMAN	EST11585 Unius Homo sapiens cDNA 5' end
4065	17101		3.7	8.9E-02	Q00288	SWISSPROT	TRANSSCRIPTION INITIATION FACTOR TF1D 135 KDA SUBUNIT (TAFII135) (TAFII130) (TAFII130)
4287	17293		1.26	8.9E-02	4502804	NT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4331	17359		2.3	8.9E-02	4580423	NT	Homo sapiens paired box gene 6 (enitidia, teratilis) (PAX6), isoform b, mRNA
7792	20744		0.86	8.9E-02	D117620.1	NT	Sheep mRNA for angiotensinogen, complete cds
8339	22304	35732	1.32	8.9E-02	AA151872.1	EST_HUMAN	z199605.s1 Strategic clone (#837204) Homo sapiens cDNA clone IMAGE:566288 3'
11453	24366	37941	3.43	8.9E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11453	24368	37942	3.43	8.9E-02	BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11593	24531	36088	5.78	8.9E-02	AL040129.1	EST_HUMAN	DKFZ434D1313.1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZ434D1313 5'
12441	25204	31827	2.4	8.9E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF_YNL285w
1654	14685	27681	1.55	8.7E-02	AI167281.1	EST_HUMAN	ox6501.s1 Sources_NRHMPU_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3707	16750	26865	3.84	8.7E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3707	16750	26865	3.84	8.7E-02	U82685.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4736	17756	30650	1.2	8.7E-02	AF176839.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5138	18147		1.02	8.7E-02	AE000865.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 149) of the complete genome
5165	18175	31053	0.97	8.7E-02	6563384	NT	Homo sapiens protein kinase C, nu (PRKN), mRNA
5387	18460	31365	6.04	8.7E-02	AA266875.1	EST_HUMAN	z55508.s1 NCI CGAP GC31 Homo sapiens cDNA clone IMAGE:701438 3'
5387	18460	31366	6.04	8.7E-02	AA266875.1	EST_HUMAN	z55508.s1 NCI CGAP GC31 Homo sapiens cDNA clone IMAGE:701438 3'
7022	20147	33468	0.81	8.7E-02	AJ271865.2	NT	Mus musculus partial Kcnk1 gene for potassium channel protein, exons 10-14
7022	20147	33467	0.81	8.7E-02	AJ271865.2	NT	Mus musculus partial Kcnk1 gene for potassium channel protein, exons 10-14
7243	19678	33276	0.63	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein-1 mRNA, partial cds
8860	21827	35250	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8860	21827	35250	0.71	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
11067	24030		2.16	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11641	24578	38144	1.78	8.7E-02	AJ007763.1	NT	Glycobacter oxydans RNA-III and RNA-Ala genes

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12123	24892	38593	1.89	8.7E-02	Z74060.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL012c
12123	24892	38594	1.89	8.7E-02	Z74060.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL012c
12428	25196		1.6	8.7E-02	X17118.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
1237	14292	27256	6.2	8.6E-02	AJ271736.1	NT	Human sapiens Xa pseudocapsid region; segment 22
2256	16295	28295	1.96	8.6E-02	BE408667.1	EST_HUMAN	601504016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3202	16257	29176	4.47	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (blub1) gene, complete cds
3658	16701		4.37	8.6E-02	AF143302.1	NT	Dicystidium discoidum adenylyl cyclase (accA) gene, complete cds
3793	16834		0.66	8.6E-02	U29487.1	NT	Mus musculus long incubation prion protein (Prn <sup>ob</sup> ) and prion-like protein (Prn <sup>d</sup> ) genes, complete cds
4512	17537	30421	0.67	8.6E-02	U88179.1	NT	Oryctolagus cuniculus galactin-3 gene, untranscribed exon and 5' flanking region
5170	18179		1.09	8.6E-02	L134119.1	NT	Chromatium vinosum tetraether cytochrome c gene, 3' end, bacterial ankyrin homologue, flavocytochrome c heme subunit fccA (complete cds) and flavin subunit, fccB (3' end)
5276	18282		1.09	8.6E-02	AB011163.1	NT	Homo sapiens mRNA for KIAA0591 protein, partial cds
8213	19287	32520	4.24	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6510	19574	32628	1.48	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-452, mu switch region (part a)
6510	19574	32629	1.48	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-452, mu switch region (part a)
7834	20781	34159	1.01	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8282	21231	34640	1.33	8.6E-02	5730066	NT	Homo sapiens Smi2-related GTP activator protein (SRGAP) mRNA
8292	21231	34641	1.33	8.6E-02	5730068	NT	Homo sapiens Smi2-related GTP activator protein (SRGAP) mRNA
8405	21374	34782	0.66	8.6E-02	11427428	NT	Homo sapiens hypodermal protein FLJ11008 (PLJ11005), mRNA
8469	21438		0.81	8.6E-02	U60168.1	NT	Dicystidium discoidum proteasome subunit C2 homolog P4C (prtC) gene, complete cds
10084	23020	36495	1.04	8.6E-02	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
10131	23037		1.97	8.6E-02	AW062163.1	EST_HUMAN	H20048.X1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872846 3'
10513	23435	36933	0.97	8.6E-02	AF026504.1	NT	Rattus norvegicus SFA-1 like protein p1284 mRNA, complete cds
11579	24517	39072	2.47	8.6E-02	BF306008.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11679	24817	39073	2.47	8.6E-02	BF306009.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11767	23922	37441	0.23	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11901	24782	36370	1.97	8.6E-02	AF283690.1	NT	Acetivibrio stearothermophilus BarFI methylase (FIN) and BarFI restriction endonuclease (FIR) genes, complete cds
2406	15413	28437	2.86	8.6E-02	AE000652.1	NT	Helicobacter pylori Z6959 section 130 of 134 of the complete genome
5762	18946	32028	0.71	8.6E-02	AA085491.1	EST_HUMAN	068307.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592917 3' similar to gbK01144 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
5763	18995		1.92	8.6E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6127	19205	32428	6.34	8.6E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8953	21910	35345	1.92	8.5E-02	BT64779	NT	Mus musculus myosin XV (Myo15), mRNA
10186	23121	36507	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC3-O10037-200700-014-005 OT0037 Homo sapiens cDNA
10196	23121	36508	3.17	8.5E-02	BE833054.1	EST_HUMAN	RC3-O10037-200700-014-005 OT0037 Homo sapiens cDNA
10338	23252	36742	0.44	8.5E-02	AI1140818.1	EST_HUMAN	qet505.k1 Scores, tests NHT Homo sapiens cDNA clone IMAGE:1738138 3'
10728	23650	37143	0.56	8.5E-02	X76731.1	NT	V.ammodys gene for ammodys C
10851	23771	37270	1	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11480	24433		8.1	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11507	24449	37999	4.05	8.5E-02	AB001962.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12985	25547		6.78	8.5E-02	AA302304.1	EST_HUMAN	ST64411.r1 Scores, fetal heart_NbHH19W Homo sapiens cDNA 5' end
2875	16001	28690	3.69	8.4E-02	W69330.1	EST_HUMAN	z44411.r1 Scores, fetal heart_NbHH19W Homo sapiens cDNA 5' end
4381	17409	30290	1.02	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4391	17409	30291	1.02	8.4E-02	AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
5235	18243	31115	0.98	8.4E-02	5453817	NT	Homo sapiens nucleodindin 1 (NUCD1), mRNA
5385	18468	31363	8.74	8.4E-02	BE287153.1	EST_HUMAN	BT0190438F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534383 5'
6847	19500	33194	1.88	8.4E-02	AK024458.1	NT	Human sapiens mRNA for FLJ00050 protein, partial cds
8363	21332	34744	7.84	8.4E-02	BE095074.1	EST_HUMAN	CM8-B10780-200400-182-405 BT0780 Homo sapiens cDNA
8784	22160	35588	1.02	8.4E-02	AF218680.1	NT	Homo sapiens atracilin precursor (ATRNL) gene, exon 2
10727	23849	37142	1.9	8.4E-02	AI735184.1	EST_HUMAN	ea88g10.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2335642 3' similar to TR:088312
12351	25146	31853	1.48	8.4E-02	R76408.1	EST_HUMAN	O88312 GDB-4.;
2027	15047	28060	0.87	8.3E-02	5835680	NT	h83h12.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2027	15047	28061	0.87	8.3E-02	5835680	NT	h83h12.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3008	16851	29588	6.11	8.3E-02	P75534	SWISSPROT	h83h12.r1 Scores hexagenus mitochondrion, complete genome
3334	16877	29590	0.96	8.3E-02	AI436797.1	EST_HUMAN	HYPOPHYSICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3334	16877	29591	0.96	8.3E-02	AI436797.1	EST_HUMAN	h83h12.r1 Scores, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19457	32702	0.78	8.3E-02	AI942338.1	EST_HUMAN	h83h12.r1 Scores, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6902	19566	32818	2.54	8.3E-02	AF052683.1	NT	h83h12.r1 Scores, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
8313	21282	34694	3.61	8.3E-02	AF195787.1	NT	Homo sapiens protactin 43 gene, exon 1
8346	21315		1.19	8.3E-02	AA865285.1	EST_HUMAN	h83h12.r1 Scores, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
8642	21610		1.54	8.3E-02	AA987873.1	EST_HUMAN	h83h12.r1 Scores, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
9896	22949	36306	1.58	8.3E-02	AA683503.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;
9899	22730		2.18	8.3E-02	AA161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10708	23628		0.6	8.3E-02	AF020409.1	NT	Dichostelium discoideum DocA (docA) mRNA, complete cds
12444	25024		1.48	8.3E-02	BE958458.1	EST_HUMAN	60164770F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3926863 5'
1379	14413		7.44	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBSCN protein gamma isoform
1494	14827	27499	1.77	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3089	16147		2.24	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
3815	16855		1.61	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10'
4033	17071	26972	1.22	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4313	17342	30222	5.93	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
4313	17342	30223	5.93	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
4313	17342	30224	5.93	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
5108	18118	30992	1.29	8.2E-02	AF240778.1	NT	Mus musculus pepsinogen F (PepF) mRNA, complete cds
5118	18128	31004	4.13	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5000	18128	31004	0.95	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5408	18511	31389	1.47	8.2E-02	BE897030.1	EST_HUMAN	601439078F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7221	20243	33577	2.84	8.2E-02	AF306555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8005	20944		0.6	8.2E-02	AV743341.1	EST_HUMAN	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
9057	22023		0.45	8.2E-02	U26397.1	NT	Rattus norvegicus plasma membrane Ca <sup>2+</sup> -ATPase isoform 3 (PMCA3) gene, 5' flanking region
9124	22090	35518	2.75	8.2E-02	AW875128.1	EST_HUMAN	RC2-P10004-031299-011-d05 P10004 Homo sapiens cDNA
9958	22895	36348	5.43	8.2E-02	X04187.1	NT	Beet neotrophic yellow vein virus RNA-2
10121	23047	36526	2.38	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355569 5'
12450	25209	31631	6.88	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12835	25710		5.74	8.2E-02	AF275968.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1493	14526	27498	1.05	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
5948	18038	32123	1.05	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19579	32836	1.38	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7403	20371		0.81	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7835	20782		0.9	8.1E-02	AI692881.1	EST_HUMAN	wb8606.xt NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:238503 3'
8683	21651	35072	0.53	8.1E-02	11426974	NT	Homo sapiens hypophyseal protein FLJ10090 (FLJ10060), mRNA
8883	21651	35073	0.53	8.1E-02	11426974	NT	Homo sapiens hypophyseal protein FLJ10090 (FLJ10060), mRNA
10272	23187		1.58	8.1E-02	AY005190.1	NT	Homo sapiens extracellular glycoprotein laminin precursor, gene, complete cds
11827	24710	38294	1.53	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	16830	26028	4.82	8.0E-02	AW954653.1	EST_HUMAN	EST386723 IMAGE resequences, IMAGE Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1709	16876	27722	13.83	8.0E-02	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1709	15975	27723	13.93	8.0E-02	D26835.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1919	14949	27636	4.07	8.0E-02	BE067219.1	EST_HUMAN	PM3-3T10347-170200-001-308 3T10347 Homo sapiens cDNA
2384	15392	28417	1.05	8.0E-02	D80915.1	NT	Synecocystis sp. PCC6803 complete genome, 1727, 2137259-2267259
2384	15392	28418	1.05	8.0E-02	D80915.1	NT	Synecocystis sp. PCC6803 complete genome, 1727, 2137259-2267259
2478	16482		4.99	8.0E-02	BF246744.1	EST_HUMAN	60185548F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075619 5'
2831	14137	27088	0.99	8.0E-02	M23449.1	NT	Dicorythella discoidum cyclic nucleotide phosphodiesterase gene, complete cds
2911	15969	28692	0.76	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3830	16870	29772	8.94	8.0E-02	AY565118.1	EST_HUMAN	EST378191 MAGS ressequences, MAG1 Homo sapiens cDNA
4810	17827	30724	1.7	8.0E-02	AI434202.1	EST_HUMAN	431902.X1 NCI_CGAP_G64 Homo sapiens cDNA clone IMAGE:2192114 3'
4818	17835	30733	0.99	8.0E-02	AF116599.1	NT	Arabidopsis thaliana putative transcription factor (HUA2) mRNA, complete cds
4852	17969		7.57	8.0E-02	X72784.1	NT	M. musculus gene for gelatinase B
5832	18322	32105	0.71	8.0E-02	AW651139.1	EST_HUMAN	EST368309 MAGS ressequences, MAGA Homo sapiens cDNA
5893	18077	32274	3.28	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7398	18077	32274	1.44	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8465	21434	34851	3.74	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9744	22985	36139	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9744	22985	36140	1.21	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10519	23441		0.6	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11145	24105	37632	2.19	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 (lka-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP-1) genes, complete cds
12483	25230	31788	6.54	8.0E-02	AJ005375.1	NT	Drosophila orexin hunchback region
13036	18342		2.06	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2184	15199	28219	4.38	7.9E-02	BE250008.1	EST_HUMAN	60064318F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2992	16060	28971	8.43	7.9E-02	AI592029.1	EST_HUMAN	605 RIBOSOMAL PROTEIN L38 (HUMAN);
3894	16903	29808	5.98	7.9E-02	6681044	NT	ar6e08.x1 Brested colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z28876
3894	16903	29809	5.98	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1) mRNA
4722	17742	30633	1.08	7.9E-02	BF344654.1	EST_HUMAN	Mus musculus colony stimulating factor 1 receptor (Csfr1) mRNA
4849	17968		1.49	7.9E-02	AB080819.1	NT	60201970F1 NCI_CGAP_Bint67 Homo sapiens cDNA clone IMAGE:4155401 5'
6855	19803		1.06	7.9E-02	BF368016.1	EST_HUMAN	Arabidopsis thaliana RFW24L mRNA, partial cds
8366	21335	34747	3.26	7.9E-02	U27632.1	NT	RC3-GR0042-310500-024-d11 GN0042 Homo sapiens cDNA
10388	23310	30788	4.89	7.9E-02	AJ081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of Mif2 Sm14p (SM14) gene, complete cds
							oe08b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
							CDC80B11

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10385	23310	39789	4.89	7.8E-02	AJ081944.1	EST_HUMAN	cd03905.s1 NCL_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08811 ;
1215	14253	27210	1.69	7.8E-02	AJ793275.1	EST_HUMAN	cd59402.v5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1 repetitive element ;
1215	14253	27211	1.89	7.8E-02	AJ793275.1	EST_HUMAN	cd59402.v5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1 repetitive element ;
5123	16904		3.26	7.8E-02	BE250048.1	EST_HUMAN	600943055FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
7279	20013	33317	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7279	20013	33318	1.29	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
9137	22103	35529	1.26	7.8E-02	BE937647.1	EST_HUMAN	60144035FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925448 5'
9232	22198	35528	0.6	7.8E-02	X78344.1	NT	S cerevisiae CAT8 gene
9408	22373	35908	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9408	22373	35909	0.66	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9716	22744	36195	1.23	7.8E-02	AA469354.1	EST_HUMAN	nc08808.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:771931
10161	23086	35593	0.65	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
12114	24984	35585	1.84	7.8E-02	BF025981.1	EST_HUMAN	601665979FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3953083 5'
1309	16567	27402	0.93	7.7E-02	AF181907.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3600	16045		2.05	7.7E-02	AJ238993.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5622	18718	31877	0.61	7.7E-02	AF062636.1	NT	Gallus gallus collagen type XII alpha-1 (COL12A1) gene, promoter region and partial cds
8241	21210	34915	7.94	7.7E-02	AA402949.1	EST_HUMAN	zu83411.r1 Soares ovary tumor NishOT Homo sapiens cDNA clone IMAGE:741717 5' similar to
10185	23120	36505	3.76	7.7E-02	F30590	SWISSPROT	TR.G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
10480	23412	36909	0.76	7.7E-02	AJ318662.1	EST_HUMAN	probable SERINE/THREONINE-PROTEIN KINASE YB0359C
10480	23412	36910	0.76	7.7E-02	AJ318662.1	EST_HUMAN	la60508.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
11352	24302	37629	4.65	7.7E-02	11422757	NT	la60508.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
12971	25785		1.91	7.7E-02	11439859	NT	Homo sapiens KIA00823 gene product (KIA00823), mRNA
							Homo sapiens interferon regulatory factor 7 (IRF7), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3398	16447	29373	2.43	7.6E-02	BE514432.1	EST_HUMAN	601311426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3894903 5'
3419	16487	29387	1	7.6E-02	AA288447.1	EST_HUMAN	EST111214 Cerebellum II Homo sapiens cDNA 5' end similar to protocadherin 43
6216	19290	32533	0.72	7.6E-02	AJ001275.1	EST_HUMAN	4n25d02.x1 Gassler/Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
6491	19556	32606	0.87	7.6E-02	BE379328.1	EST_HUMAN	601230402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9725	22753	36206	1.35	7.6E-02	AL131016.1	NT	Homo sapiens SCL gene locus
10237	23182	36206	1.42	7.6E-02	AL135078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10560	23502	36904	0.47	7.6E-02	BE708002.1	EST_HUMAN	RC1-LHT0545-020800-017-008 HT0545 Homo sapiens cDNA
10714	23636	37384	0.68	7.6E-02	BE696938.2	EST_HUMAN	601864915F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3838810 3'
10952	23872	37385	0.67	7.6E-02	X92658.1	NT	L esculentum mRNA for tissue phosphatase translocator
10952	23872	37385	0.67	7.6E-02	X92658.1	NT	L esculentum mRNA for tissue phosphatase translocator
11388	24683	38459	1.9	7.6E-02	AW96845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
785	13845	28780	2.89	7.5E-02	5902093	NT	Homo sapiens edula carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA
785	13845	28791	2.89	7.5E-02	5902093	NT	Homo sapiens edula carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC8A9), mRNA
1935	14950	27055	0.93	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4538	17659	30447	0.93	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, Intronic 1 and exon 2
5952	19037	32233	0.71	7.5E-02	AJ948714.1	EST_HUMAN	wq2h09.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8631	21649	35071	1.01	7.5E-02	AJ894367.1	EST_HUMAN	w62h02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN)
8652	21819	35239	1.29	7.5E-02	AJ116973.1	EST_HUMAN	AJ116973 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10392	23314		0.46	7.5E-02	BF221730.1	EST_HUMAN	7c671005.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:3576504 3' similar to contains element MER27 repetitive element 1
10859	23779	37278	0.9	7.5E-02	BF208909.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10953	23873	37380	0.96	7.5E-02	X78460.1	NT	C.fiml DSM 20113 76S rDNA
478	13560	28478	1.24	7.4E-02	AW83547.1	EST_HUMAN	RC6-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1458	14488		1.08	7.4E-02	AF930027.1	NT	Equine herpesvirus 4 strain NS0567 complete genome
2935	15589		0.99	7.4E-02	6759069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
3608	16653	29571	1.07	7.4E-02	AJ807895.1	EST_HUMAN	W439101.T1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2555895 3'
4733	17763	30646	1.09	7.4E-02	L78910.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4833	17850	30760	3.24	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
4978	17894	30883	2.92	7.4E-02	6878492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchp), mRNA
6843	18701		1.8	7.4E-02	R17477.1	EST_HUMAN	Y07406.R1 Soares infant brain IN18 Homo sapiens cDNA clone IMAGE:32339 5'
7707	20684	34031	0.79	7.4E-02	AA605132.1	EST_HUMAN	Y07402.e1 NCL_CGAP_AAT1 Homo sapiens cDNA clone IMAGE:1112259 3'

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8233	21202	34608	1.2	7.4E-02	BE930112.1	EST_HUMAN	001493366F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3895264 5'
8846	21813	35233	1.01	7.4E-02	U155039.1	NT	Human peroxid tyrosinase protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9821	22484	35830	1.02	7.4E-02	AW42905.1	EST_HUMAN	Hb7d11.1Y1 NCI CGAP GLI1 Homo sapiens cDNA clone IMAGE:2987861 5' similar to SW:SCA2_HUMAN
9821	22484	35931	1.02	7.4E-02	AW62905.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.1
9794	21117	34510	0.48	7.4E-02	AB072938.1	EST_HUMAN	Hb7d11.1Y1 NCI CGAP GLI1 Homo sapiens cDNA clone IMAGE:2987861 5' similar to SW:SCA2_HUMAN
9794	21117	34517	0.48	7.4E-02	AB072938.1	EST_HUMAN	we74d02.x1 Soares Dieckgrafe, colon, NHGD Homo sapiens cDNA clone IMAGE:2346819 3'
10173	23098	36578	1.07	7.4E-02	U62283.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10301	23226	36708	0.93	7.4E-02	BFF12878.1	EST_HUMAN	UJ-HBW1-ang-g-98-Q1 at NCI CGAP Sub77 Homo sapiens cDNA clone IMAGE:3069888 3'
12408	25181		1.47	7.4E-02	11529893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12665	25903		2.51	7.4E-02	AW370431.1	EST_HUMAN	CM4-H10243-081195-037-d11 H10243 Homo sapiens cDNA
489	13542	26468	1.3	7.3E-02	BE964951.2	EST_HUMAN	601659738R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886209 3'
489	13542	26469	1.3	7.3E-02	BE964951.2	EST_HUMAN	601659738R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886209 3'
886	13748	26674	6.48	7.3E-02	AE001789.1	NT	Thermatoga maritima section 101 of 136 of the complete genome
1477	15869	27486	3.94	7.3E-02	AW900281.1	EST_HUMAN	CMC-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1862	15979		15.78	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TORBV27S1P, TORBV22S1A2N1T, TORBV6S1A1T, TORBV7S1A1N2T, TORBV6S1A1T1, TORBV13S3, TORBV6S7P, TORBV7S3A2T, TORBV13S2A1T, TORBV6S2A2PT, TORBV7S2A1N4T,
3785	16826		0.72	7.3E-02	U660359.1	NT	TCRBV13S8/13S2
5032	18046		1.06	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6586	19855	32927	1.04	7.3E-02	AA779977.1	EST_HUMAN	g24c02.s1 Soares fetal_liver_spleen_1NF.L3_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7706	20963	34029	2.47	7.3E-02	P05143	SWISSPROT	g24c02.s1 Soares fetal_liver_spleen_1NF.L3_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7706	20963	34030	2.47	7.3E-02	P05143	SWISSPROT	g24c02.s1 Soares fetal_liver_spleen_1NF.L3_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
8508	21476		1.2	7.3E-02	7662107	NT	PROLINE-RICH PROTEIN MP-3
9655	22527		1.39	7.3E-02	AB011090.1	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
							Homo sapiens mRNA for KIAA0358 protein, partial cds
11552	19855	32927	1.89	7.3E-02	AA779977.1	EST_HUMAN	g24c02.s1 Soares fetal_liver_spleen_1NF.L3_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
12925	25510		1.33	7.3E-02	Z73597.1	NT	g24c02.s1 Soares fetal_liver_spleen_1NF.L3_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
							S. cerevisiae chromosome XVI reading frame ORF YPL241c.
120	13229	26156	0.7	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from basins 1028155 to 1039934 (section 88 of 148) of the complete genome



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
120	13229	26157	0.7	7.2E-02	AE000892.1	NT	Methanobacterium thermoautotrophicum from bases 1020165 to 1039834 (section 88 of 148) of the complete genome
1472	14505	27478	2.71	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1472	14505	27478	2.71	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2558	13558		2.98	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3900	16940	29851	0.74	7.2E-02	AW298322.1	EST_HUMAN	U1H-BW0-ajl-a-95-Q-U1.at NCL_CGAP_Sub85 Homo sapiens cDNA clone IMAGE:2732049 3'
4373	17400	30280	4.57	7.2E-02	BF572307.1	EST_HUMAN	602077757Ft NIH_MGC 82 Homo sapiens cDNA clone IMAGE:4251950 5'
5360	18485	31336	2.81	7.2E-02	U87531.1	NT	Methanococcus jannaschii section 73 of 180 of the complete genome
5361	18486	31337	9.14	7.2E-02	P11120	SWISSPROT	CALMODULIN
6239	18312		0.73	7.2E-02	BF217596.1	EST_HUMAN	601883908Ft NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4096224 5'
7374	20344	33695	1.76	7.2E-02	BF216088.1	EST_HUMAN	601883558Ft NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4095710 5'
7391	20360	33712	0.6	7.2E-02	AF221128.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7417	20384		1.74	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8529	21497	34912	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8529	21497	34913	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9419	22384		0.82	7.2E-02	Y17217.1	NT	Leidococcus leicis casE gene
9934	22881		0.83	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9970	22997	36660	1.98	7.2E-02	AV712452.1	EST_HUMAN	AV712462 DCA Homo sapiens cDNA clone DCAUG01 5'
10117	23043	36523	3.63	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10274	23109	36683	1.17	7.2E-02	BF126399.1	EST_HUMAN	601763523Ft NIH_MGC 20 Homo sapiens cDNA clone IMAGE:4026436 5'
10382	23285	36782	2.29	7.2E-02	AW873187.1	EST_HUMAN	hg4411.xt NCL_CGAP_Adt1 Homo sapiens cDNA clone IMAGE:3120393 3' similar to TR:Q82340 Q82340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
10552	23474	36680	0.64	7.2E-02	AA768204.1	EST_HUMAN	ca62207.st NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10717	23639	37132	2.17	7.2E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and bcl2can (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10840	23760	37260	5.41	7.2E-02	BE565003.1	EST_HUMAN	601343828Ft NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3686951 5'
10894	23784		3.24	7.2E-02	BE339214.1	EST_HUMAN	601065794Ft NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3451659 5'
11258	24210	37733	4.17	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12311	25119	31642	1.58	7.2E-02	AJ270966.1	EST_HUMAN	h87ab0.1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:1048308 5'
12330	25145		5.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230786 Homo sapiens library (Seranikd P) Homo sapiens cDNA clone PS1306 3'

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12469	25218		3.99	7.2E-02	U82828.1	NT	Homo sapiens alaxia islanclactasia (ATM) gene, complete cds
12484	25764		8.41	7.2E-02	AW609682.1	EST_HUMAN	CM4-NN1009-200000-116-c11 NN1009 Homo sapiens cDNA
12880	25933		1.45	7.2E-02	AF020439.1	NT	Homo sapiens ATP-citrate lyase gene, intron 3
12964	25533		1.85	7.2E-02	AA401770.1	EST_HUMAN	2557c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454.5
1820	14944	27940	1.83	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D8) proviral structural capsid protein (gag) gene; partial cds
2300	15112	28332	6.39	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981.5
8239	21208	34612	0.97	7.1E-02	A1126284.1	EST_HUMAN	q82a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922.3
12163	25038		8.33	7.1E-02	BE394764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234.5
528	13600	28518	1.42	7.0E-02	Q07082	SWISSPROT	COLLAGEN ALPHA 1(XVII) CHAIN PRECURSOR
1499	14632		1.82	7.0E-02	X98977.1	NT	Martellia Mrcut-1 gene
1776	14605	27781	1.18	7.0E-02	AA056343.1	EST_HUMAN	Z166104.s1 Strazigene colon (#937204) Homo sapiens cDNA clone IMAGE:309559.3
3042	16100	29015	1.76	7.0E-02	AW138152.1	EST_HUMAN	UJH-381-acy-c-07-Q-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020.3
3913	16553	28864	0.88	7.0E-02	AA815438.1	EST_HUMAN	a85a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:309559.3
4074	17110	30004	1.05	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN)
4164	17195		1.24	7.0E-02	AW762882.1	EST_HUMAN	QV4-BT0407-280100-090-010 BT0407 Homo sapiens cDNA
4242	17271	30156	1.28	7.0E-02	AF077821.1	NT	CMQ-UN10001-060300-270-e12 UN10001 Homo sapiens cDNA
4865	17981	30871	8.41	7.0E-02	BF381987.1	EST_HUMAN	Cardia familiaris inducible nitric oxide synthase mRNA, complete cds
5457	18537		1.03	7.0E-02	Y08143.2	NT	601818251F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071.5
7630	20590	33953	0.9	7.0E-02	AV693285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
7884	20808	34185	0.6	7.0E-02	Y19187.1	NT	AV69285 GKC Homo sapiens cDNA clone GKCCAE08.5
9454	22418	35856	1.2	7.0E-02		NT	Gallus gallus fever virus, complete genome
9856	22863	36346	1.21	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10312	23236	38718	0.76	7.0E-02	U12768.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11700	24655	39242	2.23	7.0E-02	AA724255.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
12303	25519	31710	1.88	7.0E-02	11421638	NT	ah69a05.e1 Soares_NFL_J_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184.3 similar to gb:L14837
515	13586	26504	11.2	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN)
515	13586	26505	11.2	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1336	14370		1.68	6.9E-02	4507668	NT	Homo sapiens chromosome 21 segment HS21C010
3807	16647	29764	1.37	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gs-selective protein signalling (ZGAP1) mRNA, and translated products
3807	16647	29755	1.37	6.9E-02	Q06364	SWISSPROT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3807	16647	29755	1.37	6.9E-02	Q06364	SWISSPROT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5151	18161	31041	0.97	6.9E-02	AA670289.1	EST_HUMAN	af2560.s1 Soares, total_fetus_Nb2H-Fa_9w Homo sapiens cDNA clone IMAGE:1032710 3'
6028	19109		0.57	6.9E-02	AF161934.1	NT	Homo sapiens HSPC101 mRNA, partial cds
7676	20820		0.67	6.9E-02	AF164957.1	NT	Carline distemper virus strain AT517, complete genome
8387	21359		1.18	6.9E-02	U12022.1	NT	Human calmodulin (CALM) gene, exons 2,3,4,5 and 6, and complete cds
8699	21865	35287	1.08	6.9E-02	BE567435.1	EST_HUMAN	60134-0681F4 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8699	21865	35288	1.08	6.9E-02	BE567435.1	EST_HUMAN	60134-0681F4 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9475	22439	35879	0.55	6.9E-02	U22867.1	NT	Barbican duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
12343	25141		2.17	6.9E-02	X74315.1	NT	X.lievis XF02 mRNA for fork head protein
12519	25250		1.75	6.9E-02	P44821	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFCHOMOLOG
13112	25631	31648	3.89	6.9E-02	BF352899.1	EST_HUMAN	IL3-HT00618-110700-210-C04 HT0619 Homo sapiens cDNA
						EST_HUMAN	aa30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1859	14924	27918	1.18	6.8E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1859	14924	27918	1.18	6.8E-02	AA496759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1822	14946	27942	4.77	6.8E-02	AF165873.1	NT	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
3117	16174	29084	1.05	6.8E-02	AA781966.1	EST_HUMAN	af75a08.s1 Soares, testis_NHT Homo sapiens cDNA clone 1376626 3'
3117	16174	29085	1.05	6.8E-02	AA781966.1	EST_HUMAN	af75a08.s1 Soares, testis_NHT Homo sapiens cDNA clone 1376626 3'
3117	16174	29086	1.05	6.8E-02	AA781966.1	EST_HUMAN	af75a08.s1 Soares, testis_NHT Homo sapiens cDNA clone 1376626 3'
4583	17605		0.71	6.8E-02	BE141076.1	EST_HUMAN	MR04-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
6293	18289		0.76	6.8E-02	T03013.1	EST_HUMAN	FB20A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB20A8 3' end
6776	19631		0.69	6.8E-02	P20792	SWISSPROT	CELL-SURFACE RECEPTOR DAF-1 PRECURSOR
7084	20018		1.05	6.8E-02	BE061880.1	EST_HUMAN	RC1-BT0254-090300-017-409 BT0254 Homo sapiens cDNA
7407	20482	33822	7.18	6.8E-02	AL183268.2	NT	Homo sapiens chromosome 21 segment HS21C068
7448	20899	34280	0.64	6.8E-02	U16956.1	NT	Dicofactin discoidin domain myosin heavy chain kinase A (MHOK A) mRNA, complete cds
8631	21569	35020	5.44	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
8631	21569	35021	6.44	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
12140	25949		3.73	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12274	25044		2.52	6.8E-02	AA758074.1	EST_HUMAN	af67005.s1 Soares, testis_NHT Homo sapiens cDNA clone 1320705 3'
12832	25449		1.68	6.8E-02	AW675839.1	EST_HUMAN	EST3787048 MAOE retrotransposon, MAGN Homo sapiens cDNA
12894	25490		2.35	6.8E-02	6910385	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1531	14564		1.63	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1.101 allele, complete cds
1910	14934	27690	1.99	6.7E-02	AJ220285.1	EST_HUMAN	q779e04.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3730	16772	28983	4.34	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD4 (HOXD4)
8183	21153	34590	1.01	6.7E-02	X62955.1	NT	H. sapiens DNA for cGMP phosphodiesterase (exons 4-22)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8183	21153	34581	1.01	6.7E-02 X02995.1	NT	EST_HUMAN	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8781	35170	35170	0.45	6.7E-02 AW082688.1	EST_HUMAN	EST_HUMAN	xb61c11.x1 Scores NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2880788 3'
9859	22386	36347	0.73	6.7E-02 AW137358.1	EST_HUMAN	EST_HUMAN	U-H-811-act-g-91-Q-J1.s1 NCI CGAP Su33 Homo sapiens cDNA clone IMAGE:2715433 3'
9859	22386	36348	0.73	6.7E-02 AW137358.1	EST_HUMAN	EST_HUMAN	U-H-811-act-g-91-Q-J1.s1 NCI CGAP Su33 Homo sapiens cDNA clone IMAGE:2715433 3'
1371	14405	27376	0.6	6.8E-02 AF245116.1	NT	NT	Drosophila melanogaster actin mRNA, complete cds
2162	15207	28226	2.66	6.8E-02 AJ286241.1	NT	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3477	16523	29447	1.07	6.8E-02 R84306.1	EST_HUMAN	EST_HUMAN	y11b70.s1 Scores placenta N2b-P Homo sapiens cDNA clone IMAGE:139579 3'
3491	16637	29462	2.1	6.8E-02 7108357	NT	EST_HUMAN	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3491	16637	29463	2.1	6.8E-02 7108357	NT	EST_HUMAN	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4107	17141	30036	1.45	6.8E-02 AF260225.1	NT	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5015	18029	30913	9.23	6.8E-02 Q61703	SWISSPROT	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5015	18029	30914	9.23	6.8E-02 Q61703	SWISSPROT	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
6736	19792	33073	3.87	6.8E-02 X06411.1	NT	NT	P.vulgaris mRNA for chalcone synthase
6967	19823	33105	0.55	6.8E-02 P28159	SWISSPROT	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6967	19823	33106	0.55	6.8E-02 P28159	SWISSPROT	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
8152	21050		0.57	6.8E-02 D14567.1	NT	SWISSPROT	Penicillium urticae mitochondrial rRNA (large rRNA) gene and its flanking region
8279	21248	34680	1.6	6.8E-02 AF052572.1	NT	NT	Dictyostellum discoideum dad1 (dad) gene, complete cds
8871	21784	35208	0.67	6.8E-02 AF006355.1	NT	NT	Human respiratory syncytial virus, complete genome
9273	22239	35686	0.67	6.8E-02 9629198	NT	NT	Human respiratory syncytial virus, complete genome
9273	22239	35687	0.67	6.8E-02 9629198	NT	NT	Human respiratory syncytial virus, complete genome
10311	23235	36717	0.52	6.8E-02 A1458752.1	EST_HUMAN	EST_HUMAN	[97G03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2149488 3'
10447	23369	36860	1.05	6.8E-02 Y07848.1	NT	NT	Homo sapiens EWS, grr22, rrr22, and bam22 genes
10481	23403		0.3	6.8E-02 11430589	NT	NT	Homo sapiens vinculin (VCL), mRNA
11310	24260	37786	4.9	6.8E-02 BF374248.1	EST_HUMAN	EST_HUMAN	MR1-SN0064-07000-006-at12 SN0064 Homo sapiens cDNA
12003	24939		1.73	6.8E-02 C05789.1	EST_HUMAN	EST_HUMAN	C05789 Human pancreatic islet Homo sapiens cDNA clone hbc5156
12719	25373		2.53	6.8E-02 9837991	NT	NT	Mus musculus DfPB gene (DfPB), mRNA
13024	25672		1.31	6.8E-02 AF167430.1	NT	NT	Rattus norvegicus cyclochrome P450 2E1 (CYP2E1) gene, 5' flanking region
984	13652	26566	2.67	6.8E-02 BF027639.1	EST_HUMAN	EST_HUMAN	50167/046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3354176 5'
989	14041	26866	1.95	6.8E-02 7709068	NT	NT	Homo sapiens E2F-like protein (LOC31270), mRNA
1332	14426	27396	3.5	6.8E-02 U47624.1	NT	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1749	14778	27763	2.08	6.8E-02 AE000784.1	NT	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5638	18734	31886	1.71	6.8E-02 AA443991.1	EST_HUMAN	EST_HUMAN	z46h12.s1 Scores ovary tumor NHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6933	19750	33027	0.83	6.8E-02 BF665340.1	EST_HUMAN	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN),
							902118887F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278028 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7185	18396	31241	1.17	6.6E-02	U22681.1	NT	Azobacter vinelandii ATCC 8048 negative regulator MucB (mucB) gene, partial cds
10302	23227	36709	0.95	6.6E-02	BE693200.2	EST_HUMAN	60165681T1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3865637 3'
10302	23227	36710	0.65	6.6E-02	BE693200.2	EST_HUMAN	60165681T1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3865637 3'
10332	23753	37252	0.93	6.6E-02	BF10830.1	EST_HUMAN	60182361T1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4043138 5'
11002	23668	37462	4.51	6.6E-02	AA195648.1	EST_HUMAN	2323605.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:565144 3'
12184	25017		4.16	6.6E-02	M21498.1	NT	Rabbit microsomal epoxide hydrolase
12256	25255		7.31	6.6E-02	AF102363.1	NT	Neceria haemolysos kinsin related protein 2 (KRP2) gene, complete cds
577	13646	26556	1.74	6.4E-02	X94549.1	NT	A. carlesii precursor of peridinin-chlorophyll-protein (PCP) gene
1746	14775	27760	0.93	6.4E-02	AE001777.1	NT	Thermotoga maritima section 69 of 138 of the complete genome
1746	14775	27761	0.93	6.4E-02	AE001777.1	NT	Thermotoga maritima section 69 of 138 of the complete genome
4833	16085	29007	1.16	6.4E-02	6959923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5282	18270		2.56	6.4E-02	AA147572.1	EST_HUMAN	z515r04.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505470 5' similar to contains Alu repetitive element
5525	18624	31559	1.18	6.4E-02	A191958.1	EST_HUMAN	qp07d01.x1 Soares_basils_NHT Homo sapiens cDNA clone IMAGE:1738246 3' similar to contains LTR8.b3 LTR8 repetitive element
5992	19067	32295	1.16	6.4E-02	7305188	NT	Mus musculus IFN-response element binding factor 1 (IREBF-1), mRNA
6234	19307	32539	4.16	6.4E-02	AF052733.1	NT	Helicodora glycinyl-beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6234	19307	32540	4.16	6.4E-02	AF052733.1	NT	Helicodora glycinyl-beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6542	19604	32866	0.72	6.4E-02	AB72896.1	EST_HUMAN	w67312.x1 Soares_Diacytrafo_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6960	20213	33542	4.94	6.4E-02	BE974448.1	EST_HUMAN	60168042B2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3960503 3'
7693	20851	34015	0.52	6.4E-02	AL162767.2	NT	Neseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8079	21647		2.76	6.4E-02	6753323	NT	Neseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
8012	21978	33397	0.92	6.4E-02	AA093005.1	EST_HUMAN	k1419.seq F Human fetal heart, Lambda Zap Express Homo sapiens cDNA 5'
9483	22447	35587	0.92	6.4E-02	AF150195.1	EST_HUMAN	AF150188 Human mRNA from c634+ stem cells Homo sapiens cDNA clone CBDA1A10
5944	22871		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT10083-150600-014-g06 OT10083 Homo sapiens cDNA
10075	23002	36472	1.75	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10624	23546	37045	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10624	23546	37047	0.59	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12018	24895	38492	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RchRt gene, and sodium phosphate transporter (NPT3) gene, complete cds
12018	24895	38493	2.18	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RchRt gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12424	25681		5.38	6.4E-02	AF107890.1	NT	Homo sapiens mucin 6B (MUC6B) gene, partial cds
12476	25224	31793	5.68	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1769	14798	27784	2.78	6.3E-02	AF106905.1	NT	Mus musculus major histocompatibility/locus class III regions Hsc70i gene, partial cds; snRNP, G7A, NG23, MUs homolog, CLCP, NG24, NG25, and NG28 genes, complete cds, and unknown genes
3618	16692		2.71	6.3E-02	P37062	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6259	19332	32553	1.08	6.3E-02	BF210735.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087469 5'
7463	20419		1.39	6.3E-02	X67865.1	NT	H. sapiens gene encoding La autoantigen
8646	22590	36039	1.01	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dominia gene, exons 1-3
10374	23297	36773	2.98	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-162
10634	23556		0.81	6.3E-02	AV686070.1	EST_HUMAN	AV686070 GKC Homo sapiens cDNA clone GKCAHE01 5'
11070	19392	32553	2.76	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087469 5'
4278	17307	30165	2.48	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4365	17392		1.12	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4812	17633		0.56	6.2E-02	Q82191	SWISSPROT	62 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO82)
6853	20183	33513	0.97	6.2E-02	U46830.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7889	20633	34212	0.79	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8158	21096		0.68	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9299	26007		0.63	6.2E-02	M61101.1	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 45
9639	22552	36706	0.63	6.2E-02	AA178450.1	EST_HUMAN	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9835	22771	36228	1.25	6.2E-02		NT	At2G06361 Soares total, fetus, N2HIF8, 9w Homo sapiens cDNA clone IMAGE:1032178 3'
12259	25979		15.66	6.2E-02	AE000790.1	EST_HUMAN	Mus musculus stromal cell derived factor receptor 2 (Sdrf2), mRNA
12596	25299		1.38	6.2E-02	BE793095.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12676	25346	31764	3.54	6.2E-02	BF112039.1	EST_HUMAN	601883737F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
268	13563	26278	3.09	6.1E-02	D16471.1	NT	737N08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
4017	17056		15.65	6.1E-02	U73325.1	NT	Human mRNA, 3' terminal portion
6043	19125	32330	0.62	6.1E-02	7662463	NT	Arabidopsis thaliana K <sup>+</sup> inward rectifying channel protein (AKG1) gene, complete cds
6043	19125	32331	0.62	6.1E-02	7662463	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
8235	18308		1.64	6.1E-02	4507070	NT	Homo sapiens KIAA1052 protein (KIAA1052), mRNA
8606	21574	34688	3.52	6.1E-02	X69288.1	NT	Homo sapiens SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8008	21974		1.93	6.1E-02	BE671863.1	EST_HUMAN	H. sapiens mRNA for B-HLH DNA binding protein
							601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9008	21974	35594	1.93	6.1E-02	BE971853.1	EST_HUMAN	307.051068RT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
11082	24044	37596	3.44	6.1E-02	BE179543.1	EST_HUMAN	IL3HT0818-110500-135-008 HT0818 Homo sapiens cDNA
1216	25997		2.42	6.1E-02	T07089.1	NT	Sjögren's syndrome mRNA for salivary enzyme
12179	25774		1.35	6.1E-02	AI886811.1	EST_HUMAN	259907.x1 NCL CGAP_Ox36 Homo sapiens cDNA clone IMAGE:2292301 3'
12912	25491		7.44	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1287	14302	27063	1.25	6.0E-02	AE001777.1	NT	Thermococcus maritima section 89 of 138 of the complete genome
2884	16590	28598	1.17	6.0E-02	AW698948.1	EST_HUMAN	EST338024 IMAGE resources, MAGJ Homo sapiens cDNA
2763	15775		1.98	6.0E-02	AB031288.1	NT	Mesocricetus auratus mitochondrial DNA, NADH dehydrogenase subunit 2
2848	13213	28137	1.47	6.0E-02	AB031288.1	NT	ATPase subunit 6, and NADH dehydrogenase subunit 2
2848	13213	28138	1.47	6.0E-02	AA188730.1	EST_HUMAN	Zp7804.1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:628310 5'
3243	16298	29222	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST84260 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3243	16298	29223	1.52	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
5472	18573		0.76	6.0E-02	AW370211.1	EST_HUMAN	RC3-3T0263-01109-013-b04 B10263 Homo sapiens cDNA
6341	18410	32851	0.98	6.0E-02	AB07837.1	EST_HUMAN	Wf4805.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358973 3' similar to contains L1/L1 L1 repetitive element
7180	18411	31212	2.79	6.0E-02	5174598	NT	Homo sapiens stimulated T-lymphocyte factor (50 kDa) (STAF50) mRNA
7180	18411	31213	2.79	6.0E-02	5174598	NT	Homo sapiens stimulated T-lymphocyte factor (50 kDa) (STAF50) mRNA
7384	20682	33714	2.08	6.0E-02	BF382349.1	EST_HUMAN	801815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049228 5'
7508	20473	33833	0.57	6.0E-02	BF210488.1	EST_HUMAN	801817410F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101074 5'
7844	20988	34277	1.71	6.0E-02	AI204276.1	EST_HUMAN	qf58808.x1 Soares_testis NIH Homo sapiens cDNA clone IMAGE:1764199 3'
8765	21732		0.52	6.0E-02	11466495	NT	Reclinomonas americana mitochondrion, complete genome
9827	22571	36020	1.17	6.0E-02	AB23167.1	EST_HUMAN	h78a08.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
9827	22571	36021	1.17	6.0E-02	AB23167.1	EST_HUMAN	h78a08.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
9761	22702	36159	2.03	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9761	22702	36160	2.03	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10255	23190	36675	0.65	6.0E-02	AA309797.1	EST_HUMAN	EST180954 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
10255	23190	36675	0.65	6.0E-02	AA309797.1	EST_HUMAN	EST180954 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
12475	25223	31792	3.08	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12845	25455		3.16	6.0E-02	AB09273.1	EST_HUMAN	W68H03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR-O60258
232	13332	28255	5.34	5.9E-02	AW634718.1	EST_HUMAN	CG0298 KIAA0551 PROTEIN; RCH-T01001-280100-072-e10 DT0001 Homo sapiens cDNA

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Antibodies Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Database BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2698	16054	28975	3.42	5.9E-02	AF160269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4905	17922	30814	0.94	5.9E-02	AF068304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7077	26574	33409	0.82	5.9E-02	AF146800.1	NT	Drosophila melanogaster LD23107 slling (slling) mRNA, complete cds
8854	21830	33355	1.92	5.9E-02	8055249.1	EST	Mus musculus iroquois related homeobox 5 (Drosophila) (iro5) mRNA
9808	21129		0.82	5.9E-02	BF242748.1	EST	601877609F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:4706994 5'
11138	24098		3.23	5.9E-02	6879870.1	NT	Mus musculus tollistatin-like (Fsl) mRNA
833	13989		0.93	5.9E-02	D80110.1	NT	Thiobacillus ferrooxidans metC, metA genes and URF-1
2872	15032		0.98	5.9E-02	AJ223821.1	NT	Populus trichocarpa CCoA-metC1 gene, exon 1 to exon 5
3976	16719	29633	1.32	5.9E-02	AJ223821.1	NT	Thermidopsis maritima section 87 of t38 of the complete genome
4392	17410	30292	5.33	5.9E-02	AW051827.1	EST	w24c402.x1 NCI_CGAP_Ki671 Homo sapiens cDNA clone IMAGE:2544578 3'
4392	17410	30293	5.33	5.9E-02	AW051927.1	EST	w24c402.x1 NCI_CGAP_Ki671 Homo sapiens cDNA clone IMAGE:2544578 3'
4578	17600	30495	4.73	5.9E-02	AJ247905.1	EST	gb1M13142 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1846697 3' similar to gb1M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4578	17600	30496	4.73	5.9E-02	AJ247905.1	EST	gb1M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4804	17625		2.93	5.9E-02	AF070264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6014	18037	32298	0.33	5.9E-02	AI190894.1	EST	z980a11.s1 Stragansia Helia cell s3 937216 Homo sapiens cDNA clone IMAGE:627069 3'
7841	20893	34273	2.52	5.9E-02	M69160.1	NT	Human polymorphic microsatellite DNA
7841	20893	34274	2.52	5.9E-02	M69160.1	NT	Human polymorphic microsatellite DNA
9014	21990	35399	0.39	5.9E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment H321C083
12655	25698		10.6	5.9E-02	AA604269.1	EST	nc275a11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112694 3'
3070	16127	29038	1.27	5.7E-02	AI081944.1	EST	ou6305.61 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
3086	16143	29055	1.61	5.7E-02	AF119117.1	NT	CE088111
3814	16854	26761	2.47	5.7E-02	AW068791.1	EST	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
5189	18209	31082	0.91	5.7E-02	AJ251973.1	NT	EST1378865 MAGE resequences, MAGI Homo sapiens cDNA
5308	18039		1.18	5.7E-02	6754625	NT	Mus musculus parvalbumin-1 gene
5979	19064		0.59	5.7E-02	AF275948.1	NT	Mus musculus low density lipoprotein receptor (Ldlr) mRNA
7704	20861	34025	0.69	5.7E-02	BE687191.1	EST	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7704	20861	34026	0.69	5.7E-02	BE687191.1	EST	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7785	20739	34111	0.88	5.7E-02	D786003.1	EST	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3951685 5'
7785	20739	34112	0.88	5.7E-02	D786003.1	EST	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3951685 5'
8495	21463	34876	1.74	5.7E-02	AI290090.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
10279	23134	36621	0.65	5.7E-02	AF260261.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
							Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
							Mus musculus scd2 oxysterol (Ecd2) mRNA



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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10930	23850	37395	0.48	5.7E-02 Z46983.1	NT	EST_HUMAN	L.mexicana cbp1 gene
11521	24482	38013	3.22	5.7E-02 A1752885.1	EST_HUMAN	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11521	24482	38014	3.22	5.7E-02 A1752885.1	EST_HUMAN	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11678	24542		1.89	5.7E-02 AL163303.2	NT	NT	Homo sapiens chromosome 21 segment HS21C103
12573	25782		8.27	5.7E-02 D50320.1	NT	NT	Pig DNA for SPAl-2, complete cds
12794	26855		3.72	5.7E-02 AF217490.1	NT	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12990	26958		5.55	5.7E-02 AF261280.1	NT	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1529	14552	27533	1.85	5.8E-02 AF094455.1	NT	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4671	17692	30578	1.92	5.8E-02 AB013100.1	NT	NT	Lycopodium obscurum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4725	17745	30536	1.21	5.8E-02 AA305589.1	EST_HUMAN	EST_HUMAN	z445001.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416.3'
6817	19871	33160	5.93	5.8E-02 AW172708.1	EST_HUMAN	EST_HUMAN	x02070.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2656050.3' similar to TR-O84979 O84979 KIAA0905 PROTEIN. ;
7076	20097	33407	0.77	5.8E-02 AA866182.1	EST_HUMAN	EST_HUMAN	0447712.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119.3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7558	20328	33677	2.94	5.8E-02 BE008001.1	EST_HUMAN	EST_HUMAN	QYCBN0147-250403-214-g07 BN0147 Homo sapiens cDNA
8141	21078	34478	0.81	5.8E-02 A1183583.1	EST_HUMAN	EST_HUMAN	qdb4g111.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734308.3'
9154	22120	35548	2.47	5.8E-02 BE542663.1	EST_HUMAN	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279.5'
9154	22120	35549	2.47	5.8E-02 BE542663.1	EST_HUMAN	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279.5'
10171	23098	36578	1.08	5.8E-02 AA482864.1	EST_HUMAN	EST_HUMAN	n146d07.st NCI_CGAP_A01 Homo sapiens cDNA clone IMAGE:923245 similar to TR-G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE IC. ;
11891	24772		1.87	5.8E-02 AF260225.1	NT	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2563	15680	29678	8.23	5.8E-02 X97869.1	NT	NT	H. sapiens gene encoding La autoantigen
3228	16283	29207	3.44	5.8E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4244	17273	30157	1.13	5.8E-02 L41561.1	NT	NT	Gallus herpesvirus mRNA fragment
5742	18836	32017	3.09	5.8E-02 Q01174	SWISSPROT	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6141	18838	32017	3.81	5.8E-02 Q01174	SWISSPROT	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7603	20564	33925	1.95	5.8E-02	6755902	NT	Mus musculus titin 1 (Tt1), mRNA
8457	21428	34842	0.89	5.8E-02 AF170911.1	NT	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8457	21428	34843	0.89	5.8E-02 AF170911.1	NT	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
10013	22940	36405	0.93	5.8E-02	10947034	NT	Homo sapiens eIF-4E-transporter (4E-T), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10013	22940	36406	0.83	5.9E-02	U0947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10107	23033	36510	1.45	5.9E-02	U094822.1	NT	Mus musculus second IL11 receptor alpha chain (L11Ra2) gene, exons 1 and 2
11360	24309	37836	6.48	5.9E-02	U08771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhak), 1,3-propanediol dehydrogenase (dhaf), glycerol dehydrogenase (dhaf), >
13089	25920	31303	1.89	5.9E-02	11421332	NT	Homo sapiens hypophthalic protein SRR-b2 (SRR-b2), mRNA
3032	16090		1.02	5.4E-02	AJ277488.1	NT	Oryza sativa fbh3-1 gene for putative Bowman Birk trypsin inhibitor
3433	18523		6.87	5.4E-02	BE073488.1	EST_HUMAN	RC5-B10559-1.02010-012-C03 B10559 Homo sapiens cDNA
3831	16971	29885	0.7	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8462	21431		1.05	5.4E-02	Z98116.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
9428	22390	36828	0.83	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11057	24020	37543	1.54	5.4E-02	U02760.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
1056	14102	27052	1.81	5.3E-02	AW391248.1	EST_HUMAN	QVQ-ST0213-021299-062-ad9 ST0213 Homo sapiens cDNA
1059	14102	27053	1.81	5.3E-02	AW391248.1	EST_HUMAN	QVQ-ST0213-021299-062-ad9 ST0213 Homo sapiens cDNA
1506	14539	27511	18.63	5.3E-02	T04759.1	EST_HUMAN	yeS7H12.11 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2504	15507	26533	2.12	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgs gene
2953	16011	26937	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster leminin B2 gene, complete cds
2953	16011	26938	0.95	5.3E-02	M58417.1	NT	Drosophila melanogaster leminin B2 gene, complete cds
3167	16222	29137	5.38	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgs gene
4941	17652	30550	0.9	5.3E-02	AJ011048.1	NT	Arabidopsis thaliana cils gene, exons 1-11
5125	18134	31011	8.41	5.3E-02	M80483.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5328	18436	31372	1.8	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5392	18495	31373	1.8	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6222	19295	32530	3.03	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7088	20090	33398	3.84	5.3E-02		NT	Lymphocytic choriomeningitis virus 1, complete genome
7259	20271	33009	1.23	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7585	20546		2.12	5.3E-02	S76221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4953 nt]
8209	21108	34507	0.61	5.3E-02	P38742	SWISSPROT	HYPOPHthalic 130.0 kD PROTEIN IN SNF6-SPOT11 INTERGENIC REGION
8748	21718		0.5	5.3E-02	U10088.1	NT	Mus musculus 120Sv ovalbumin C (cst3) gene, complete cds
9481	22445	35886	2.05	5.3E-02	X03127.1	NT	Podopara anserina mitochondrial epsilon-sen DNA
10491	23413	36911	0.81	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds
10491	23413	36912	0.81	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12699	25359		1.75	5.1E-02	AF082467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
12697	25531		1.8	5.1E-02	AA531104.1	EST_HUMAN	h73602.61 NCI CGAP PR10 Homo sapiens cDNA clone IMAGE:998199
483	13556	28481	2.16	6.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
935	13888	28938	4.55	5.0E-02	Z33886.1	NT	O. virginianus (HEL37) microsatellite DNA
1209	14247	27205	4.03	5.0E-02	Z69104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
2007	15028	28036	4.94	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 12 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (P1F-F1P1-F3) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2829	14040	26995	1.92	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase [UGT2B13] mRNA, complete cds
3348	16399		1.34	5.0E-02	Z305810	NT	Mus musculus Ubc-51 like kinase 2 (G. elegans) (Ulk2), mRNA
3609	16854		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3695	18730	26852	13.52	5.0E-02	U12769.2	NT	Anthraxa penryl period clock protein homolog mRNA, complete cds
6253	19326	32657	0.77	5.0E-02	AF098264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
8441	19505		1.25	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7181	18412	31214	0.6	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7785	20738	34110	12.03	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8008	20946		0.52	5.0E-02	AW062464.1	EST_HUMAN	MRQ-CT0094-100899-002-g10 CT0064 Homo sapiens cDNA
10560	23482	36977	1.26	5.0E-02	AF05238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fie3) mRNA, complete cds
11820	24703	38285	2.47	6.0E-02	U87600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
12226	25516		6.4	5.0E-02	Q04947	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
228	13325		27.61	4.9E-02	M14230.1	NT	Chicken 28-40a vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
359	13455	26384	2.98	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
359	13455	26385	2.96	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3302	16355	28274	1.84	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
3584	16828		0.7	4.9E-02	AA188940.1	EST_HUMAN	z47842.61 Strabagone INT neuron. (#637233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
3605	16850	26656	0.96	4.9E-02	AA400914.1	EST_HUMAN	z178a03.61 Soares testis, NHT Homo sapiens cDNA clone IMAGE:728428 3'
3605	16850	26657	0.96	4.9E-02	AA400914.1	EST_HUMAN	z178a03.61 Soares testis, NHT Homo sapiens cDNA clone IMAGE:728428 3'
4877	17894	30783	2.11	4.9E-02	AA167821.1	EST_HUMAN	xg58g10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:263288 3'
4877	17894	30784	2.11	4.9E-02	AA167821.1	EST_HUMAN	xg58g10.x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:263288 3'
5444	18546	31458	1.71	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
6444	18546	31459	1.71	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7349	20319	33689	2.83	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8693	21928		0.91	4.9E-02	AE002399.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8707	22073	36550	0.8	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10656	23578	37075	0.63	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11730	24616	38193	3.44	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12879	25473		6.66	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
330	13420	26344	1.08	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
331	13420	26344	2.41	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
489	13562	28486	12.99	4.9E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
							2c49b2.61 Soares, senescent, fibroblasts, NIH/3T3 Homo sapiens cDNA clone IMAGE:325811 3' similar to
2281	15294	28318	2.24	4.9E-02	N191983.1	EST_HUMAN	gbM300538 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3222	16277	29202	1.63	4.9E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4698	17719		1.24	4.9E-02	Z64280.1	NT	S. aureus gene for skeletal muscle myosin receptor
5174	18183	31060	0.63	4.9E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
8477	21446	34863	1.55	4.9E-02	AW389497.1	EST_HUMAN	MR2-ST0728-221096-012-602 ST0728 Homo sapiens cDNA
9485	22449	35689	0.76	4.9E-02	AJ001398.1	NT	Fugu rubripes rpa24 gene
9485	22449	35690	0.76	4.9E-02	AJ001398.1	NT	Fugu rubripes rpa24 gene
12505	25242		1.35	4.9E-02	8632893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
							yc3709.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu
7004	20130	33445	3.77	4.7E-02	V01153.1	EST_HUMAN	repulsive element
7069	20091	33399	0.88	4.7E-02	BF686625.1	EST_HUMAN	802143564Ft NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7069	20091	33400	0.88	4.7E-02	BF686625.1	EST_HUMAN	802143564Ft NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7103	20037	33340	1.56	4.7E-02	M62732.1	NT	Rat statin-related protein (s1) gene, complete CDS
8604	21562	34878	8.56	4.7E-02	X15543.1	NT	H. sapiens mRNA for RF-36-DNA-binding protein
9305	22270	35701	1.85	4.7E-02	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
9327	22292		2.51	4.7E-02	AB028678.1	NT	Gallus gallus Wp161-8 gene, complete cds
9582	22544	35695	0.56	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
10005	22632	36395	0.56	4.7E-02	BF030527.1	EST_HUMAN	801802892Ft NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
10092	23018		0.66	4.7E-02	AB73042.1	EST_HUMAN	we78c1d.x1 Soares, NFL_T, GBC_S1 Homo sapiens cDNA clone IMAGE:2347314.3'
12783	25970		1.97	4.7E-02	P52961	SWISSPROT	HOMEOBOX PROTEIN GBX2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
13022	25570		1.56	4.7E-02	AJ277692.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
270	13366	26292	1.08	4.6E-02	BE153583.1	EST_HUMAN	PNC-HT10336-231199-003-g05 HT10339 Homo sapiens cDNA
741	13802	26741	3.47	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1391	14395	27966	3.62	4.6E-02	AV727095.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW001 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2466	15490	26525	4.32	4.6E-02	AW236023.1	EST_HUMAN	xm2403.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
2819	13300	26292	1.03	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1;
3020	16078	26599	0.87	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3342	16078	26599	0.97	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3342	16078	26599	0.97	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3507	16078	26599	0.61	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4149	17160		1.24	4.6E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase II(Gu ddx21) gene, complete cds
5252	18260	31128	0.94	4.6E-02	AA078157.1	EST_HUMAN	zmr2010.s1 Striatum ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:543594 3' similar to gb:XA03212 KERATIN, TYPE II CYTOSKELETAL 7 (HUMAN);
5823	18913	32066	1.42	4.6E-02	AF076982.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6357	19426	32563	4.48	4.6E-02	X81624.1	NT	C.reinhardtii ap2 (apB) mRNA
6357	19426	32569	4.48	4.6E-02	X81624.1	NT	C.reinhardtii ap2 (apB) mRNA
6968	20191	33518	1.51	4.6E-02	A1149574.1	EST_HUMAN	gc00000.x1 Soares_p1acenta_80cweeks_2NHP8B6uW Homo sapiens cDNA clone IMAGE:1719371 3' similar to contains L1 t3 L1 repetitive element;
8134	21071	34470	0.60	4.6E-02	6978720	NT	Rattus norvegicus Cathelin H (CthH), mRNA
9003	21069	35391	2.89	4.6E-02	BE154006.1	EST_HUMAN	PMO-HT0339-060400-008-G12 HT0339 Homo sapiens cDNA
11731	24617	38164	5.31	4.6E-02	AA013328.1	EST_HUMAN	q27h09.s1 Soares_NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
12761	26987		1.99	4.6E-02	L11692.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
12982	25552		8.41	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
447	13520	28453	1.9	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1222	14250	27217	0.78	4.5E-02	AF005720.1	NT	Meibing virus strain MIS.AfricaJohannesburg/1975/Ozolin VP35 gene, complete cds
1222	14250	27218	0.78	4.5E-02	AF005730.1	NT	Meibing virus strain MIS.AfricaJohannesburg/1975/Ozolin VP35 gene, complete cds
1821	14848	27841	4.23	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2119	15139	28150	3.34	4.5E-02	AE003584.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3736	16778	28681	4.42	4.5E-02	AL153278.2	NT	Homo sapiens chromosome 21 segment HS210078
6359	19427	32870	1.63	4.5E-02	AL400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene and C11orf17 gene
6656	19713	32950	0.94	4.5E-02	AL169280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7062	20084	33592	0.98	4.5E-02	L26487.1	NT	Methanococcus frida carbon monoxide dehydrogenase large subunit (cdhIA) gene, carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
7062	20084	33593	0.98	4.5E-02	L26487.1	NT	Methanococcus frida carbon monoxide dehydrogenase large subunit (cdhIA) gene, carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
8736	21704	35128	2.34	4.5E-02	AF036684.1	NT	Arabidopsis thaliana COCAAT-box binding factor HAP3 homolog gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10309	23233	38715	4.93	4.9E-02	AA325210.1	EST_HUMAN	EST128167 Cerebellum II Homo sapiens cDNA 5' and similar to neuro-D4 protein
10460	23382	38975	0.43	4.5E-02	X95508.1	NT	A.europaeum mRNA for leucine-like protein
10571	23469	36991	0.81	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12440	25203	31826	2.95	4.5E-02	11418013	NT	Gallus gallus ref finger protein-like 3 (RFPL3), mRNA
12823	23663	31440	7.3	4.5E-02	AA191087.1	EST_HUMAN	243311.11 Stragarene INT neuron (8937233) Homo sapiens cDNA clone IMAGE:632493 5'
222	13322		4.84	4.4E-02	BE872733.1	EST_HUMAN	160162154FT NIH_MGC: 82 Homo sapiens cDNA clone IMAGE:393588 5'
2107	15124		0.38	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2498	15501	28527	2.11	4.4E-02	AW87457.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3654	16697	29812	2.01	4.4E-02	AF159160.1	NT	Mycobacterium vanthius serine/threonine kinase Pkn10 (pkn10) gene, complete cds; and S171 gene, partial cds
4657	17678	30593	1.25	4.4E-02	AF109007.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4657	17678	30564	1.25	4.4E-02	AF109007.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4771	17791		0.84	4.4E-02	AF222659.1	NT	Ovite cdas CCAAT-enhancer binding protein epsilon gene
7325	20298	33639	0.59	4.4E-02	AF095824.1	NT	Caris familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7325	20298	33640	0.69	4.4E-02	AF095824.1	NT	Caris familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8105	22071	35497	2.17	4.4E-02	AA736569.1	EST_HUMAN	nt13h03.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239221 3'
11409	24353	37898	3.75	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
11533	24474	38025	2.55	4.4E-02	AA498739.1	EST_HUMAN	ad3304.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12159	25014		2.22	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12346	25980		1.83	4.4E-02	BF241245.1	EST_HUMAN	601878749FT NIH_MGC: 55 Homo sapiens cDNA clone IMAGE:4107418 5'
781	13841	26766	5.93	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2575	15579	28995	1.4	4.3E-02	AY704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAO108 5'
3443	16490	29409	8.93	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3671	16714		1.25	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6944	19702	32977	4.82	4.3E-02	P30427	SWISSPROT	PLECTIN
6844	19702	32978	4.82	4.3E-02	P30427	SWISSPROT	PLECTIN
6859	19548	33245	0.73	4.3E-02	AA65286.1	EST_HUMAN	hs8612.s1 NCI_CGAP_F22 Homo sapiens cDNA clone IMAGE:118886
8658	21826	35248	0.9	4.3E-02	AF263359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9153	22119	35548	0.95	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9153	22119	35547	0.95	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
823	13881	26632	1.85	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
837	13923		2.69	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'

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Probe ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13852	897	28910	0.83	4.2E-02	AW003845.1	EST_HUMAN	wk3dgl01.x1 NCI_CGAP_P1H1 Homo sapiens cDNA clone IMAGE:2545894.3' similar to TR-Q63281 Q63291 L1 Retroplasma, ORF2 mRNA, contains L1.8 L1 L1 repetitive element ;
1733	14783		1.54	4.2E-02	AL445068.1	NT	Theroplasma acidophilum complete genome, segment 4/5
1763	14822	27806	1.02	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3877	16720	28634	2.18	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4774	17794	30698	0.73	4.2E-02	BF342895.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152872 5'
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5699	18794	31867	0.85	4.2E-02	AF280107.1	NT	Homo



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8042	20979	34376	2.63	4.1E-02	AF020188.1	NT	Ragu subtypes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8549	21617	34936	0.58	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (ADAMTS-1) (ADAM-TS1)
8590	21956	35581	0.57	4.1E-02	P34887	SWISSPROT	CUTICLE COLLAGEN 34
9509	22472	35916	0.83	4.1E-02	AA372388.1	EST_HUMAN	ESTB42891 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
13013	25609	31423	4.48	4.1E-02	AJ271909.1	NT	Brassica napus gin gene for plastid glutamine synthetase, exons 1-12
13102	25625	31679	1.33	4.1E-02	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
1549	14681	27654	1.21	4.0E-02	AB075392.1	EST_HUMAN	W58B101.X1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313745 3'
3258	16312	26233	2.57	4.0E-02	AB040604.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5453	18555	31486	5.39	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6339	19408	32848	1.43	4.0E-02	BF110434.1	EST_HUMAN	7h2h07.X1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568390 3' similar to TR:075299 075299
7554	20895	34288	6.1	4.0E-02	L23638.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
8025	20983		0.68	4.0E-02	AL181533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
8043	20980	34378	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GH-anchored molecule-like protein, complete cds
8043	20980	34377	0.85	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GH-anchored molecule-like protein, complete cds
9087	22033	35459	2.78	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOAMYLASE)
10022	22929		0.71	4.0E-02	BF079376.1	EST_HUMAN	60215384.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284724 5'
10027	22954	35423	2.95	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thioflumarate reductase subunit A
10344	23288		0.92	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
12089	24041		1.48	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca <sup>2+</sup> ATPase
12331	25730	31614	3.52	4.0E-02	AJ001058.1	NT	Ovis aries mRNA for acyl-CoA carboxylase
1122	14166	27118	3.13	3.9E-02	BF516749.1	EST_HUMAN	U1H-BW1-anch-HB-CUI.1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1348	14383	27351	1.9	3.9E-02	P41047	SWISSPROT	PAS ANTIGEN LIGAND
1978	14699	28001	2.82	3.9E-02	AJ463368.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2715	15700		2.12	3.9E-02	4509862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15KD (SDHC) mRNA
5191	18200	31072	0.65	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0289-171199-021-C08 ST0259 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5573	18669	31630	0.74	3.9E-02	D50608.1	NT	Rat gene for cholesterylkin type-A receptor (CKAR), complete cds
5573	18669	31631	0.74	3.9E-02	D50608.1	NT	Rat gene for cholesterylkin type-A receptor (CKAR), complete cds
5820	18910	32094	1.08	3.9E-02	BE66884.1	EST_HUMAN	60164087/4F1 NIH_MGC 74 Homo sapiens cDNA clone IMAGE:3933642 5'
5957	19042	32241	0.71	3.9E-02	BF675203.1	EST_HUMAN	602138132/FT1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4274910 5'
7259	18694	33281	1.1	3.9E-02	BE271437.1	EST_HUMAN	601140729/FT1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3049830 5'
8167	21105	34504	0.53	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
8172	21142	34548	1.07	3.9E-02	BF238613.1	EST_HUMAN	601606848/FT1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4134779 5'
8395	21364	34772	0.63	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8395	21364	34773	0.83	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11737	21105	34504	1.61	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12164	25872		14.17	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12949	25794		5.15	3.9E-02	AL049865.2	NT	Mus musculus chromosome X contig8; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, rrmxq28orf
1899	14990	27893	1.13	3.9E-02	BE685137.1	EST_HUMAN	60151089/FT1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912215 5'
2129	15148		1.1	3.9E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
4906	17923	30815	0.92	3.9E-02	BE393276.1	EST_HUMAN	601308498/FT1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3626757 5'
4906	17923	30816	0.92	3.9E-02	BE393276.1	EST_HUMAN	601308498/FT1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3626757 5'
4955	17980	30870	1.4	3.9E-02	AJ124122.1	EST_HUMAN	AJ124122 NT28M2 Homo sapiens cDNA clone NT28M2001688 5'
6616	18616	31648	1.2	3.9E-02	MT1228.1	NT	Human protein C gene, complete cds
6208	19280	32513	1.04	3.9E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOXB4 (HOX-2.6)
7540	20503	33662	1.43	3.9E-02	P10284	SWISSPROT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8011	21977		1.28	3.9E-02	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
11014	23878	37505	2.04	3.9E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
12009	24883	39481	1.53	3.9E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR
12009	24886	39482	1.53	3.9E-02	P01641	SWISSPROT	IG KAPPA CHAIN V-V REGION MOPC 173B PRECURSOR
694	14045	26869	4.76	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1389	14423	27392	0.85	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2246	15260	28287	4.68	3.7E-02	AJ94606.1	EST_HUMAN	wf5604x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
3063	16120	29034	1.27	3.7E-02	P79944	SWISSPROT	ECOMESODERMIN
3065	16122	29035	4.14	3.7E-02	BF312663.1	EST_HUMAN	601889233/FT1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4125984 5'
3469	16514		1.03	3.7E-02	6880541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kerms3), mRNA
5279	18285	31148	0.76	3.7E-02	AF168106.1	NT	Bufo virginianus cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7281	25998		0.79	3.7E-02	AF0000683.1	NT	Aeropyrum pernix genomic DNA, section 67
7956	20897	34290	0.64	3.7E-02	AE003975.1	NT	Xyella fastidiosa, section 121 of 229 of the complete genome
10376	23298		0.89	3.7E-02	AA782516.1	EST_HUMAN	h55d09.61 Soares parathyroid tumor Nbr-IPA Homo sapiens cDNA clone 1360912.3
12275	25051	36828	5.94	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024673.6
12883	25762	31520	2.34	3.7E-02	11418392	NT	HuJugarc Sst1 gene for sucrose synthase
3667	16710	29625	1.04	3.6E-02	X73221.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosomes 10[10q26.3] of Homo sapiens
3674	16717	29631	0.75	3.6E-02	AL096808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosomes 10[10q26.3] of Homo sapiens
5253	18281	31130	2.27	3.6E-02	AL096810.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5501	18601	31514	0.8	3.6E-02	X56403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5501	18601	31530	0.8	3.6E-02	X56403.1	NT	Homo sapiens RUA2AS (RU2) mRNA, complete cds
5578	18674	31638	0.68	3.6E-02	AF161722.1	NT	CM2-EN0013-110500-192-b70 EN0013 Homo sapiens cDNA
6895	19018	33212	4.97	3.6E-02	AW946516.1	EST_HUMAN	CM2-EN0013-110500-192-b70 EN0013 Homo sapiens cDNA
6895	19018	33213	4.97	3.6E-02	AW946516.1	EST_HUMAN	Methanococcus jannaschii section 117 of 150 of the complete genome
7150	18382	31270	0.5	3.6E-02	U67575.1	NT	Chromatium vinosum sulfur globule protein Cx2 precursor (sp22) gene, complete cds
7291	20263	33597	1.7	3.6E-02	AF025662.1	NT	TM20605.s1 NCI_CGAP_GG80 Homo sapiens cDNA clone IMAGE:1241024.3 similar to gb:J00314.1ma2
7527	20491	33653	2.75	3.6E-02	AA714521.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
7895	20338	34218	1.08	3.6E-02	BE143078.1	EST_HUMAN	MRO-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
8746	22687	36142	1.85	3.6E-02	U20608.1	NT	Dicystatellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
8746	22687	36143	1.85	3.6E-02	U20608.1	NT	Dicystatellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
8971	22998	36361	0.68	3.6E-02	BF347599.1	EST_HUMAN	602020453F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156116.5
896	13951	26909	0.9	3.6E-02	U09506.1	NT	Drosophila melanogaster igitrin mRNA, complete cds
1010	14059	27011	1.38	3.6E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1566	14590	27574	1.3	3.6E-02	BF78085.1	EST_HUMAN	602086136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377.5
1566	14590	27575	1.3	3.6E-02	BF78085.1	EST_HUMAN	602086136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377.5
4241	17270	30155	1.95	3.6E-02	AE001773.1	NT	Thermoplasma maritima section 65 of 138 of the complete genome
4344	17371	30253	3.67	3.6E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5285	18273		1.04	3.9E-02	P47144	SWISSPROT	HYPOTHETICAL 83.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
6347	18418	32657	1.74	3.9E-02	J01238.1	NT	Maize actin 1 gene (MAct1), complete cds
8310	21279		0.76	3.9E-02	H29951.1	EST_HUMAN	Yp4405.r1 Soares retina N2B5HR Homo sapiens cDNA clone IMAGE:3929737 3'
8970	21535	35582	2.87	3.9E-02	BE556970.1	EST_HUMAN	Liactis MG1363 gPPE and chak genes
10378	23301	36777	1.99	3.9E-02	X76642.1	NT	PM1344681FT NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677694 5'
10425	23347	36832	0.47	3.9E-02	BE591042.1	EST_HUMAN	PM1-CT0326-291298-002-H03 CT0326 Homo sapiens cDNA
11823	24703	38288	1.61	3.4E-02	AW861841.1	EST_HUMAN	PM1-CT0326-291298-002-H03 CT0326 Homo sapiens cDNA
11823	24703	38289	1.61	3.4E-02	AW861841.1	EST_HUMAN	PM1-CT0326-291298-002-H03 CT0326 Homo sapiens cDNA
12877	25508		6.77	3.9E-02	BE276948.1	EST_HUMAN	Homo sapiens mRNA for FLJ00013 protein, partial cds
580	13649	26592	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
580	13649	26593	0.91	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13649	26592	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
581	13649	26593	3.42	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1053	14099	27049	2.4	3.4E-02	AW274020.1	EST_HUMAN	X02607.XT Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW-0211_HUMAN PS3801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR.
1211	14249		6.61	3.4E-02	11345459	NT	Homo sapiens hypodermal protein FLJ13220 (FLJ13220), mRNA
2401	15408	28432	2.51	3.4E-02	T57160.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3444	16491	29410	1.19	3.4E-02	AL763208.2	NT	MER29 repetitive element
3942	16982	29897	3.71	3.4E-02	AW754952.1	EST_HUMAN	ROG-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4628	17649	30837	3.05	3.4E-02	X59789.1	NT	M. musculus S-antigen gene promoter region
5100	18110		2.48	3.4E-02	Q23487	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5114	18124	30899	1.93	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6330	19400		0.63	3.4E-02	BF131628.1	EST_HUMAN	601820448FT NIH_MGC_98 Homo sapiens cDNA clone IMAGE:4052434 5'
7032	18354	31281	3.97	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8604	21672		3.14	3.4E-02	A869929.1	EST_HUMAN	M6904.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
9100	22068	35492	1.66	3.4E-02	AA684886.1	EST_HUMAN	hu7008.s1 NCI CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element;
							zq04711.s1 Stratiene muscle 837209 Homo sapiens cDNA clone IMAGE:028749 3' similar to TR-G1017425 G1017425
9288	22334		6.2	3.4E-02	AA194306.1	EST_HUMAN	IPISKPLPKVTLSDQGVPLKATNRNFNTAENLTINKESVTADAGRYEITAAANSSGTTKAFINIVLDRPG
10136	23062		0.64	3.4E-02	AA092719.1	EST_HUMAN	PPT GRVVISDITEESVTLKVEPKYDGGSOVTNYLLKRETSIAWTEVSATVARTANKVKL ...;
							0298108.x1 Soares_papillary tumor_NbHFA Homo sapiens cDNA clone IMAGE:1883519 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
372	13458		0.24	3.3E-02	AA398735.1	EST_HUMAN	275603 at Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728108 3'
1171	14212	27166	14.48	3.3E-02	AB035887.1	NT	Cheteculus gireus CYP2A7 mRNA for cytochrome P450 2A17, complete cds
1945	14677	27650	1.73	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1753	14782		1.29	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2098	15113		1.76	3.3E-02	R08112.1	EST_HUMAN	Y25603 r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127888 5'
2498	15462	28485	1.31	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp98 (Ttra1), mRNA
3372	16422	29347	8.85	3.3E-02	H02389.1	EST_HUMAN	J359102 r1 Soares placenta N2bHP Homo sapiens cDNA clone IMAGE:150771 5'
4205	16677	27650	2.36	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4494	17519	30407	1.81	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp98 (Ttra1), mRNA
4848	17865	30759	0.86	3.3E-02	AW275695.1	EST_HUMAN	Xp4004.x1 NCL CGAP_HNT1 Homo sapiens cDNA clone IMAGE:2742790 3'
6570	18630	32895	20.14	3.3E-02	BF245895.1	EST_HUMAN	601853910FT NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5'
6570	18630	32897	20.14	3.3E-02	BF245895.1	EST_HUMAN	601853910FT NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073787 5'
6671	22630	36084	0.71	3.3E-02	BF115621.1	EST_HUMAN	7m92404.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9677	22630	35085	0.71	3.3E-02	BF115621.1	EST_HUMAN	7m92404.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9779	22720	36174	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad0809 st Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb.X70944_cds1
							MYOBLAST CELL SURFACE ANTIGEN 24-1D5 (HUMAN);
9779	22720	36175	0.72	3.3E-02	AA488202.1	EST_HUMAN	ad0809 st Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb.X70944_cds1
10884	23884		0.46	3.3E-02	H38109.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24-1D5 (HUMAN);
11465	24988	37945	2.47	3.3E-02	BF691107.1	EST_HUMAN	3p51111 st Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190989 3'
12647	25270		3.71	3.3E-02	T86545.1	EST_HUMAN	3p224777FT NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4332487 5'
12647	25270		1.69	3.3E-02	P28955.1	NT	3p48111 st Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101 5'
12677	25286		3.04	3.3E-02	M81800.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
132	13237	28188	1.27	3.2E-02	AF002005.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
1128	14171	27122	10.01	3.2E-02	AF068275.1	NT	Cytocollus cuticularis gene encoding ileal sodium-dependent bile acid transporter
1128	14171	27123	10.01	3.2E-02	AF068275.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88 allele, complete cds
2127	15144		3.6	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88 allele, complete cds
3151	16203	29122	9.61	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
4248	17275		16.99	3.2E-02	X94768.1	NT	3p1442431FT NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3846727 5'
							H. sapiens RP3 gene (XLRP gene 3)
4801	17818	30712	3.75	3.2E-02	AF114182.1	NT	Sadfraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5303	18306		1.34	3.2E-02	Y08824.1	NT	P. falciparum mRNA for AARP2 protein
5613	18709	31886	1.56	3.2E-02	X88709.1	NT	S. griseocaudum whiG-Stv gene
5613	18709	31887	1.56	3.2E-02	X88709.1	NT	S. griseocaudum whiG-Stv gene

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6873	19730	33008	2.23	3.2E-02	M32437.1	NT	Rat polyomavirus left junction in cell line W68.14
6876	19733			3.2E-02	T89387.1	EST_HUMAN	Y839h12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element/contains LTR1 repetitive element
6763	19817	33097	4.01	3.2E-02	AF173845.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
8039	20676	34372	0.82	3.2E-02	11424049	NT	Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B), mRNA
8643	21611	35033	2.84	3.2E-02	6680553	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9283	22258		0.7	3.2E-02	AF106718.1	NT	Homo sapiens chromosome 3 subtelomeric region
9580	22642	35592	1.02	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1892063 3'
9580	22642	35593	1.02	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1892063 3'
10417	23339		4.18	3.2E-02	AA716795.1	EST_HUMAN	z654b12.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gblL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
10723	23645	37138	0.98	3.2E-02	U96762.1	NT	Macaca mulatta chemokine receptor CCR3 mRNA, complete cds
12612	25076		1.43	3.2E-02	V00574.1	NT	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-res-1) with four exons
1265	14300		2.28	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1308	14344	27309	1.67	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1909	14933	27929	1	3.1E-02	6671594	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1991	16012		1.18	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
5336	18441	31194	1.28	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5434	18536		2.26	3.1E-02	AA278478.1	EST_HUMAN	z881a06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5731	18826	32006	0.81	3.1E-02	BF687742.1	EST_HUMAN	592068783.F1 NHIMGCB7 Homo sapiens cDNA clone IMAGE:4065789 5'
5803	25545	32078	0.52	3.1E-02	AJ391284.1	NT	Nakaseia meningitidis DNA for region 2 (flaB- and fliaC-homologs, unknown genes) and flanking genes, strain FAM18
10391	23313	35793	2.55	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1627	14680		2.21	3.0E-02	AF187125.1	NT	Phykolines minutus cytochrome oxidase 1 gene, partial cds; mitochondrial gene for mitochondrial product z653h03.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:727263 5'
2590	15591	28608	0.97	3.0E-02	AA40242.1	EST_HUMAN	Sec6h03.1 Soares testis stem-loop mutation suppressor SSL2 gene, complete cds
3579	16524	29545	0.91	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3683	16709	28624	2.77	3.0E-02	AF247684.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3768	18769		0.98	3.0E-02	AW620223.1	EST_HUMAN	QV2-ST0298-180200-Q00-Q09 ST0298 Homo sapiens cDNA
3969	17009		1.45	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pined gland II Homo sapiens cDNA 5' end
5092	18102	30977	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5092	18102	30978	7.41	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
6465	18587		2.99	3.0E-02	AB048793.1	NT	Homo sapiens mRNA for KIAA1673 protein, partial cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6383	19451	32593	0.58	3.0E-02	N89615.1	EST_HUMAN	z39a10.1t Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6383	19451	32594	0.58	3.0E-02	N89615.1	EST_HUMAN	z39a10.1t Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6957	20182	33505	3.17	3.0E-02	AJ24205.1	NT	Cyprinid carpio mRNA for inducible nitric oxide synthase (NOS gene)
7091	20025	33327	2.8	3.0E-02	BE86948.1	EST_HUMAN	801612206FT NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3913848 5'
7091	20025	33328	2.8	3.0E-02	BE86948.1	EST_HUMAN	801612206FT NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3913848 5'
7274	20009	33310	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7274	20009	33311	2.29	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7442	20408	33760	1.29	3.0E-02	M89524.1	NT	Human dystrophin gene
7838	20783		0.76	3.0E-02	BF246361.1	EST_HUMAN	601854081FT NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4074548 5'
8463	21432		0.48	3.0E-02	BF973706.1	EST_HUMAN	602154364FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4295654 5'
8688	21954	36378	0.74	3.0E-02	BF353889.1	EST_HUMAN	ILCH10704-230600-108-cd4 HT0704 Homo sapiens cDNA
9145	22111		1.62	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10326	23747	37248	1.89	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
11566	24506	38063	2.38	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11697	24874	38470	7.84	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCJ_CGAP_Kdrt Homo sapiens cDNA clone IMAGE:391283
12529	25590	31316	2.02	3.0E-02	R32019.1	EST_HUMAN	Y839d4.s1 Scores placenta N22HP Homo sapiens cDNA clone IMAGE:134407 3'
12663	25470		2.06	3.0E-02	AIW89555.1	EST_HUMAN	QV4-NN0038-270400-187-h65 NN0038 Homo sapiens cDNA
12908	25954		1.96	3.0E-02	AF046987.1	NT	Rattus norvegicus UDP-Gal:glucose/keramide beta-1,4-galactosyltransferase mRNA, complete cds
2442	15803	28487	1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRO1) gene, complete cds, alternatively spliced
3005	16003	28982	1.14	2.6E-02	BE565944.1	EST_HUMAN	601338428FT NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3680695 5'
3005	16003	28983	1.14	2.6E-02	BE565944.1	EST_HUMAN	601338428FT NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3680695 5'
3573	16618	29540	0.8	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
3650	16960	29508	0.72	2.9E-02	HT2805.1	EST_HUMAN	y07610.t Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:233130 5'
6181	19256	32499	1.13	2.9E-02	AF060221.1	NT	Sus scrofa dioxynucleotase II mRNA, complete cds
6424	19491	32743	7.33	2.8E-02	BF032233.1	EST_HUMAN	801452601FT NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3656598 5'
7142	20118	33431	0.52	2.6E-02	AJ391284.1	NT	Neisseria meningitidis DNA for region 2 (haB- and haC-homologs, unknown genes) and flanking genes, aroA FAM18
7460	20428	33782	10.95	2.8E-02	BE271437.1	EST_HUMAN	601140728F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3049830 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7857	20817	33382	0.67	2.9E-02	D28214.1	EST_HUMAN	HUMN282 Human epidermal keratinocyte Homo sapiens cDNA clone 282
8169	21107	34506	0.53	2.9E-02	AE003932.1	NT	Xylaria festuicosa, section 79 of 229 of the complete genome
8331	21300	34716	0.83	2.9E-02	AF128279.1	NT	Buchnera aphidicola natural-host Schlectendallia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
8331	21300	34717	0.83	2.9E-02	AF128279.1	NT	Buchnera aphidicola natural-host Schlectendallia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
10016	22943	36409	2.26	2.9E-02	AW875978.1	EST_HUMAN	OM3-PT0014-071269-051-c04 PT0014 Homo sapiens cDNA
10016	22943	36410	2.26	2.9E-02	AW875978.1	EST_HUMAN	OM3-PT0014-071269-051-c04 PT0014 Homo sapiens cDNA
10233	23158	37127	0.67	2.9E-02	AW976597.1	EST_HUMAN	EST3388708 MAGE resequences, MAGN Homo sapiens cDNA
10710	23632	37127	1.07	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 777
11388	16618	29540	1.6	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12531	26870		1.46	2.9E-02	ALU13587.1	EST_HUMAN	EST338224 MAGE resequences, MAGK Homo sapiens cDNA
567	13637		1.93	2.9E-02	AW970153.1	EST_HUMAN	EST338224 MAGE resequences, MAGK Homo sapiens cDNA
3380	16429	26355	1.27	2.9E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3380	16429	26356	1.27	2.9E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4341	17398		0.67	2.9E-02	6893751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5206	18215	31090	3.2	2.9E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, LaminB ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-GUANINE TRANSGLYCOSYLASE
5294	18289		0.93	2.9E-02	M69483.1	NT	Dengue virus type 2 non-structural protein 1 (NS1) gene, partial cds
5565	18632	31622	10.99	2.9E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948067 5'
6881	20204	33533	1.13	2.9E-02	T76980.1	EST_HUMAN	XZ15081T Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:108855 5'
8871	21633	35063	2.24	2.9E-02	ALJ08920.1	NT	Craterosigma plantaginum mRNA for homeodomain leucine zipper protein (hb-1)
9371	22336	33706	0.82	2.9E-02	AA280782.1	EST_HUMAN	Z59606.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9563	22525	35974	1.03	2.9E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9697	23920	36071	1.01	2.9E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
10380	23300	37413	0.42	2.9E-02	BF62744.1	EST_HUMAN	602039477F2 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4177287 5'
12809	25801		1.6	2.9E-02	F08606.1	EST_HUMAN	Xf12h02.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:126675 5'
12816	26438		1.57	2.9E-02	X06322.1	NT	Yeast CN31C chromosome III RAHS DNA (right arm transcription hot-spot)
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRCBV27S1P, TCRCBV22S1A2N1T, TCRCBV9S1A1T, TCRCBV7S1A1N2T, TCRCBV6S1A1T, TCRCBV13S3, TCRCBV67P, TCRCBV7S3A2T, TCRCBV13S2A1T, TCRCBV6S2A2P, TCRCBV7S2A1N4T, TCRCBV13S9/13S>
1485	14518	27491	1.07	2.7E-02	U60059.1	NT	Arbidolipiditaliana DNA chromosome 4, contig fragment No. 6
3445	16462	29411	1.88	2.7E-02	AL161494.2	NT	Arbidolipiditaliana DNA chromosome 4, contig fragment No. 6
4230	17259	30143	2.01	2.7E-02	N47258.1	EST_HUMAN	Y68H121T Soares_multiple_sclerosis_2NDRMSP Homo sapiens cDNA clone IMAGE:280487 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	17269	30144	2.01	2.7E-02	N47288.1	EST_HUMAN	y68h12.r1 Soares, multiple sclerosis, 2NHNSP Homo sapiens cDNA clone IMAGE:280487 5'
5319	18425	31176	0.92	2.7E-02	BF245072.1	EST_HUMAN	601664811FT NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4083075 5'
5616	18616	31549	1.09	2.7E-02	R12246.1	EST_HUMAN	y33d09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6005	19088	32288	0.88	2.7E-02	X61670.1	NT	T.aestivum pT120 mRNA for wheat type V lichen
6087	19187	32379	0.81	2.7E-02	AB004788.1	NT	Oryza sativa mRNA for ascorbate oxidase, partial cds
6764	19808	32780	1.03	2.7E-02	X97880.1	NT	A.babingtonii pglA gene
7269	20004	33304	1.93	2.7E-02	AA93571.1	EST_HUMAN	y96h03.s1 Soares, total, fetus Nb21F9, 9w Homo sapiens cDNA clone IMAGE:1624931 3'
8140	21077		0.83	2.7E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00248 protein, partial cds
8180	21068	34497	0.89	2.7E-02	6256542	NT	Mus musculus G21 protein (G21), mRNA
8697	21965		1.23	2.7E-02	AI377036.1	EST_HUMAN	tc25g08.x1 Soares, total, fetus Nb21F9, 9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
573	13542	26556	1.25	2.8E-02	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C082
2374	15382	28404	2.54	2.8E-02	AA490221.1	EST_HUMAN	ab0202.s1 Strategene fetal retina 037202 Homo sapiens cDNA clone IMAGE:839606 3'
2376	15384	28406	3.05	2.8E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2378	15384	28407	3.05	2.8E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2828	15984		1.52	2.8E-02	AF108908.1	NT	Mus musculus MHC class III region RD gene, partial cds; B2, C2, G9, NG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; GTA gene, partial cds; and unknown genes
3683	17028		0.91	2.8E-02	AW181945.1	EST_HUMAN	x68f09.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2652409 3'
4942	17958	30848	3.26	2.8E-02	L12032.1	NT	Chicken ovalbumin mRNA, complete cds
5104	18114	30887	1.8	2.8E-02	AE002014.1	NT	Dicrocoelium radicum R1 section 151 of 229 of the complete chromosome 1
5128	18137	31014	3.05	2.8E-02	AW241154.1	EST_HUMAN	x62b04.x1 NCI CGAP Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
5944	19030		0.6	2.8E-02	AL161563.2	NT	O15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5992	19076		0.85	2.8E-02	AL161563.2	NT	A.adiopis italiana DNA chromosome 4, contig fragment No. 63
6345	19414		6.36	2.8E-02	AI206030.1	EST_HUMAN	Arabiopsis italiana DNA chromosome 4, contig fragment No. 63
6565	19925	32890	1.88	2.8E-02	BE821748.1	EST_HUMAN	g927f11.x1 NCI CGAP K48 Homo sapiens cDNA clone IMAGE:1792317 3'
7001	20127	33441	0.82	2.8E-02	Z69064.1	NT	601493473T1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3895578 3'
7001	20127	33441	0.82	2.8E-02	Z69064.1	NT	Vaccinia virus ORF1L strain Wyeth
7001	20127	33441	0.82	2.8E-02	Z69064.1	NT	Vaccinia virus ORF1L strain Wyeth
7095	20029	33333	6.03	2.8E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngf), mRNA
7516	20481	33842	0.55	2.8E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8850	21817	35237	0.71	2.8E-02	AA860946.1	EST_HUMAN	ak2204.s1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1406719 3'
9715	22743	36184	1.27	2.8E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10072	22999	39469	0.7	2.8E-02	AF114952.1	NT	Saccharomyces deliensalis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	22999	39469	0.7	2.8E-02	AF114952.1	NT	Saccharomyces deliensalis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10768	23699	37685	4.31	2.8E-02	AF163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11717	24890	37165	2.02	2.8E-02	AA279331.1	EST_HUMAN	zsf4402.1f1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704182 5'
11889	24770	38359	1.91	2.8E-02	AF505947.1	EST_HUMAN	UJHFB-BND-af4-e-10-UJH NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
12457	25944	31313	1.66	2.8E-02	BF343827.1	EST_HUMAN	602070562FT NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4150944 5'
533	13804	26522	1.85	2.8E-02	AF793130.1	EST_HUMAN	602606.y5 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1557827 5'
533	13804	26523	1.85	2.8E-02	AF793130.1	EST_HUMAN	602606.y5 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1557827 5'
810	13968	26617	8.19	2.8E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850665 3'
870	13928	26684	6.9	2.8E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850665 3'
2773	15765	28949	2.26	2.8E-02	U12571.1	NT	Rattus norvegicus rephillin-3A mRNA, complete cds
2968	16026	28949	3.43	2.8E-02	X9697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2968	16026	28950	3.43	2.8E-02	X9697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4075	18316	30005	1.02	2.8E-02	BE701195.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4075	18316	30006	1.02	2.8E-02	BE701195.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4233	17262	30146	8.52	2.8E-02	AW592114.1	EST_HUMAN	R36808.x1 Scores_NFI_L_CBG_S1 Homo sapiens cDNA clone IMAGE:2634015 3'
5789	18991	32073	0.65	2.8E-02	AI732716.1	EST_HUMAN	263510.xd Scores ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:810354 3'
6317	18368		4.71	2.8E-02	BE670128.1	EST_HUMAN	763009.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 repetitive element 1
6334	18403		4.42	2.8E-02	BE746898.1	EST_HUMAN	601576363FT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
8470	18335	32783	0.87	2.8E-02	L28028.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7927	20870	34268	1.48	2.8E-02	BF526722.1	EST_HUMAN	602070562FT NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213408 5'
7927	20870	34269	1.48	2.8E-02	BF526722.1	EST_HUMAN	602070562FT NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213408 5'
8137	21074	34474	0.54	2.8E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA photolyase (Phr2) gene, complete cds
9171	22143	35570	0.82	2.8E-02	Q81713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9315	22280	35710	0.46	2.8E-02	AW025821.1	EST_HUMAN	hw08c10.x1 NCI_CGAP_GCB8 Homo sapiens cDNA clone IMAGE:2510370 3'
10426	23348		0.85	2.8E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10947	23967	37381	0.67	2.8E-02	AI147616.1	EST_HUMAN	qb22a08.x1 Scores_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:1696982 3'
11161	24119	37646	2.15	2.8E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11161	24119	37647	2.15	2.8E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11227	24180		3.01	2.9E-02	AF090157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (A1pha) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-2
12059	24932		1.47	2.9E-02	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds
12416	25985		3.35	2.9E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H_sapiens) (LOC59634), mRNA
12598	25751		1.47	2.9E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12686	25953		2.24	2.9E-02	U90169.1	NT	Ductalactone disaccharide putative protein kinase Mica (mika) gene, complete cds
12709	25495	31170	3.42	2.9E-02	BE973327.1	EST_HUMAN	601552305F2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3035573 3'
175	13276	26203	0.69	2.4E-02	A137692.1	EST_HUMAN	lc72d07.x1 Soares, NIH/MPU, S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1802	14834	27610	2.24	2.4E-02	H65884.1	EST_HUMAN	375f11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:21149 5'
2060	16884	28068	1.73	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2060	16884	28098	1.73	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4396	17424	30308	1.43	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4549	17572	30461	1.43	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4549	17572	30462	1.43	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5227	18235		0.8	2.4E-02	AL161955.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6340	19409	32650	0.97	2.4E-02	W86580.1	EST_HUMAN	zh89h04.s1 Soares, fetal liver, spleen, 1NfLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
6496	19560	32811	0.95	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
6496	19560	32812	0.95	2.4E-02	M31650.1	NT	Chicken myristoylated alanine-rich C kinase substrate (MARCKS) mRNA, complete cds
7431	20398	33750	1.38	2.4E-02	Z20573.1	EST_HUMAN	HSAACAKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7448	20414	33787	1.05	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7448	20414	33788	1.05	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8159	21097	34495	0.52	2.4E-02	P98092	SWISSPROT	HEMOCTIN PRECURSOR (HUMORAL LECTIN)
8159	21097	34496	0.52	2.4E-02	P98092	SWISSPROT	HEMOCTIN PRECURSOR (HUMORAL LECTIN)
8222	21101		0.57	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-018-h08 ST0186 Homo sapiens cDNA
8276	21244		0.58	2.4E-02	U16180.1	NT	Homo reticulospinos 3' long terminal repeat
8784	21751		0.93	2.4E-02	H78376.1	EST_HUMAN	yt12d05.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:233678 3' similar to contains Alu repetitive element/contains A3R repetitive element
8876	21843	35265	11.43	2.4E-02	N69442.1	EST_HUMAN	z83g11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:294589 3' similar to gk102909J2R7SR7K Rat (RNA) contains A3R b1 A3R repetitive element;
9398	22503	35731	0.49	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 79) of the complete genome
9393	22328	35757	0.81	2.4E-02	AA625660.1	EST_HUMAN	z091cd6.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN) contains Alu repetitive element/contains element XTR XTR repetitive element;

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10050	22877	36443	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurase (mbs) gene, complete cds
10050	22977	36444	0.46	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurase (mbs) gene, complete cds
10165	23090	36659	2.57	2.4E-02	AF692854.1	EST_HUMAN	AV692854 GKX Homo sapiens cDNA clone GKX3CQ3 5'
10340	23284	36743	2.76	2.4E-02	AA493864.1	EST_HUMAN	rh07612.x1 NCL CGAP_T101 Homo sapiens cDNA clone IMAGE:943563 similar to contains Alu repetitive element; contains element P1R3 repetitive element;
10976	23898		1.35	2.4E-02	BE387111.1	EST_HUMAN	801274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615802 5'
11800	24781	36368	1.81	2.4E-02	AF109005.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, GTA, NG23, Mds1 homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11800	24781	36369	1.81	2.4E-02	AF109005.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, GTA, NG23, Mds1 homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
12383	25152	31855	1.7	2.4E-02	6627809	NT	Bacteriophage BIL37, complete genome
12418	25188	31823	3.48	2.4E-02	BE928693.1	EST_HUMAN	Mus musculus DnB1 homolog 1 (E cd) (DnB1), mRNA
12474	25222	31791	1.59	2.4E-02	U78167.1	NT	MR0-F10175-310800-202-a06 F10175 Homo sapiens cDNA
12474	25222	31833	1.59	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF) mRNA, complete cds
12643	25327		7.88	2.4E-02	AB006599.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF) mRNA, complete cds
1888	14913		5.26	2.3E-02	W05340.1	EST_HUMAN	Ceanothus thibetensis cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF) mRNA, complete cds
1904	14928		8.44	2.3E-02	U594165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2358	15366	26368	3.16	2.3E-02	Z74293.1	NT	S cerevisiae chromosome IV reading frame ORF YOL245c
3694	16737	29650	4.2	2.3E-02	Z20377.1	EST_HUMAN	HSAAACACADH P, Human fetal Brain White tissue Homo sapiens cDNA
4176	17207	30063	0.8	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4176	17207	30094	0.8	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4450	17476	30364	1.52	2.3E-02	AW599107.1	EST_HUMAN	GM4-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4477	17503	30388	0.78	2.3E-02	BE936225.1	EST_HUMAN	GM4-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4477	17503	30389	0.78	2.3E-02	BE936225.1	EST_HUMAN	GM4-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4478	18317	30390	1.23	2.3E-02	AW593953.1	EST_HUMAN	xs25408.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4478	18317	30391	1.23	2.3E-02	AW593953.1	EST_HUMAN	xs25408.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4626	17846	30534	2.80	2.3E-02	BF028487.1	EST_HUMAN	601672270F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'
4626	17846	30535	2.80	2.3E-02	BF028487.1	EST_HUMAN	601672270F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955388 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5203	18212	31086	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5203	18212	31087	1.19	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5449	18851	31463	3.35	2.3E-02	U86503.1	NT	Caulobacter crescentus topoisomerase IV PaeE subunit (paeE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6363	19432	32675	0.95	2.3E-02	BF108464.1	EST_HUMAN	60182292R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042828 3'
6774	19829	33112	4.22	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7172	18403	31201	0.84	2.3E-02	BE141475.1	EST_HUMAN	MFG-HT0080-011039-002-009 HT0080 Homo sapiens cDNA
7685	20553	34016	0.52	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8208	21178	34688	5.65	2.3E-02	U63910.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8815	21782	35207	0.87	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9044	22010	35431	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
9044	22010	35431	0.74	2.3E-02	AF685380.1	EST_HUMAN	wa78h10.x1 Soares, NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9493	22457	35857	0.89	2.3E-02	AF685380.1	EST_HUMAN	wa78h10.x1 Soares, NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2302147 3'
10218	23149	36532	0.77	2.3E-02	P41998	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10360	23312	36791	1.47	2.3E-02	AE000166.1	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10360	23312	36792	1.47	2.3E-02	AE000166.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11135	24095	37624	1.71	2.3E-02	P08640	SWISSPROT	GLUCANAMYLASE S1S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12338	26738	31755	7.99	2.3E-02	BE278331.1	EST_HUMAN	60117858R1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3548567 5'
12742	25392	31755	1.5	2.3E-02	BF528462.1	EST_HUMAN	60204352P1 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12742	25392	31756	1.5	2.3E-02	BF528462.1	EST_HUMAN	60204352P1 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12843	25453	31724	3.2	2.3E-02	U36394.1	NT	Streptomyces sp. alpha-1,3/4-lucosidase precursor gene, complete cds
12897	25983		2.48	2.3E-02	U11077.1	NT	Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
13100	25633		1.82	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
739	13800	28739	4.3	2.2E-02	AF018267.1	NT	Columbia IVa nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1762	14791		1.99	2.2E-02	4557448	NT	Homo sapiens chromodomain release DNA binding protein 2 (ChD2) mRNA
2031	16050	28055	1.68	2.2E-02	Z82001.1	NT	S.pneumoniae popA gene and open reading frames
3448	16495		2.15	2.2E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NC1_CGAP_Gast1 Homo sapiens cDNA clone IMAGE:1084782 3'
3600	16703		3.48	2.2E-02	AF083094.1	NT	Infectious burial disease virus segment B strain IL4 VP1 gene, complete cds
3887	18006	29814	1.26	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-70100-004-103 BT0340 Homo sapiens cDNA
3941	16891	29896	0.74	2.2E-02	Z74263.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5105	18115	30688	1.17	2.2E-02	Z73597.1	NT	Saccharibiosidase chromosom XVI reading frame ORF YPL241c
7458	20424	33780	3.37	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GK3 Homo sapiens cDNA clone GK6AND03.3
8714	21882	35100	2.28	2.2E-02	AL161616.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8714	21882	35110	2.28	2.2E-02	AL161616.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9161	22127	35555	0.77	2.2E-02	X79468.1	NT	P. vulgaris alpha tub 2 mRNA
10045	22972	36438	2.26	2.2E-02	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10045	22972	36438	2.26	2.2E-02	AB026888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10565	23487		0.91	2.2E-02	6978140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
11540	24481	38033	1.8	2.2E-02	BE797801.1	EST_HUMAN	601684309F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938571.5'
12602	26304		6.72	2.2E-02	AA603553.1	EST_HUMAN	nc47107.s1 NCJ_CGAP_C03 Homo sapiens cDNA clone IMAGE:900541.3' similar to contains Alu repetitive element
419	13492		5.37	2.1E-02	AV781502.1	EST_HUMAN	AV781502.NDS Homo sapiens cDNA clone MDSADG01.5'
449	13522		8.77	2.1E-02	AF029726.1	NT	Dicystallum discobium histidine kinase C (dhkC) mRNA, complete cds
1268	14303	27264	8.3	2.1E-02	U72073.1	NT	Bacillus subtilis coxLM cluster, OatK (coxK), OatC (coxL), and spore coat protein OatM (coxM) genes, complete cds
1367	14420	27386	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1367	14420	27386	0.99	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1767	14826	27811	1.26	2.1E-02	P02436	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1767	14826	27812	1.26	2.1E-02	P02436	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1767	14826	27813	1.26	2.1E-02	P02436	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1980	15001	28004	1.01	2.1E-02	AF180859.1	NT	Tegula aureocincta major arceosomal protein precursor (TMAP) mRNA, complete cds
2030	15069	28089	0.9	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2030	15069	28090	0.9	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2591	15592	28609	1.04	2.1E-02	AA225095.1	EST_HUMAN	nc21g03.r1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008820
2827	18339	29784	4.45	2.1E-02	N26266.1	EST_HUMAN	yx43107.r1 Scores melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:204541.5'
3164	15069	28689	1.02	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3164	15069	28690	1.02	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3587	16842	29491	0.98	2.1E-02	AA461271.1	EST_HUMAN	Z63509.r1 Scores, total fetus, N26HF8, 9w Homo sapiens cDNA clone IMAGE:786121.5'
4028	17066	29657	0.97	2.1E-02	BF203471.1	EST_HUMAN	601689800F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098407.5'
4157	17188	30076	0.94	2.1E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YOL245c
4339	17366	30246	1.4	2.1E-02	BF343955.1	EST_HUMAN	G02015305F1 NCJ_CGAP_Bmed4 Homo sapiens cDNA clone IMAGE:4161161.5'
4473	17499	30384	2.15	2.1E-02	U44614.1	NT	Borrelia burgdorferi plasmid cp32-2, espC and erpD genes, complete cds, and unknown genes

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4483	17608	30397	1.13	2.1E-02	AI768127.1	EST_HUMAN	wg91d11.x1 Soares NSF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4739	17759	30654	5.69	2.1E-02	Y069501.1	NT	A thellena mitochondrial genome, part A
4761	17781	30977	1.5	2.1E-02	AA695737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
5255	18264	31133	1.07	2.1E-02	BF026405.1	EST_HUMAN	GM147141F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3964410 5'
5723	18817	31988	0.75	2.1E-02	AV379529.1	EST_HUMAN	CM4-H70244-11198-040-H05 HT0244 Homo sapiens cDNA
7268	20003	33303	0.65	2.1E-02	BF088199.1	EST_HUMAN	CV3-GN0058-12950-329-a12 GN0058 Homo sapiens cDNA
8884	21831	35254	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9851	22797	36250	0.51	2.1E-02	AA984288.1	EST_HUMAN	em83407.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9889	22916	36381	2.63	2.1E-02	AJ243213.1	NT	Alu repetitive element contains element MER11 repetitive element;
9989	22916	36382	2.63	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10343	23267	36746	1.13	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5 UrmD MucA homolog genes, complete cds; and unknown genes
10421	23343	36929	0.88	2.1E-02	AA984288.1	EST_HUMAN	em83407.s1 Striatogene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
12584	18345		8.95	2.1E-02	Y10213.1	NT	Alu repetitive element contains element MER11 repetitive element;
12624	25735	31617	1.4	2.1E-02	L34170.1	NT	Homo sapiens putative psithbA pseudogene for hair keratin, exons 2 to 7
13003	23557	31693	3.5	2.1E-02	AF163913.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
19	13139	26037	1.39	2.0E-02	BF002932.1	EST_HUMAN	Acropitulum brasiliense major outer membrane protein OmpA precursor (omA) gene, complete cds
20	13140	26038	10.78	2.0E-02	AW695665.1	EST_HUMAN	MER1 repetitive element;
259	13356	26280	3.29	2.0E-02	6753635	NT	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
295	13389	26317	2.85	2.0E-02	A4455535.1	EST_HUMAN	Mus musculus DnaE homolog 1 (E. coli) (DnaB1), mRNA
789	13858	26805	1.27	2.0E-02	6753635	NT	ae19b10.r1 Soares NhrHPu.S1 Homo sapiens cDNA clone IMAGE:813307 5'
1089	14133	27085	1.03	2.0E-02	AL096805.1	NT	Mus musculus DnaE homolog 1 (E. coli) (DnaB1), mRNA
1204	14243	27201	0.79	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 11(p38.33) of Homo sapiens
1204	14243	27202	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1590	14915	27609	2.08	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
1590	14915	27610	2.08	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
2810	15802		4.57	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3095	13139	26037	1.61	2.0E-02	BF002932.1	EST_HUMAN	7651c08.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:3309988 3' similar to contains MER1.13 MER1 repetitive element;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3159	19216		1.83	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3241	19296		1.8	2.0E-02	AF095988.1	NT	Arabidopsis thaliana CSH2 zinc finger protein FZF mRNA, complete cds
4032	17070	29971	1.4	2.0E-02	M18095.1	NT	P vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5153	18163		0.7	2.0E-02	A1271695.1	EST_HUMAN	g83c33.x1 NCL_CGAP_K182 Homo sapiens cDNA clone IMAGE:1866076 3'
5175	18184	31081	0.94	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5718	19812	31991	0.69	2.0E-02	U94778.1	NT	Ctenorhabdites elegans sma-2 mRNA, complete cds
6000	19063	32282	0.73	2.0E-02	L36521.2	NT	Dityrocellum discoidium class VII unconventional myosin (myo) gene, complete cds
7769	20761	34126	1.09	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
7799	20751	34127	1.09	2.0E-02	AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
10236	23161		1.69	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10726	23648	37141	1.54	2.0E-02	AI840342.1	EST_HUMAN	wat17602.x1 NCL_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2298315 3'
11005	23971	37495	1.64	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11699	24684	39241	2.26	2.0E-02	D88184.1	EST_HUMAN	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
12148	18361	31298	3.03	2.0E-02	AA456635.1	EST_HUMAN	aa16b10.r1 Scorea_NHNPuL_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12821	15802		1.99	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13076	25608		3.4	2.0E-02	T80037.1	EST_HUMAN	yt04c09.r1 Scorea Infant brain T1B1B Homo sapiens cDNA clone IMAGE:24675 5'
694	13769	26686	2.55	1.9E-02	AA572784.1	EST_HUMAN	nt19a07.s1 NCL_CGAP_Fr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1(L1 L1 repetitive element)
1619	14652	27628	1.03	1.9E-02	F18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2055	15074	28093	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2055	15074	28094	3.04	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2514	15517	28540	1.07	1.6E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2916	15974	28897	8.5	1.9E-02	AA713859.1	EST_HUMAN	mw0405.x1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1283337 3'
2984	10022	28947	1.46	1.9E-02	AV648695.1	EST_HUMAN	AV048698 GLC Homo sapiens cDNA clone GLCBLH07 3'
3273	18327		0.72	1.9E-02	AB033811.1	NT	Utricularia glaucoides mitochondrial gene for cytochrome b, complete cds
3625	16668		1.38	1.9E-02	N62250.1	EST_HUMAN	yz28b02.x1 Scorea_multiple_colicaria_2NBMHSP Homo sapiens cDNA clone IMAGE:284331 3'
3718	16761		8.23	1.9E-02	BE738088.1	EST_HUMAN	60157282F21 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839504 5'
3727	16769	28681	0.69	1.9E-02	AJ301183.1	EST_HUMAN	mp04c07.x1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains A1u repetitive element
4077	17172	30008	1.69	1.9E-02	AF11940.1	NT	Myocytoma imitans VlnA1 precursor (VlnA1) and VlnA2 precursor (VlnA2) genes, partial cds
4222	17251	30137	1.82	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4222	17251	30138	1.62	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)



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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	17594	30489	3.65	1.9E-02	AI452988.1	EST_HUMAN	ip46d0.x1 Soares NSF_Fg_3W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains A1u repetitive element;
5048	15517	28540	2.68	1.9E-02	AL181500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5389	18492	31389	0.91	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5544	18541	31581	1.25	1.9E-02	L47572.1	NT	Melanogaster galliparus paraoxonase-2 (PON2) mRNA, complete cds
5885	18974		1.24	1.9E-02	AB019507.1	NT	Drosophila karekai gene for glycerol-3-phosphate dehydrogenase, complete cds
7309	20279	33617	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7309	20279	33618	1.34	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8917	21883		1.2	1.9E-02	AL162764.2	NT	Nelusetra meningitis serogroup A strain Z2491 complete genome, segment 3/7
9886	22639	36096	0.78	1.9E-02	BF316129.1	EST_HUMAN	601884130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
10071	22968	38467	0.43	1.9E-02	L10114.1	NT	Nicotian tabacum type II phytochrome (phyE) gene, complete cds
10405	23327	36811	1.09	1.9E-02	BF69832.1	EST_HUMAN	601852395F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4076253 5'
10510	23432	36829	0.45	1.9E-02	N39160.1	EST_HUMAN	xy46f08.s1 Soares_multiple sclerosis_2NHMSP Homo sapiens cDNA clone IMAGE:276639 3'
10514	23538	37034	0.5	1.9E-02	D84601.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 253000-284794
12372	25742	31620	3.14	1.9E-02	AF101085.1	NT	Hirudo medicinalis intermediate filament gliadin mRNA, complete cds
13026	25574	31696	1.4	1.9E-02	X68271.1	NT	H. sapiens MUC18 gene exon 16
346	13435	26367	1.35	1.9E-02	AW771104.1	EST_HUMAN	h562d06.x1 NCI_LGAP_Cor17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
686	13749	26676	1.39	1.9E-02	BF308122.1	EST_HUMAN	601894328F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1164	14205	27169	1.87	1.9E-02	X17864.1	NT	H.fascioli mRNA for myelin basic protein (MBP)
2887	15983	28701	1.78	1.9E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3224	16270		1.06	1.9E-02	AB05528.1	EST_HUMAN	la52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090298 3'
3302	16842	29683	1.01	1.9E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280303-009-g04 OT0011 Homo sapiens cDNA
3802	16942	29854	1.01	1.9E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280303-009-g04 OT0011 Homo sapiens cDNA
4113	17147		1.04	1.9E-02	AA891446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4461	17487	30374	1.49	1.9E-02	AW83693.1	EST_HUMAN	QV4-DT0021-301298-071-411 DT0021 Homo sapiens cDNA
4892	18007	30895	0.98	1.9E-02	O60810	SWISSPROT	HYPOPHYSICAL PROTEIN D1845024.2
5287	18263	31154	0.68	1.9E-02	AF255711.1	NT	Oryza sativa putative histone deacetylase HD2 mRNA, complete cds
6524	18967	32845	0.59	1.9E-02	AE002518.1	NT	Nelusetra meningitis serogroup B strain MC58 section 180 of 200 of the complete genome
6524	18967	32846	0.59	1.9E-02	AE002518.1	NT	Nelusetra meningitis serogroup B strain MC58 section 180 of 200 of the complete genome
6882	20205	33534	4.59	1.9E-02	P14310	SWISSPROT	HYPOPHYSICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7889	20657	34021	0.65	1.9E-02	BF125690.1	EST_HUMAN	601763288F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7722	20657	34021	0.58	1.9E-02	BF125690.1	EST_HUMAN	601763288F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
8467	21436	34854	0.77	1.9E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8811	21778	35203	0.78	1.8E-02	AW095327.1	EST_HUMAN	QV2-NN1073-220400-159-H09 NN1073 Homo sapiens cDNA
8857	21924	35247	0.75	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9849	22785	36238	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9849	22785	36238	0.5	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
10000	22927		2.03	1.8E-02	AA897543.1	EST_HUMAN	gb2068.s1 Soares_testis_HUNT Homo sapiens cDNA clone IMAGE:194921 3' similar to gbL11672 ZINC FINGER PROTEIN 94 (HUMAN);
10423	23345	36930	1.65	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866683 5'
10586	23508	37000	1.2	1.8E-02	X98933.1	NT	L. signatus mRNA for myomodulin neuropeptide precursor
11765	23920	37436	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11765	23920	37436	1.7	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11835	24816	38413	2.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1169001-1485000 nt, position (87)
11848	24827	38422	3.16	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
13105	25626	31680	1.35	1.8E-02	R40255.1	EST_HUMAN	y80d01.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28685 3' similar to gb-M62783
13105	25626	31681	1.35	1.8E-02	R40255.1	EST_HUMAN	ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN);
507	13962	26516	0.8	1.7E-02	BE394869.1	EST_HUMAN	ALPHA-N-ACETYL GALACTOSAMINIDASE PRECURSOR (HUMAN);
1806	14834	27823	2.15	1.7E-02	AW673183.1	EST_HUMAN	601310023F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1806	14834		2.16	1.7E-02	AW573183.1	EST_HUMAN	H34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element ;
1887	14912	27824	4.23	1.7E-02	AL163204.2	NT	H34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element ;
2121	15138		11.19	1.7E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21C004
2301	15313	28333	1.03	1.7E-02	S74185.1	NT	Oryctolagus cuniculus mRNA for riboguaninidase, complete cds
2848	16846		1.18	1.7E-02	7657495	NT	[Microsatellite INRA41] (Ovis aries)-sheep, Genomic, 381 nt, segment 1 of 2
3011	16059	28690	0.96	1.7E-02	AI147615.1	EST_HUMAN	Homo sapiens putative Rab5 GDI/GTP exchange factor homolog (RABEX5), mRNA
3523	16569		5.52	1.7E-02	AW827988.1	EST_HUMAN	gb22a08.x1 Soares_Progmat, uterus, NBHPU Homo sapiens cDNA clone IMAGE:166982 3'
4198	17229		0.96	1.7E-02	AA669618.1	EST_HUMAN	hm45a04.x1 NCL CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element ;
4228	17257		2.04	1.7E-02	R02506.1	EST_HUMAN	act904.61 Stragene ovary (H37217) Homo sapiens cDNA clone IMAGE:855927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element ;
4482	17507	30396	0.7	1.7E-02	AI305278.1	EST_HUMAN	ye85f08.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:124647 5'
							gm08a07.x1 NCL CGAP_Lus Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb-X52359 ZINC FINGER PROTEIN 30 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4557	17590	30471	1.52	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 repetitive element;
4744	17764	30658	1.54	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish ( <i>Lophius americanus</i> ) somatostatin II
4851	17868		7.05	1.7E-02	AI015078.1	EST_HUMAN	ovf1a02.ct1 Soares_bat1a_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
5105	18116	30889	0.74	1.7E-02	U681289	NT	Rattus norvegicus N-rangine diase convertase 1 (Ndr1), mRNA
5229	18237		0.91	1.7E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AM1.1 and CBR1 on chromosome 21q22; segment 1/3
6248	18321	32551	1.63	1.7E-02	AJ760247.1	EST_HUMAN	wg3503b.x1 Soares_NSIF_F8_gW_OT_PA_2_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6618	18676		0.64	1.7E-02	AJ760247.1	NT	T. niivium (ATCC34821) simA gene for cyclopropane synthetase
6731	18787	33065	1.37	1.7E-02	AI038280.1	EST_HUMAN	oy65f03.x1 Soares_fetal_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
7251	19968	33284	1.31	1.7E-02	AF160930.1	NT	Maceca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7411	20378	33729	1.95	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7681	20543	33902	0.85	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7581	20543	33903	0.85	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
8016	20954		1.98	1.7E-02	AJ010107.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase, exon 1-50
8781	21114	34614	0.91	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF-1 protein gene, complete cds
10057	22884	39463	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZP4340314.1_1_434 (synonym: hba3) Homo sapiens cDNA clone DKFZP4340314 5'
12084	24958	38551	1.59	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MASE55), mRNA
12810	25910	31424	3.15	1.7E-02	AW603482.1	EST_HUMAN	CM4-NN1535-0-040-030-065 NN1030 Homo sapiens cDNA
13059	25995	31687	1.31	1.7E-02	AA846926.1	EST_HUMAN	oe0804.s1 NCL_GGAP_OV2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSRT1 repetitive element;
512	13583		2.22	1.6E-02	AL021928.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1685	14697	27873	0.91	1.6E-02	Y18888.1	NT	Tropomyosin mallophilum flab2, flab23 and flab24 genes for flagellin subunit proteins and CAP protein homologue
2571	16573	28593	0.95	1.6E-02	AJ006346.1	NT	Homo sapiens KVLQ17 gene
2852	16648	28671	1.46	1.6E-02	AA484872.1	EST_HUMAN	ne81008.s1 NCL_GGAP_Ewt Homo sapiens cDNA clone IMAGE:910667
2704	15700		1.37	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIA0634 protein, partial cds
3537	16553	28506	4.46	1.6E-02	AW650652.1	EST_HUMAN	IL3-CT0219-160200-063-007 CT0219 Homo sapiens cDNA
4204	17235		2.14	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NC27, NC28, RPS28, NADH oxidoreductase, NC29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4328	17357	30245	0.96	1.6E-02	AW1875407.1	EST_HUMAN	QV52-PT0012-140100-030-007 PT0012 Homo sapiens cDNA
5172	18181		0.76	1.6E-02	N80156.1	EST_HUMAN	zef6507.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone IMAGE:287444 3'
5325	18431	31183	0.49	1.6E-02	AI281385.1	EST_HUMAN	qu42603.s1 NCL_GGAP_Lym5 Homo sapiens cDNA clone IMAGE:1987417 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5705	18800	31977	1.33	1.9E-02	6871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6789	18853	33138	2.07	1.9E-02	AB015281.1	NT	Candida albicans CaCGR3 gene, complete cds
7117	20051	33354	0.93	1.9E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7117	20051	33355	0.93	1.9E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7878	20917	34308	1.08	1.9E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8458	21427	34844	0.72	1.9E-02	ALJ27662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8519	21487		1.5	1.9E-02	X05151.1	NT	Human spcC-II gene for preprocalciprotein C-II
10400	23322		1.98	1.9E-02	AF078764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10785	23706	37206	1.2	1.9E-02	AA572818.1	EST_HUMAN	AF1903 st NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RAB1T
10785	23706	37207	1.2	1.9E-02	AA572818.1	EST_HUMAN	AF1903 st NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RAB1T
11255	25705	37730	1.83	1.9E-02	Z94828.1	NT	P29284 TELOKIN, [1];
11547	24488	38042	1.7	1.9E-02	AL161508.2	NT	G.allius microsatellite DNA (LE10260 (=116111))
11547	24488	38043	1.7	1.9E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11839	24722	38307	1.66	1.9E-02	AL373858.1	EST_HUMAN	q28e10.XT Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12347	18334	31172	1.39	1.9E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12347	18334	31173	1.39	1.9E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
1752	13813		20.75	1.9E-02	8623734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2162	15768	28184	4.44	1.9E-02	N39521.1	EST_HUMAN	Y27607.st Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:243925 3'
2185	15200	28220	1.82	1.9E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3074	16131	29043	2.54	1.9E-02	ALJ06218.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3074	16131	29044	2.54	1.9E-02	ALJ06218.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3737	16779	29692	1.08	1.9E-02	BF092842.1	EST_HUMAN	MR4-TN0115-060906-201-4512 TN0115 Homo sapiens cDNA
6426	19493	32745	1.33	1.9E-02	Q09711	SWISSPROT	HYPOPHOSPHATE CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7541	20304		1.59	1.9E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7831	20591	33954	1.38	1.9E-02	AL1618713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8208	21176	34583	1.5	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8213	21182	34593	4.62	1.9E-02	11417739	NT	Homo sapiens wily-1 RNA synthetase 2 (VAR52), mRNA
9182	22148	35575	0.93	1.9E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Bri87 Homo sapiens cDNA clone IMAGE:4154604 5'
9823	22672		0.58	1.9E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9829	22812	36286	1.58	1.9E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10170	23095	36674	0.95	1.9E-02	R32667.1	EST_HUMAN	Y194B10.1T Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:133531 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10170	23095	36576	0.95	1.8E-02	R32667.1	EST_HUMAN	Y64b10.r1 Soares placenta N26HP Homo sapiens cDNA clone IMAGE:133631 5'
11503	24445	37967	2.75	1.9E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
11537	24478	38028	2.82	1.9E-02	AL111288.1	NT	Bakvyle chinese strain T4 cDNA library under conditions of nitrogen deprivation
12664	25783		2.04	1.9E-02	AW780334.1	EST_HUMAN	RC4-CH0049-140100-011-c11 CN0049 Homo sapiens cDNA
13078	25610		1.3	1.8E-02	AF183127.1	EST_HUMAN	w06h003.x1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2389483 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element ;
417	13490		1.99	1.4E-02	AE002230.2	EST_HUMAN	Chlamydia pneumoniae AR39, section 56 of B4 of the complete genome
1120	14164	27115	5.44	1.4E-02	7705890	NT	Homo sapiens NESH protein (LOC51225), mRNA
1261	14286		1.74	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1301	14337		3.4	1.4E-02	U07778.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1520	14552		1.03	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBA-HP117 5'
3226	16261	26204	2.04	1.4E-02	AF160689.2	NT	Bifidobacterium longum Ncr/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglI) genes, complete cds; and N-acetylglucosaminylxylase repressor protein (nagC/xylR) gene, partial cds
3409	16458	29380	0.98	1.4E-02	AW074212.1	EST_HUMAN	x5b0d06.x1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2575793 3'
3468	16543	29497	6.29	1.4E-02	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3468	16543	29498	6.29	1.4E-02	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3589	16712	29627	6.69	1.4E-02	6968918	NT	Mus musculus histocompatibility 2, complement component factor B (H2.B), mRNA
4516	17541	30427	6.1	1.4E-02	AW962888.1	EST_HUMAN	EST1374761 MAGE resequences, MAGEG Homo sapiens cDNA
4516	17541	30428	6.1	1.4E-02	AW962888.1	EST_HUMAN	EST1374761 MAGE resequences, MAGEG Homo sapiens cDNA
4911	17928	30818	8.08	1.4E-02	BE73142.1	EST_HUMAN	601567403FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4911	17928	30819	8.08	1.4E-02	BE73142.1	EST_HUMAN	601567403FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5130	18139	31017	1.01	1.4E-02	AW946453.1	EST_HUMAN	CNO-FN0041-120500-370-R09 FN0041 Homo sapiens cDNA
5888	25992		0.95	1.4E-02	X91338.1	NT	H.sapiens LaS5-B pseudogene 3
6555	19615	32680	4.9	1.4E-02	AA559030.1	EST_HUMAN	n11t04.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1025980 3' similar to contains Alu repetitive element;
6555	19615	32681	4.9	1.4E-02	AA559030.1	EST_HUMAN	n11t04.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1025980 3' similar to contains Alu repetitive element;
8478	21447		1.61	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 89/162
9249	22215	35643	0.77	1.4E-02	M81702.1	NT	Candida badoili methylal oxidase (AOX1) gene, complete cds
9510	22473	35617	0.9	1.4E-02	AL272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-3
9755	22699	35133	2.15	1.4E-02	BE544581.1	EST_HUMAN	601078293FT NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
10923	23643		0.66	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12554	25080	38172	2.14	1.4E-02	X60458.1	NT	Human IPNAR gene for Interferon alpha/beta receptor
12616	25312		1.47	1.4E-02	AF324955.1	NT	Arabidopsis thaliana P21J9.2 mRNA, complete cds
12882	26474		1.68	1.4E-02	11426993	NT	Human spleen spm associated antigen 7 (SPAG7), mRNA
1972	14893	27694	2.05	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3227	16282	28205	2.31	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3277	16282	28206	2.31	1.3E-02	BF697081.1	EST_HUMAN	602128475F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3993	17033		1.38	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
4984	17679	30869	1.06	1.3E-02	U66061.1	NT	Human germ-line T-cell receptor beta chain TORBV17S1A1T, TORBV2S1, TORBV10S1P, TORBV28S1P, TORBV19S1P, TORBV16S1, TORBV11S1A1T, HVB relic, TORBV28S1P, TORBV34S1, TORBV14S1, TORBV3S1, TORBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBV1S1, TORBV1S2>
5317	18423	31225	1.79	1.3E-02	AL049668.2	NT	Mus musculus chromosome X contig8: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmoq28orf
5317	18423	31226	1.79	1.3E-02	AL049668.2	NT	Mus musculus chromosome X contig8: X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmoq28orf
6288	19360	32597	1.21	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p47 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6322	19363	32634	0.7	1.3E-02	M82662.1	NT	G.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7164	18366	31228	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7154	18366	31229	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7826	20777	34155	4.86	1.3E-02	A031593.1	EST_HUMAN	ov05g05.x1 Soares_papillary_tumor_Nb-HPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8828	21780	35216	1.48	1.3E-02	AF156951.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10907	23489	35981	2.18	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10941	23563	37059	0.63	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10989	23508	37421	0.44	1.3E-02	AA107741.1	EST_HUMAN	zh24607.s1 Soares_pituitary_gland_N3-HPG Homo sapiens cDNA clone IMAGE:412680 3'
11336	24286	37609	3.74	1.3E-02	AW269593.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11336	24286	37610	3.74	1.3E-02	AW269593.1	EST_HUMAN	xx34e03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12622	25923		1.4	1.3E-02	Z89117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2594431 to 2812870
12714	25368		2.51	1.3E-02	9633099	NT	Human herpesvirus 6B, complete genome
12896	25718		16.88	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
214	13314		0.67	1.2E-02	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
355	13443	28368	4.67	1.2E-02	AA058299.1	EST_HUMAN	z65g01.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
453	13526	26456	1.81	1.2E-02	P38888	SWISSPROT	HYPOPHOSPHATASE 17.3 KD PROTEIN IN PUR5 3 REGION
740	13801	26740	3.32	1.2E-02	AI183522.1	EST_HUMAN	cd88a12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1.11 L1 repetitive element;
2187	15202	28222	1.82	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2190	15205	28225	1.44	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2449	15454	28476	1.65	1.2E-02	AW172350.1	EST_HUMAN	X37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2505	15508	28534	0.99	1.2E-02	BE59310.1	EST_HUMAN	601089406.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2506	15509	28535	0.99	1.2E-02	BE59310.1	EST_HUMAN	601089406.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2843	15454	28476	1.31	1.2E-02	AW172350.1	EST_HUMAN	X37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2843	15454	28476	1.31	1.2E-02	AW172350.1	EST_HUMAN	z65g01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:3454608 5'
3118	16175	28273	2.62	1.2E-02	AA075418.1	EST_HUMAN	W11D08.e1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:345020 5'
3301	16354	28273	2.62	1.2E-02	R62805.1	EST_HUMAN	W11D08.e1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:345020 5'
4817	17934	30828	8.36	1.2E-02	6754387	NT	Mus musculus interferon regulatory factor 5 (irf5), mRNA
4953	17988	30858	1.66	1.2E-02	U91928.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	18090		1.54	1.2E-02	AB019789.1	NT	Onchop pyrophosphate CplBqT mRNA, partial cds
5121	18131	31008	2.09	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5259	18287	31135	1.01	1.2E-02	AF165576.1	NT	Mus musculus POZ/zinc finger transcription factor ODA-8 mRNA, complete cds
5769	18361		0.5	1.2E-02	AA759018.1	EST_HUMAN	cd8910.x1 Soares_testis_NHT Homo sapiens cDNA clone 1344235 3'
5846	18336	32120	1.72	1.2E-02	D78569.1	NT	Rana rugosa mRNA for cathectin, complete cds
6238	18311	32543	0.88	1.2E-02	AF045555.1	NT	Homo sapiens wbcrt (WBSCR1) and wbcrt2 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7203	20227	33560	5.57	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7510	20475	33839	1.07	1.2E-02	H02197.1	EST_HUMAN	y34h12.e1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150995 3'
7534	20487	33858	8.5	1.2E-02	AV132093.1	EST_HUMAN	X37c09.x1 HTF Homo sapiens cDNA clone HTFBUC09 5'
7805	20755	34131	0.54	1.2E-02	BF216550.1	EST_HUMAN	601852949.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4059253 5'
8330	21299	34715	2.29	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8534	21502	34819	1.31	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8534	21502	34920	1.31	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
9242	22208		1.1	1.2E-02	T76987.1	EST_HUMAN	XBT2008.st Soares fetal liver spleen INFLUS Homo sapiens cDNA clone IMAGE:113774 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9997	22924	36389	2.63	1.1E-02	AB031013.1	NT	Nonviral-like virus genogroup 2 gene for capsid protein, complete cds
10330	22957	36425	1.29	1.1E-02	AJ246003.1	NT	Homo sapiens Speet gene for speatin protein
12310	25118	31841	2.74	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU1) (HPER)
12998	25482		5.61	1.2E-02	C18118.1	EST_HUMAN	C18119 Human placenta cDNA (Tf- $\beta$ -liver) Homo sapiens cDNA clone GEN-557G06.5'
12718	14309	27270	1.74	1.1E-02	AA070364.1	EST_HUMAN	h18991.1 (S) Stralagene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:500924.3'
1719	14749	27734	1.8	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
1719	14749	27735	1.79	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
2054	15073	28092	4.08	1.1E-02	BF345263.1	EST_HUMAN	002018037F1 NCI CGAP Brn77 Homo sapiens cDNA clone IMAGE:4153608.5'
2889	15948		3.91	1.1E-02	N69523.1	EST_HUMAN	zaf0c05.11 Scores fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:295040.5'
3335	16591	29505	2.75	1.1E-02	AI653508.1	EST_HUMAN	ig95b10.x1 NCI CGAP OV23 Homo sapiens cDNA clone IMAGE:295040.5'
4051	17088		1.32	1.1E-02	BE144637.1	EST_HUMAN	Q62889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL :
4133	17165		0.71	1.1E-02	AW813768.1	EST_HUMAN	PM3-HT0175-300989-001-H08 HT0175 Homo sapiens cDNA
4687	17884	30772	2.22	1.1E-02	AL046383.2	EST_HUMAN	RC3-ST0197-120200-015-011 ST0197 Homo sapiens cDNA
							DKFZp596E0924_s1 558 (synonym: tute3) Homo sapiens cDNA clone DKFZp596E0924
6272	19345	32578	1.02	1.1E-02	U60480.1	NT	Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaH (ynaH), YnaB (ynaB), YnaC (ynaC), YnaD (ynaD), YnaE (ynae), YnaF (ynaf), YnaG (ynag), YnaH (ynah), YnaI (ynai), YnaJ (ynaj), xylan beta-1,4-xylosyl
7855	20300	34176	2.47	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-H07 HT0256 Homo sapiens cDNA
8105	21042	34441	3.79	1.1E-02	9631284	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
8987	21953	35377	0.7	1.1E-02	AW995160.1	EST_HUMAN	QV3-BN0046-220300-128-H02 BN0046 Homo sapiens cDNA
9174	22140	35566	0.66	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NH0C4040
9253	22210	36680	7.21	1.1E-02	Q61082	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10289	23214	36698	2.1	1.1E-02	AA082578.1	EST_HUMAN	znc24d0.1 L1 Stralagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328.5'
10454	23376	36859	3.79	1.1E-02	AA314695.1	EST_HUMAN	EST186944 Cdon carcinooma (HCC) cell line II Homo sapiens cDNA 5' end
11324	24274	37802	2.01	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
12194	25039		3.52	1.1E-02	AA686239.1	EST_HUMAN	ab77111.1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:953005.3' similar to contains
12960	17165		1.67	1.1E-02	AW813768.1	EST_HUMAN	Alu repetitive element
7	13127	26027	0.68	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1526	14559	27530	1.07	1.0E-02	AW398128.1	EST_HUMAN	MR3-CT0176-111098-003-010 CT0176 Homo sapiens cDNA
2578	15579		1.26	1.0E-02	AA803389.1	EST_HUMAN	CM2-HT0177-041099-017-H12 HT0177 Homo sapiens cDNA
3106	16163	29075	2.7	1.0E-02	BE935593.1	EST_HUMAN	sc22108.1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1350495.3'
3276	16330	29251	1.33	1.0E-02	BE969696.1	EST_HUMAN	RC0-FN0025-250500-021-002 FN0025 Homo sapiens cDNA
							BDT6498987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689.3'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3520	16566		0.85	1.0E-02	AW845621.1	EST_HUMAN	NR0-CT0090-081099-003-h10 CT0060 Homo sapiens cDNA
3895	16935	28845	0.76	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
3811	16951	28862	1.08	1.0E-02	AI163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4811	17828	30872	4.97	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4881	17898	30787	5.01	1.0E-02	R68567.1	EST_HUMAN	Xp4001.11 Scores fetal liver spleen TNF1.3 Homo sapiens cDNA clone IMAGE:196535 5'
5036	18049	30828	0.63	1.0E-02	AI161593.2	NT	Arbidopsis thaliana DNA chromosome 4, contig fragment No. 89
5490	18590	31501	0.86	1.0E-02	H52681.1	EST_HUMAN	Xp3911.11 Scores ovary tumor N18HOT Homo sapiens cDNA clone IMAGE:235941 5'
5840	18930	32114	0.82	1.0E-02	AF305388.1	NT	Mus musculus transcription complex subunit NF-A1C4 (N1alc4) gene, exons 1 and 2
6237	19310	32542	1.02	1.0E-02	AF257303.1	NT	Mus musculus synaptobrevin II (SY2) gene, complete cds
6305	19376	32614	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6305	19376	32615	2.49	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6828	20150	33470	2.15	1.0E-02	Z25642.1	NT	Z.mays U3snRNA pseudogene
9748	22689	36145	4.78	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663177 5'
9748	22689	36146	4.79	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663177 5'
11594	24532		1.96	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for
11695	24560	38238	2.05	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDG10 5'
12091	24962		1.47	1.0E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12276	25990		1.99	1.0E-02	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A69)
12337	25757	31518	3.9	1.0E-02	AW835521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12356	25816		5.66	1.0E-02	ST0330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12722	25769		2.07	1.0E-02	AL275950.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12873	25973		4.78	1.0E-02	X82664.1	NT	H. sapiens gene for M64971C053 antigen
13094	25920	31676	1.7	1.0E-02	AB039897.1	NT	Homo sapiens WDRA gene for WD repeat protein, complete cds
804	13049	26607	1.77	9.0E-03	AI1796126.1	EST_HUMAN	WH4209.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1289	14304		1.88	9.0E-03	BE781692.1	EST_HUMAN	MER22 MER22 repetitive element
1478	14510	27465	0.97	9.0E-03	AE001270.1	NT	601470243F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3373346 5'
2405	15412	28436	2.87	9.0E-03	AL161593.2	NT	Tropomyosin piliun section 86 of 87 of the complete genome
2413	15420	28444	0.95	9.0E-03	AF099934.1	NT	Arbidopsis thaliana DNA chromosome 4, contig fragment No. 59
2917	15975	28698	0.69	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2917	15975	28699	0.69	9.0E-03	AI251744.1	EST_HUMAN	qhs0009.x1 Scores_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3382	16725	29638	0.87	9.0E-03	J05184.1	NT	qhs0009.x1 Scores_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5061	18071	30650	1.01	9.0E-03	T70044.1	EST_HUMAN	S. acidothermus thermopain gene, complete cds
							yc17508.st Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80919 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5061	18071	30851	1.01	9.0E-03	T70044.1	EST_HUMAN	yct7b08.a1 Stratigene lung (#637210) Homo sapiens cDNA clone IMAGE:80919.3'
5260	18268	31136	0.96	9.0E-03	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2). mRNA
5908	18994		1.2	9.0E-03	AI809702.1	EST_HUMAN	hw7f704.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2361631.3'
6785	19840		4	9.0E-03	BE745968.1	EST_HUMAN	601573438F1.NH_MGC.B Homo sapiens cDNA clone IMAGE:3834752.5'
7688	20659	34020	0.93	9.0E-03	AI242219.1	EST_HUMAN	qib7o12.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:165974.3'
7712	20659	34036	0.81	9.0E-03	8622570	NT	Homo sapiens hypothetetical protein FLJ10680 (FLJ10680). mRNA
8207	21177		0.99	9.0E-03	AL039591.1	EST_HUMAN	DKFZp434L0412.1_1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412.5'
8592	21560		0.55	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10221	23146	36635	1.42	9.0E-03	P20608	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
11331	24281		1.6	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
12680	25985		2.12	9.0E-03	BE348385.1	EST_HUMAN	hw7f709.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183181.3'
12689	25549		15.47	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281298-001-e09 HT0452 Homo sapiens cDNA
502	13574		3.01	8.0E-03	AA720007.1	EST_HUMAN	zib3o03.s1 Soares_phleal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413586.3' similar to contains Alu repetitive element
691	14043	26997	19.52	8.0E-03	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2166	15182	29202	1.96	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3321	16372	29203	1.12	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3370	16420	29345	0.93	8.0E-03	AI310161.1	NT	Homo sapiens SCL gene locus
3689	16732	29644	1.25	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3689	16732	29645	1.25	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4285	17314	30103	1.08	8.0E-03	BE840049.1	EST_HUMAN	QVC-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4410	17433	30326	6.3	8.0E-03	BF563327.1	EST_HUMAN	CM4-NN0119-300800-223-b05 NN0119 Homo sapiens cDNA
4747	17787	30692	0.95	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4747	17787	30693	0.95	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5901	18897	31698	2.98	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27_NG28_RPS28_NADH oxidoreductase, NG28_K1FC1_Fas-binding protein, BING1, Ixasein, RadGS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sec21 gene, partial>
6323	25958	32835	1.39	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (27)
6913	19965	33281	4.24	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE YANA
7104	20038		1.4	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7415	20382	33733	1.88	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (tag cell), exon 1, 5' end
7790	20743		1.81	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9235	22201	35631	0.58	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
9261	22227	35657	3.77	8.0E-03	AW808992.1	EST_HUMAN	MR1-3T0111-111169-011-H06 S10111 Homo sapiens cDNA
9270	22238	35665	0.52	8.0E-03	AL130075.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/6
9331	22262	35726	0.58	8.0E-03	9789956	EST	Mus musculus fusion 2 (human) (Fus2) mRNA
10308	22323		5.16	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0877-04-000-131-g03 BT0877 Homo sapiens cDNA
11118	24078	37602	1.99	8.0E-03	BE788441.1	EST_HUMAN	S1475619F1 NH <sub>2</sub> MGC 88 Homo sapiens cDNA clone IMAGE:3878405 5'
11330	24280		2.66	8.0E-03	Z49652.1	NT	60 chromosomes X reading frame ORF YJR152w
11649	24686	38156	2.99	8.0E-03	BF93327.1	EST_HUMAN	CM4-NN0119-300630-223-055 NN0119 Homo sapiens cDNA
11710	24676	38252	1.55	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11710	24676	38253	1.55	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12024	24900	38405	3.74	8.0E-03	AF04559.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12205	25047		2.04	8.0E-03	M69035.1	NT	Cyclodextrin glucanase eIF-2a kinase mRNA, complete cds
12249	25077		2.6	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
695	13757	26687	18.14	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
695	13757	26688	18.14	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
978	14020	26983	4.66	7.0E-03	AF243378.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1118	14162	27113	4.38	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZ10 5'
1366	14400		1.16	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF1B) TRANSCRIPTION FACTOR GENESIS (HEPATOCTYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HIF-2)
1306	14430	27369	3.03	7.0E-03	AA662268.1	EST_HUMAN	ab79509.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1502	14535	27506	3.04	7.0E-03	AW303589.1	EST_HUMAN	x21b02.s1 Scortea_NFL_T_CBC S1 Homo sapiens cDNA clone IMAGE:2813739 3'
1758	14785	27769	1.03	7.0E-03	AW960396.1	EST_HUMAN	EST1362628 MAGE resequences; MAGE Homo sapiens cDNA
1758	14785	27770	1.03	7.0E-03	AW960396.1	EST_HUMAN	EST1362628 MAGE resequences; MAGE Homo sapiens cDNA
2287	16889	28307	2.08	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3371	16916	29537	0.97	7.0E-03	AI150273.1	EST_HUMAN	q3402.s1 Scortea testis NHT Homo sapiens cDNA clone IMAGE:1751952 3'
3778	16920	29728	0.93	7.0E-03	AW444463.1	EST_HUMAN	U1H-B13-alk-e-10-0-UJ s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735691 3'
3825	16965	29769	1.45	7.0E-03	AF196344.1	NT	Rattus norvegicus nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4048	16920	29728	0.93	7.0E-03	AW444463.1	EST_HUMAN	U1H-B13-alk-e-10-0-UJ s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735691 3'
4366	17393		0.86	7.0E-03	U60088.1	NT	Dichostellum discoidium multidrug resistance transporter/Ser protease (logC) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4565	17988		1	7.0E-03	AW117711.1	EST_HUMAN	x33409.x1 NCI_CGAP_Uni Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR-Q12987 Q12987
4629	17650		1.47	7.0E-03	AW630888.1	EST_HUMAN	ACIDIC 82 KDA CGAP ;
5024	18038		1.81	7.0E-03	AL163278.2	NT	h182605.Y1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:266936 5'
5228	18234	31108	1.4	7.0E-03	AV724419.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5228	18234	31109	1.4	7.0E-03	AV724419.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCEC08 5'
5918	19004		0.83	7.0E-03	H71108.1	EST_HUMAN	AV724419 HTB Homo sapiens cDNA clone HTBCEC08 5'
6233	25658		6.11	7.0E-03	AW861059.1	EST_HUMAN	y82601.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6447	16512	32762	1.38	7.0E-03	W68251.1	EST_HUMAN	9b214723 CLUSTERIN PRECURSOR (HUMAN);
6687	16744	33018	3.16	7.0E-03	AA327128.1	EST_HUMAN	IC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
6717	16773	33052	0.81	7.0E-03	BE857365.1	EST_HUMAN	Z833T01.1 Soares_fetal_liver_NbHH19W Homo sapiens cDNA
7284	20051	33397	1.82	7.0E-03	BE528133.1	EST_HUMAN	EST30974 Colon 1 Homo sapiens cDNA 5' end
7763	20716	34088	6.31	7.0E-03	Z35838.1	NT	7g34810.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR-Q13387
7763	20716	34088	6.31	7.0E-03	Z35838.1	NT	Q13387 HYPOTHETICAL PROTEIN 394D8_2, contains TAR1.12 TAR1 repetitive element ;
8180	21150	34537	0.45	7.0E-03	AJ229043.1	NT	GM2-CT0478-230300-347-b11 CT0478 Homo sapiens cDNA
8180	21150	34558	0.45	7.0E-03	AJ229043.1	NT	S.cerevisiae chromosome II reading frame ORF_YBL077w
8448	21417	34830	2.48	7.0E-03	BE179667.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8991	21927	35354	0.49	7.0E-03	AF281074.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9752	22693		0.71	7.0E-03	AF111682.2	NT	RC6-HT0562-163030-011-D02 HT0562 Homo sapiens cDNA
9953	22880	36344	0.85	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10078	23005	36476	2.84	7.0E-03	P48682	SWISSPROT	Homo sapiens serine palmitoyl transferase, subunit II, gene, complete cds; and unknown genes
10078	23005	36476	2.84	7.0E-03	P48682	SWISSPROT	y48610.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
10698	23590		1.06	7.0E-03	AV887378.1	EST_HUMAN	Alu repetitive element
10698	23590		1.06	7.0E-03	AV887378.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10853	23773		0.95	7.0E-03	AJ769734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
11248	24201	37682	2.23	7.0E-03	AB008652.1	NT	AV697379 GKC Homo sapiens cDNA clone GKCAFO7 5'
11248	24201	37722	1.51	7.0E-03	AJ004862.1	NT	wc37409.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'
11248	24201	37723	1.51	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NRP52, complete cds
12734	25977		1.53	7.0E-03	H84065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12741	25991		1.91	7.0E-03	BE263253.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12834	28461		1.09	7.0E-03	Y17455.1	NT	Y15101.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
							Alu repetitive element
							301145154F2.NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
							Homo sapiens LSRF2 gene, penultimate exon

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1245	14282	27244	9.99	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXK_HUMAN 075468 ORPHAN NUCLEAR RECEPTOR PXR;
1245	14282	27245	9.98	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXK_HUMAN 075468 ORPHAN NUCLEAR RECEPTOR PXR;
2782	15774	28793	1.32	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2801	15960	28879	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2801	15960	28880	4.82	6.0E-03	AA759135.1	EST_HUMAN	ah78a11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
3260	16314		2.26	6.0E-03	H75990.1	EST_HUMAN	yf7704.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3393	16442	29369	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isoboln, fatty acid binding protein, sepiapterin reductase and vasodiln genes, complete cds
3393	16442	29369	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isoboln, fatty acid binding protein, sepiapterin reductase and vasodiln genes, complete cds
3557	16803		1.28	6.0E-03	W37085.1	EST_HUMAN	zcf13a11.l1 Soares_parenchymal tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3572	16718	29829	4.48	6.0E-03	BF510983.1	EST_HUMAN	UJ-H-B4-epm-c-06-OJ1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3708	16751	29887	1.21	6.0E-03	BE077393.1	EST_HUMAN	RC1-B10606-280400-014-a07 B10606 Homo sapiens cDNA
3760	16831	29737	1.19	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3944	16984	28600	0.87	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240399-021-b10 CT0204 Homo sapiens cDNA
3979	17019		0.9	6.0E-03	BE250108.1	EST_HUMAN	600942604F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4391	17419		1.81	6.0E-03	A016633.1	EST_HUMAN	oa33c1.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4724	17744	30635	5.97	6.0E-03	AA324242.1	EST_HUMAN	EST127116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
6276	25657	32581	0.9	6.0E-03	9627521	NT	Varola virus, complete genome
6699	20212	33541	0.87	6.0E-03	Q14994	SWISSPROT	SYNAPSIN III
7034	18366	31253	0.84	6.0E-03	BE253748.1	EST_HUMAN	60112363F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7461	20427	33793	0.83	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7461	20427	33784	0.83	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7909	20951	34238	0.93	6.0E-03	AF128954.1	NT	Homo sapiens telomerase reverse transcriptase (TER1) gene, exons 7-16 and complete cds
8100	21036	34436	0.82	6.0E-03	P17904	SWISSPROT	RAS-RELATED PROTEIN RAP-2B
8136	21073	34473	0.5	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
8181	21161	34571	6.56	6.0E-03	A033980.1	EST_HUMAN	ovt13a04.x1 Soares_parenchymal tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646570 3' similar to contains MER10.b1 MER10 repetitive element;
8307	21276	34687	2.54	6.0E-03	AW759337.1	EST_HUMAN	RCO-UJ00051-210300-032-g02 UJ00051 Homo sapiens cDNA
8381	21350		1.51	6.0E-03	BF038198.1	EST_HUMAN	60146195F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3356628 5'
8912	22733	36188	8.57	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10403	23325		2.08	6.0E-03	AL432861.1	EST_HUMAN	U22022.X1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SWR13A_HUMAN
10523	23445	39643	0.97	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fndD gene
10659	23581		1.03	6.0E-03	AF084555.1	NT	Homo sapiens cdc42le acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10768	23580	37187	0.88	6.0E-03	X68388.1	NT	M.thermophilum complete plasmid pFV1 DNA
11096	24056	37580	1.61	6.0E-03	AW062184.1	EST_HUMAN	EST374237 MAGE resequenced, MAGE Homo sapiens cDNA
11162	24120		1.55	6.0E-03	11548814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011) mRNA
11327	24277		3.99	6.0E-03	U14559.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11328	24278	37805	2.66	6.0E-03	BE373895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12319	25129		2.28	6.0E-03	AF010498.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12422	25812		1.52	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12446	25744		5.26	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 425182 to 450236 (section 39 of 148) of the complete genome
12525	25807		2.71	6.0E-03	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcgr1) gene, complete cds
12576	25285		1.48	6.0E-03	Q62209	SWISSPROT	SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1) PROTEIN
12850	25459		2.16	6.0E-03	BE789019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3845386 5'
12869	25471		1.53	6.0E-03	AL245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
13043	26594		1.76	6.0E-03	BF110288.1	EST_HUMAN	7036811.X1 NCL CGAP_L028 Homo sapiens cDNA clone IMAGE:3668564 3'
670	13735	26581	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocacyl-ARNa synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
670	13735	26582	2.34	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocacyl-ARNa synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
671	13735	26581	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocacyl-ARNa synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
671	13735	26582	3.43	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminocacyl-ARNa synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1114	14158	27109	1.03	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
1574	14607		1.02	5.0E-03	A1138977.1	EST_HUMAN	q278005.X1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2990	15988	28703	2.63	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2947	16005	28630	3.86	5.0E-03	BE266057.1	EST_HUMAN	601184798F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3338799 5'
3153	16210	29125	3.86	5.0E-03	T87623.1	EST_HUMAN	xe81609.e1 Soares infant brain NIH Homo sapiens cDNA clone IMAGE:22365 3'
3169	16224		3.05	5.0E-03	AL101491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3181	16236	28153	1.22	5.0E-03	R71794.1	EST_HUMAN	y88g02.x1 Scores breast 2NHBat Homo sapiens cDNA clone IMAGE:155568 3'
3291	16344		0.94	5.0E-03	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3679	16722	29635	0.97	5.0E-03	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C085
3713	16756	29570	4.03	5.0E-03	AF147448.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3771	16813	28722	1	5.0E-03	U938914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
3965	17035		2	5.0E-03	AA299875.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4333	17391	30246	0.69	5.0E-03	H78355.1	EST_HUMAN	y47g010.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240068 5'
4335	16813	26722	1.02	5.0E-03	U33914.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4601	17622	30515	1.02	5.0E-03	U46891.1	NT	Human putative chromatin structure regulator (SUP16H) mRNA, complete cds
4638	17656	30546	1.13	5.0E-03	AJ131018.1	NT	Homo sapiens SCL gene locus
4749	17769	30665	1.34	5.0E-03	AJ752387.1	EST_HUMAN	cm15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm15c02 random
4970	17895	30875	1.08	5.0E-03	P15265	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5225	18250	31105	1.69	5.0E-03	6754029	NT	Mus musculus glucocorticoid-6-phosphate dehydrogenase (G6p), mRNA
5893	18981	32172	5.69	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PAPA (PARALYTIC PROTEIN)
							PROBABLY UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN-SPECIFIC PROTEINASE FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEINASE 9, Y-CHROMOSOME)
6162	19237	32468	2.97	5.0E-03	O00507	SWISSPROT	Chlamydia pneumoniae AR39, section 62 of 94 of the complete genome
6168	19272		0.69	5.0E-03	AE00234.2	NT	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
6747	19801		7.44	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMPD1 gene for S-adenosylmethionine decarboxylase, complete cds
7023	18355	31274	7.12	5.0E-03	AB025024.1	NT	Turkops truncatus mRNA for p40-phox, complete cds
7240	19975		0.82	5.0E-03	AB038267.1	NT	Mus musculus dydin, exon, heavy chain 11 (Dntrct1), mRNA
7295	20267	33602	0.57	5.0E-03	6753951	NT	EST030712 Fetal brain, Stragene (cat#939206) Homo sapiens cDNA clone HFB0893 similar to EST containing Alu repeat
7727	20683	34047	0.62	5.0E-03	T05124.1	EST_HUMAN	RC3-CT0255-031099-01-107 CT0255 Homo sapiens cDNA
7859	20801		1.17	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
8044	20981	34378	6.8	5.0E-03	AB016816.1	NT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8097	21033	34431	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8097	21033	34432	0.49	5.0E-03	Q9R001	SWISSPROT	ADAM-TS 5 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (IMPLANTIN)
8931	21549	34967	2.12	5.0E-03	P48962	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8959	21825		5.83	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Database Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	22126	35554	1.08	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
9292	22258	39988	0.61	5.0E-03	M25980.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10109	23124	36911	0.97	5.0E-03	L21710.1	NT	Plasmidium berghii 58 kDa phosphoprotein mRNA, partial cds
10330	23254	39732	0.68	5.0E-03	AW821898.1	EST_HUMAN	RCO-ST0379-210100-032-002 ST0379 Homo sapiens cDNA
10518	23440	36338	0.44	5.0E-03	AA539143.1	EST_HUMAN	h48h10.s1 NCI CGAP_P08 Homo sapiens cDNA clone IMAGE:985587
10896	23618	37112	0.47	5.0E-03	7652557	NT	Homo sapiens PROCA71 protein (PROCA71), mRNA
10844	23784	37112	0.51	5.0E-03	AA653261.1	EST_HUMAN	ag46c10.s1 Gesler Wilms tumor Homo sapiens cDNA clone IMAGE:126590 3'
11075	24037		4.17	5.0E-03	T16598.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
11287	24237	37764	2.15	5.0E-03	AW170394.1	EST_HUMAN	x159g05.x1 Soares_NHC6c, cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12.L1 repetitive element;
11287	24237	37765	2.15	5.0E-03	AW170394.1	EST_HUMAN	x159g05.x1 Soares_NHC6c, cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1.12.L1 repetitive element;
11381	24328	37857	1.55	5.0E-03	T49153.1	EST_HUMAN	1405a04.L1 Stralagene placenta (#337225) Homo sapiens cDNA clone IMAGE:70688 5'
11659	24595		3.92	5.0E-03	BE048055.1	EST_HUMAN	1248c04.y1 NCI CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2291622 5'
12463	25038		5.42	5.0E-03	AF047874.1	NT	Callus gallus glyceraldhyde-3-phosphate dehydrogenase mRNA, complete cds
12595	25298		3.7	5.0E-03	AF067263.1	NT	Brugia malayi Y chromosome marker
12693	25355		3.19	5.0E-03	L10347.1	NT	Human pro-alpha1 type I collagen (COL2A1) gene exons 1-54, complete cds
12718	26572		1.89	5.0E-03	AA165697.1	EST_HUMAN	z27a03.s1 Soares_oven/tumor NbcHOT Homo sapiens cDNA clone IMAGE:805648 3' similar to
12743	25752		5.87	5.0E-03	BF972332.1	EST_HUMAN	SWDXA2_MOUSE P14885 PROBABLE DIAPHENOL OXIDASE A2 COMPONENT ;
12922	26493	31702	3.21	5.0E-03	AW449109.1	EST_HUMAN	602077747.F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
235	13335	26259	2.6	4.0E-03	AW600196.1	EST_HUMAN	UJH-B19-akf-1408-0-01.s1 NCI CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734215 3'
321	13413	26337	2.12	4.0E-03	R46492.1	EST_HUMAN	UJH-B19-akf-1408-0-01.s1 NCI CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3076831 5'
443	13516	26449	1.15	4.0E-03	P54675	SWISSPROT	y651e04.s1 Soares_infant brain INIB Homo sapiens cDNA clone IMAGE:35983 3'
605	13672	26586	4.63	4.0E-03	AA939339.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) [PTDINS-3-KINASE] (PI3K)
878	13933	26893	1.9	4.0E-03	R46492.1	EST_HUMAN	on15g12.s1 Soares_NFL_T_GBC_ST1 Homo sapiens cDNA clone IMAGE:1862566 3'
812	13987		3.64	4.0E-03	AW749101.1	EST_HUMAN	y651e04.s1 Soares_infant brain INIB Homo sapiens cDNA clone IMAGE:35983 3'
1163	14185	27147	27.01	4.0E-03	AA099777.1	EST_HUMAN	RC3-B10333.110100-12-01.B10333 Homo sapiens cDNA
1173	14214	27198	1.92	4.0E-03	AA099777.1	EST_HUMAN	281a08.1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1308	14342	27305	1.5	4.0E-03	AA284374.1	EST_HUMAN	RCO-UM0014-170040-023-G01 UM0014 Homo sapiens cDNA
1600	14622		1.94	4.0E-03	AV1708305.1	EST_HUMAN	z59a01.L1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1769	14787	27772	2.38	4.0E-03	U33472.1	NT	AV1708305 ADC Homo sapiens cDNA clone ADCAK906 5'
2034	15053	29070	11.42	4.0E-03	AA099777.1	EST_HUMAN	Rattus norvegicus type 1 astrocyte and efferolary-limbic associated protein AT1-46 mRNA, complete cds
							281a08.1 Stralagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2269	15273		1.66	4.0E-03	BE410593.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2265	15299	28323	1.53	4.0E-03	AW784740.1	EST_HUMAN	RC8-UN0014-170400-023-G01 UN0014 Homo sapiens cDNA
2579	15580	28598	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), extracellular disphosphorylation protein >
2579	15580	28599	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), extracellular disphosphorylation protein >
2579	15580	28599	1.75	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc2/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), extracellular disphosphorylation protein >
2701	15697	28712	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2701	15697	28713	3.92	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2707	15702	28716	1.68	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3239	16294	28217	1.04	4.0E-03	BE164134.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3239	16294	28218	1.04	4.0E-03	BE164134.1	EST_HUMAN	PM1-HT0340-151299-003-H08 HT0340 Homo sapiens cDNA
3541	16597	29511	0.8	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NC1_CGAP_Cor18 Homo sapiens cDNA clone IMAGE:2665279 3'
3541	16597	29511	0.8	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NC1_CGAP_Cor18 Homo sapiens cDNA clone IMAGE:2665279 3'
3639	16932	29597	0.64	4.0E-03	Q13606	SWISSPROT	OLFATORY RECEPTOR 511(TOLFATORY RECEPTOR-LIKE PROTEIN OLF1)
4020	17038		2.14	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exon 1-11 (end joined CDS)
4643	17684	30563	1.1	4.0E-03	AJ32754.1	EST_HUMAN	ab1808.x5 Stratagene lung (R837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4805	17822	30717	3.73	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5173	18182	31050	0.98	4.0E-03	AW103719.1	EST_HUMAN	X63303.x1 NC1_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.t1 L1 L1 repetitive element ;
5220	18238	31102	0.93	4.0E-03	AA989955.1	EST_HUMAN	X66601.x1 Soares_fetal_liver_upcen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5272	18278	31142	0.93	4.0E-03	J02187.1	NT	Foot and mouth disease virus serotype A-12 19ab capsid protein VP3
5348	18453	31324	1.56	4.0E-03	AF005959.1	NT	Drosophila melanogaster anon207 (anon207) mRNA, complete cds
5473	18574	31482	23.1	4.0E-03	AF168925.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5881	18878	32171	2.72	4.0E-03	P04198	SWISSPROT	(HPRG)
5895	18983	32173	1.63	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOZYTE ANTIGEN PRECURSOR
5983	18986	32266	0.87	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7811014.1 J1 781 (synonym: ham2) Homo sapiens cDNA clone DKFZp7811014 5'
6203	19277		3.95	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6391	19430	32673	1	4.0E-03	AW50572.1	EST_HUMAN	h94607.x1 NC1_CGAP_GCS Homo sapiens cDNA clone IMAGE:2948662 3'
6442	19507	32757	1.76	4.0E-03	BES48453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481954 5'
6827	19881	33172	0.97	4.0E-03	AA813222.1	EST_HUMAN	q321f1.x1 Soares_testis_INT Homo sapiens cDNA clone 1920245 3'
6942	20166	33489	1.5	4.0E-03	U76408.1	NT	Lycopodium esculentum ltrated 3 protein (TKn3) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7273	20009	33308	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7273	20009	33309	1.22	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7404	20372	33723	4.12	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7685	20024	33988	0.89	4.0E-03	A1681483.1	EST_HUMAN	h37g12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814.3
7687	20026	33990	0.72	4.0E-03	BE670170.1	EST_HUMAN	7a31b02.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284093.3
7767	20720		0.68	4.0E-03	X927109.1	NT	H sapiens hcgX gene
8274	21243	34655	0.49	4.0E-03	Q91T92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 6) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADAM-TS 11)
8383	21352	34761	5.06	4.0E-03	AF11644.1	NT	Dicystallum discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8545	21513	34830	1.92	4.0E-03	7682087	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9084	22030	35453	7.41	4.0E-03	AI553983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013.3 similar to contains Alu repetitive element;
9241	22207		4.72	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9250	22216	35646	3.66	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10287	23212	36895	0.87	4.0E-03	H30664.1	EST_HUMAN	yp2g12.r1 Soares retina N205HR Homo sapiens cDNA clone IMAGE:190160.5
10742	23694	37158	0.78	4.0E-03	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
11178	24133	37683	1.65	4.0E-03	AW153935.1	EST_HUMAN	x047b04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2707159.3
11464	24407	37954	4.83	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
12431	26958		1.82	4.0E-03	BE81673.1	EST_HUMAN	PM4-BN0138-183603-002408 BN0138 Homo sapiens cDNA
12454	25213		2.13	4.0E-03	BE298280.1	EST_HUMAN	601118164.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028065.5
12533	25259		2.3	4.0E-03	AW504273.1	EST_HUMAN	U11H-BND-4p-0-0-0-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622.5
12755	25400		7.22	4.0E-03	BF224125.1	EST_HUMAN	7a74c06.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3 similar to contains Alu repetitive element;containing element MER31 repetitive element;
12801	26866		3.31	4.0E-03	AW614596.1	EST_HUMAN	rh02007.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2903932.3 similar to contains element LTR5 repetitive element;
12814	25437		2.73	4.0E-03	AW819141.1	EST_HUMAN	RC3-S10281-240400-015403 ST0281 Homo sapiens cDNA
13093	25519	31675	6.48	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (GABO571), mRNA
1371	13457	26837	1.89	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
680	13935	26894	3.09	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1689	14701	27676	5.52	3.0E-03	AA468110.1	EST_HUMAN	nc730d5.s1 NCL CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2268	16281		1.58	3.0E-03	AF065068.1	NT	Homo sapiens MHC class 1 region
2302	15314		8.06	3.0E-03	Z32521.1	NT	S.cereale (cv. Hilo) mRNA for triphosphate isomerase
2303	16315	28334	1.3	3.0E-03	U46856.1	NT	Mus musculus threosin trifol factor gene, partial cds

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2303	15315	28335	1.3	3.0E-03	U48658.1	NT	Mus musculus intestinal Trefol factor gene, partial cds
3006	16084		0.8	3.0E-03	Y06006.1	NT	Arabidopsis thaliana pM1 gene
3069	16156	26059	4.09	3.0E-03	BE376298.1	EST_HUMAN	601237682F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608933 5'
3168	16221	29136	2.44	3.0E-03	AW802887.1	EST_HUMAN	IL2-U00075-240300-056-D03 UM0076 Homo sapiens cDNA
3428	16478	28395	1.62	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XIII) collagen (COL18A1) gene, exon 1 and 2
3439	16486		6.72	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4002	17041	26949	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4002	17041	26950	7.18	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4057	17103	26956	1.47	3.0E-03	AI792278.1	EST_HUMAN	ai0409.j5 Gascard Wilms tumor Homo sapiens cDNA clone IMAGE:1155589 5'
4177	17209		1.08	3.0E-03	Z32921.1	NT	S.cereale (cv. Halo) mRNA for triphosphatase isomerase
4424	17451	30342	3.8	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4546	17569	30458	5.88	3.0E-03	AI598141.1	EST_HUMAN	xb8.P10.H3 confirm Homo sapiens cDNA 3'
4871	17688	30776	1.74	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.s5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4990	17907	30786	5.49	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5338	18443	31196	3.42	3.0E-03	6922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5835	18731	31893	1.22	3.0E-03	AI249681.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5708	18803	31890	0.95	3.0E-03	U38323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6705	19781	33040	10.04	3.0E-03	AA458701.1	EST_HUMAN	aa1310.1 Soares NIH-MP_u_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7224	20246	33580	0.95	3.0E-03	D37977.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, perial cds
7412	20379	33730	1.37	3.0E-03	AJ011419.1	NT	Kluweromyces marianus pop3 gene for purine-cytosine permease
7765	20718	34091	3.16	3.0E-03	AB021798.1	NT	Cytos salvia gene for bZIP protein, complete cds
8145	21082	34481	0.49	3.0E-03	P26659	SWISSPROT	DNA REPAIR HELICASE RAD15 (RHF3)
8270	21239	34650	0.91	3.0E-03	BF333058.1	EST_HUMAN	RCO-3T0812-250900-032-e07 BT0812 Homo sapiens cDNA
8270	21239	34651	0.91	3.0E-03	BF333058.1	EST_HUMAN	RCO-3T0812-250900-032-e07 BT0812 Homo sapiens cDNA
8498	21629	34680	1.31	3.0E-03	N92580.1	EST_HUMAN	ab2704.s1 Soares parathyroid tumor NHPA Homo sapiens cDNA clone IMAGE:304783 3'
8558	21628		0.77	3.0E-03	M69498.1	NT	S.cereale UGA35 gene, complete cds
8804	21771	35197	1.16	3.0E-03	P51989	SWISSPROT	PETROGENOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRP A2(A))
8827	21794	35217	1.34	3.0E-03	AI163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8933	21899		1.25	3.0E-03	Q8QNM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9343	22308		10.07	3.0E-03	AW613774.1	EST_HUMAN	hs0010.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2689131 3' similar to contains L1.11 L1 repetitive element;
9400	22366	35797	4.01	3.0E-03	AI161599.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8424	22388	35827	4.74	3.0E-03	AI016731.1	EST_HUMAN	oxd312.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:571387.1ma1
9434	22398	35936	0.83	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9764	22705		0.95	3.0E-03	D00001.1	NT	60203590F1 NCL CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4183938 5'
8802	21125	34528	0.61	3.0E-03	BE154670.1	EST_HUMAN	Synchochylis sp. PC06803 complete genome, 3/27, 271600-402289
8934	22921		0.82	3.0E-03	P03355	SWISSPROT	PM3-H10344-071298-003-007 HT0344 Homo sapiens cDNA
10055	22892		5.33	3.0E-03	P08672	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROZOITE PROTEIN PRECURSOR (OS)
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
10255	23180	36667	1.56	3.0E-03	P11369	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10355	23279	36755	1.15	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS210103
10469	23421	36920	4.39	3.0E-03	AL183303.2	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11184	24149		1.62	3.0E-03	9803028	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11708	24673	38250	1.47	3.0E-03	AF060222.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11775	23630	37451	1.86	3.0E-03	AF266285.1	NT	Homo sapiens tritricolide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11810	24695	38278	2.27	3.0E-03	AF094481.1	NT	Homo sapiens tritricolide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
11881	24763	38348	1.47	3.0E-03	P11369	SWISSPROT	promma-5.E07.7 blumer Homo sapiens cDNA 5'
12169	25765		4.08	3.0E-03	AI525055.1	EST_HUMAN	o17b7b10.61 Soares, total, fetus, NB2HF8_9v Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1:3 MER28 repetitive element;
12232	25904	38162	1.83	3.0E-03	AA983154.1	EST_HUMAN	Homo sapiens gene for CMP-N-acetylneuraminate acid hydroxylase, partial cds
12292	25895		2.42	3.0E-03	AB009668.1	NT	Rattus norvegicus mRNA for connexin38 (cx36 gene)
12478	26228	31794	2.01	3.0E-03	AJ296282.1	NT	RING CANAL PROTEIN (KELCH PROTEIN)
610	13987	29508	0.92	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
718	13687	28507	0.92	2.0E-03	Q04652	SWISSPROT	Y15h03.11 Soares fetal liver spleen 1NF.L3 Homo sapiens cDNA clone IMAGE:108341 5'
789	16851		12.64	2.0E-03	T70874.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1365	14369	27370	1.9	2.0E-03	M20783.1	NT	Homo sapiens tumor-related protein DR2 (DR2) gene, complete cds
1368	14402	27370	1.34	2.0E-03	AA661605.1	EST_HUMAN	hu8961.s1 NCL CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1376	14410	27380	12.34	2.0E-03	AF284446.1	NT	PLATELET-ENDOTHELIAL TETRAPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1486	14519	27492	1.93	2.0E-03	P48509	SWISSPROT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1519	14551	27522	3.03	2.0E-03	4557898	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1519	14951	27523	3.03	2.0E-03	4557836	NT	Homo sapiens procollagen-hyaline, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1595	14627		8.7	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
1786	14915	27800	1.26	2.0E-03	AA450138.1	EST_HUMAN	z442a10.1f Soares, total, fetus, ND2HF8, 9w Homo sapiens cDNA clone IMAGE:789114 5'
2011	15032	28042	1.52	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2261	15275	28259	1.02	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2594	15595		4.02	2.0E-03	AA137782.1	EST_HUMAN	UI-H-B17-add-g-10-Q-U1.at1 NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3427	15475	28394	4.82	2.0E-03	AA450138.1	EST_HUMAN	z442a10.1f Soares, total, fetus, ND2HF8, 9w Homo sapiens cDNA clone IMAGE:789114 5'
3434	16481	29400	0.8	2.0E-03	BF66855.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3660	16723	29638	6.1	2.0E-03	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
3973	17013	29827	0.95	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4140	17171	30059	2.1	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP38]
4203	17234	30122	1.29	2.0E-03	AA179893.1	EST_HUMAN	z43101.1f Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:503361 5'
4248	17277		9.31	2.0E-03	U08491.1	NT	Rattus norvegicus 5-hydroxytryptamine receptor gene, partial cds
4468	17484		1.01	2.0E-03	AW287380.1	EST_HUMAN	UI-H-BW0-air-g-03-Q-U1.at1 NC1 CGAP Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4462	17488	30375	1.31	2.0E-03	AJ094748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4577	17599	30483	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (sh) mRNA, complete cds
4577	17599	30484	1.99	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (sh) mRNA, complete cds
4735	17755		1.09	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4740	17760		1.84	2.0E-03	R87773.1	EST_HUMAN	y04502.s1 Soares adult brain N2644-HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5054	18086	30945	0.75	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5163	18172	31051	1.02	2.0E-03	AF187874.1	NT	8 Homo sapiens concentrative nucleoside transporter (CNT1) gene, exon 12
5281	18237	31149	2.26	2.0E-03	D88506.1	NT	Homo sapiens gene for cholesterylkin type-A receptor, complete cds
5564	18691	31607	1.33	2.0E-03	BF241410.1	EST_HUMAN	60187635F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104922 5'
5709	25543	31981	2.18	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5795	26687	32058	0.61	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-602 UM0025 Homo sapiens cDNA
5795	26687	32059	0.61	2.0E-03	AW786111.1	EST_HUMAN	MR2-UM0025-300300-102-602 UM0025 Homo sapiens cDNA
5767	18889	32071	1.73	2.0E-03	U63711.1	NT	Xenopus laevis yellin mRNA, complete cds
6231	16305	32536	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6231	16305	32537	3.79	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6480	18545	32783	15.16	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) [CARP II] (CA-XI)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
6480	19545	32794	15.16	2.0E-03	Q85203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6482	19547	32796	7.39	2.0E-03	BF308187.1	EST_HUMAN	601887434FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19584	32842	2.26	2.0E-03	Q9LKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6522	19585	32843	0.77	2.0E-03	AF708075.1	EST_HUMAN	AF708075 ADC Homo sapiens cDNA clone ADCAE08 5'
6554	19614	32879	1.38	2.0E-03	X94461.1	NT	Laculenticum mRNA for lysyl-RNA synthetase (LysRS)
6756	19810						w49h08.x1 Soares. Dieckgraeft. colon. NHCD Homo sapiens cDNA clone IMAGE:262217 3' similar to SW-RL29_HUMAN P47914 603 RUBOSOMAL PROTEIN L29 ; contains element MSR1 repetitive element ;
6794	19848	33133	0.71	2.0E-03	AA677831.1	EST_HUMAN	213811.x1 Soares. fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430552 3'
7151	18963	31271	1.08	2.0E-03	AB038502.1	NT	Ceenorhabditis elegans mRNA for galectin LEC-11, complete cds
7287	20054	33371	2.86	2.0E-03	BE097886.1	EST_HUMAN	CM4-510396-061289-054-401 BT0360 Homo sapiens cDNA
7351	20321	33688	0.64	2.0E-03	AI298883.1	EST_HUMAN	gms9411.x1 NGL CGAP_Lus Homo sapiens cDNA clone IMAGE:189685 3'
7511	20476	33637	0.77	2.0E-03	T86569.1	EST_HUMAN	y477g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114306 5'
7877	20821	34198	1.55	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8386	21355	34763	1.95	2.0E-03	AW592004.1	EST_HUMAN	H37606.x1 Soares. NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60979 Q60978 JERKY. ;
8560	21528	34947	8.01	2.0E-03	N20287.1	EST_HUMAN	y42208.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.82 L1 repetitive element ;
8560	21528	34948	6.01	2.0E-03	N20287.1	EST_HUMAN	y42208.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.82 L1 repetitive element ;
8607	21575	34890	0.57	2.0E-03	Q92350	SWISSPROT	HYPOPHYSICAL 328 KD PROTEIN C639.05 IN CHROMOSOME 1
8829	21597	35018	1.23	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8884	21652	35074	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8884	21652	35075	0.77	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8709	21677	35102	0.81	2.0E-03	AU136678.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8762	21729		0.67	2.0E-03	AI400877.1	NT	Homo sapiens ASCL3 gene, CECGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
9550	18837	32068	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UN0025-300300-102-102 UN0025 Homo sapiens cDNA
9550	18887	32069	0.66	2.0E-03	AW796111.1	EST_HUMAN	MR2-UN0025-300300-102-102 UN0025 Homo sapiens cDNA
9555	22557	35007	0.66	2.0E-03	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
9844	22837	36291	0.97	2.0E-03	H60832.1	EST_HUMAN	y86c09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'
9844	22837	36292	0.97	2.0E-03	H60832.1	EST_HUMAN	y86c09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194296 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9916	22737	36190	3.31	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MOTENOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP-150-225) (TENASCIN-C) (TN-C)
10028	22863	36421	1.02	2.0E-03	P46982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10028	22853	36422	1.02	2.0E-03	P46982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10081	23008	36476	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10081	23009	36490	0.65	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL-10) gene, complete cds
10275	23200	36694	0.94	2.0E-03	AW894289.1	EST_HUMAN	QV9-OT0064-009.000-144-e01 OT0064 Homo sapiens cDNA
10402	23324		8.44	2.0E-03	AA251376.1	EST_HUMAN	zsl0006.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754.3'
10761	23702	37200	0.46	2.0E-03	BF397386.1	EST_HUMAN	MR2-GN0030-140900-001-e05 GN0030 Homo sapiens cDNA
10969	23889	37401	0.43	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
10969	23899	37402	0.43	2.0E-03	AW361176.1	EST_HUMAN	RC1-CT0251-141099-012-d01 CT0251 Homo sapiens cDNA
11356	24306		2.4	2.0E-03	M66524.1	NT	Human dyx202 gene
11617	20621	34166	2.2	2.0E-03	P07394	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11870	24752		1.87	2.0E-03	BF330609.1	EST_HUMAN	RC3-B10333-310800-115-g04 B10333 Homo sapiens cDNA
11876	24758	38342	10.47	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
12180	25028		2.99	2.0E-03	A0925746.1	EST_HUMAN	V65H03.x1 NCI CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2283669.3' similar to SW:VATG_MANSE
12197	25042	38623	2.41	2.0E-03	AF167516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
12220	25057	38627	1.75	2.0E-03	A084325.1	EST_HUMAN	043g06.s1 Soares_papillary thyroid tumor_NHPPA Homo sapiens cDNA clone IMAGE:1666634.3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR. ;
12241	18349		11.57	2.0E-03	AL245167.1	NT	Camelus dromedarius cxhpt16 gene for immunoglobulin heavy chain variable region
12459	25932		2.03	2.0E-03	AV697696.1	EST_HUMAN	AV697696 GKC Homo sapiens cDNA clone GKCGXD05.5'
12550	25973	31777	1.83	2.0E-03	Y00508.1	NT	H. sapiens MT gene for muscarinic acetylcholine receptor
12663	26341		1.33	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12710	25795		1.55	2.0E-03	AI375037.1	EST_HUMAN	1665102.x1 Soares_fetus_Nb2-HF8_Bw Homo sapiens cDNA clone IMAGE:22049061.3' similar to contains Alu repetitive element;
12826	25445		1.6	2.0E-03	AF129795.1	NT	Homo sapiens MSH45 gene, partial cds; and CLIC1, DDAH, G8b, G6c, G6d, G6e, G6f, BAT5, G5b, GSK2B, BAT4, GA, Apo M1, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
13002	25745		1.95	2.0E-03	AV697696.1	EST_HUMAN	AV697696 GKC Homo sapiens cDNA clone GKCGXD05.5'
13095	25821		1.44	2.0E-03	P04767	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
439	13513	26444	1.72	1.0E-03	H96471.1	EST_HUMAN	Y96c08.r1 Soares_pneal_gland_N31-PG Homo sapiens cDNA clone IMAGE:222334.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Describer
830	13887	26842	2.09	1.0E-03	AJ20263.1	EST_HUMAN	as70508.x1 Barstead codon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
830	13887	26843	2.09	1.0E-03	AJ20263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYL-COA HYDRATASE. ;
1097	14141	27091	3.37	1.0E-03	AB65788.1	EST_HUMAN	as70508.x1 Barstead codon HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
1117	14161	27112	1.69	1.0E-03	AJ65467.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYL-COA HYDRATASE. ;
							w68606.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2422288 3'
							w63410.x1 NCL CGAP_Met15 Homo sapiens cDNA clone IMAGE:2551242 3'
							w68601.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Aliu repetitive element;
1170	14211	27166	1.5	1.0E-03	AJ622618.1	EST_HUMAN	HIGH MOLECULAR WEIGHT FORM OF MYOSIN (HMM/M)
2042	15061	28082	3.08	1.0E-03	P47808	SWISSPROT	Homo sapiens SCL gene locus
2163	15179	28189	9.01	1.0E-03	AJ131016.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
2893	16051	28972	1.42	1.0E-03	AB033117.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3205	16280	29176	2.08	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3205	16280	29180	2.08	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3313	16306	29286	1.23	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3553	16598	29524	0.92	1.0E-03	U66061.1	NT	Human MUC2 gene, promoter region
3553	16598	29525	0.92	1.0E-03	U66061.1	NT	Human MUC2 gene, promoter region
3678	18721		1.49	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3946	16986	29901	0.64	1.0E-03	AW170552.1	EST_HUMAN	xn63d07.x1 Scores_NHCC cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.1 TAR1 repetitive element ;
3954	16994	29910	1.11	1.0E-03	Z49549.1	NT	S cerevisiae chromosome X reading frame ORF_YJ149w
4464	17490	30377	2.27	1.0E-03	BE639162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4502	17527	30412	4.39	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4609 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP4609
4692	17713	30508	0.76	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL6) genes
4861	17878	30765	2.07	1.0E-03	AJ073488.1	EST_HUMAN	ov4504.x1 Scores_testis NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4861	17878	30766	2.07	1.0E-03	AJ073486.1	EST_HUMAN	ov4504.x1 Scores_testis NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4862	17879		4.33	1.0E-03	BE154067.1	EST_HUMAN	PWQ-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5113	18123	30898	9.53	1.0E-03	Q48409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5202	18211	31086	1.03	1.0E-03	AV685870.1	EST_HUMAN	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5331	18485	31360	1.74	1.0E-03	AA280651.1	EST_HUMAN	2s44f01.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5476	18577	31486	2.98	1.0E-03	AJ068345.1	NT	Homo sapiens KVLQ171 gene
5631	18620	31566	1.77	1.0E-03	K03332.1	NT	Epsilon-Barr Virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5531	18929	31506	1.77	1.0E-03	K03332.1	NT	Epiplatin-Barr virus (AC876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5552	18748	31916	0.93	1.0E-03	BE769491.1	EST_HUMAN	601186941FT NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3843854 5'
5558	18754	31921	1.76	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5716	18910	31988	0.7	1.0E-03	N41974.1	EST_HUMAN	X07065.1 Soares melanocytes 2NHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER8 repetitive element;
5716	18910	31989	0.7	1.0E-03	N41974.1	EST_HUMAN	X07065.1 Soares melanocytes 2NHM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER8 repetitive element;
5995	19079	32276	0.96	1.0E-03	AA773352.1	EST_HUMAN	ab05612.s1 Stragene lung carcinoma 637218 Homo sapiens cDNA clone IMAGE:845734 3'
6018	19101		0.52	1.0E-03	BF541639.1	EST_HUMAN	602068042F1 NIH_MGC.88 Homo sapiens cDNA clone IMAGE:4069507 5'
6138	19213		2.57	1.0E-03	X07680.1	NT	Mouse nucleolin gene
6177	19252	32485	1.06	1.0E-03	BE983939.2	EST_HUMAN	601657518RT NIH_MGC.88 Homo sapiens cDNA clone IMAGE:3875693 3'
6316	19387		8.39	1.0E-03	11528178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6468	19533	32781	1.05	1.0E-03	T87761.1	EST_HUMAN	X493a11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115772 5'
6549	19510		1.99	1.0E-03	AW602595.1	EST_HUMAN	QV3-N11024-250400-17-g05 NN1024 Homo sapiens cDNA
6919	19570	33266	1.78	1.0E-03	L77570.1	NT	Human gene for fourth somatostatin receptor subtype
7359	20329	33978	2.43	1.0E-03	D16828.1	NT	Homo sapiens 955 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7729	20985		2.36	1.0E-03	AJ229042.1	NT	Homo sapiens 955 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
7901	20844	34228	1.71	1.0E-03	U52111.2	NT	protein L18a (RPL18a), Cdc2/Cdkmulin-dependent protein kinase 9 (CDK9), ribosomal CDM protein (CDM), adenosine diphosphate/protein >
7975	20914	34305	3.18	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
8033	20970	34384	0.97	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC.89 Homo sapiens cDNA clone IMAGE:3893276 5'
8221	21190	34599	0.55	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8282	21291	34663	5.32	1.0E-03	AJ251973.1	NT	Homo sapiens partial elastin-1 gene
8483	21451	34899	1.01	1.0E-03	AA122270.1	EST_HUMAN	z867609.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.t1 L1 repetitive element;
8598	21554	34970	2.42	1.0E-03	AF153960.1	NT	Homo sapiens eosinophil-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8773	21740	35161	0.7	1.0E-03	U25937.1	NT	Rattus norvegicus plasma membrane Cdc2x A1Pase isoform 3 (RNC43) gene, 5' flanking region
8941	21907	35331	0.53	1.0E-03	AA001613.1	EST_HUMAN	z822606.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:427810 3'
8941	21907	35332	0.53	1.0E-03	AA001613.1	EST_HUMAN	z822606.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:427810 3'
9295	22261		1.37	1.0E-03	Y11204.1	NT	V carter gene encoding volvoxpsin
9321	22286	35716	0.6	1.0E-03	AW840353.1	EST_HUMAN	CM3-L10079-170200-092-407 L10079 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9435	22399		0.65	1.0E-03	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdz2/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT1R), CDM protein (CDM), adrenoleukodystrophy protein >
9474	22438	35877	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA clone IMAGE:1848673 3' similar to
9474	22438	35878	3.71	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA clone IMAGE:1848673 3' similar to
9855	22882		0.45	1.0E-03	AJ247482.1	EST_HUMAN	q156d01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848673 3' similar to
9868	22893	36354	1.77	1.0E-03	AF011400.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA clone IMAGE:1848673 3' similar to
9868	22893	36355	1.77	1.0E-03	AF011400.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA clone IMAGE:1848673 3' similar to
10179	23104	36585	0.8	1.0E-03	Q01129	SWISSPROT	Thermolysin neopolitana alpha-1 (3-galactosidase (glgA) gene, complete cds
10524	23446	36044	1.55	1.0E-03	AF003529.1	NT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG-40) (DERMATAN SULFATE
10529	23451		0.78	1.0E-03	AF097485.1	NT	PROTEOGLYCAN-II (DSPG)
10679	23801	37096	1.12	1.0E-03	AJ024350.1	EST_HUMAN	Homo sapiens glycin 3 (GFC3) gene, partial cds and flanking repeat regions
11025	23990	37516	1.65	1.0E-03	AW362393.1	EST_HUMAN	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
11025	23990	37517	1.65	1.0E-03	AW362393.1	EST_HUMAN	075608.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643775 3' similar to contains MER39.b1
11102	24052	37585	2.91	1.0E-03	BE170858.1	EST_HUMAN	MER39 MER39 repetitive element ;
11172	24129		2.21	1.0E-03	AJ583847.1	EST_HUMAN	RC1-CT0278-181095-011-609 CT0278 Homo sapiens cDNA
11481	24434		2.59	1.0E-03	AV759649.1	EST_HUMAN	RC1-CT0278-181095-011-609 CT0278 Homo sapiens cDNA
11662	24598	38171	6.18	1.0E-03	AA122270.1	EST_HUMAN	QV3-HT0543-220300-130-ab3 HT0543 Homo sapiens cDNA
12178	25024	38621	6.74	1.0E-03	BE594488.1	EST_HUMAN	073612.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2248448 3' similar to TR-Q26185 O.26185
12653	25915		1.53	1.0E-03	AJ347355.1	EST_HUMAN	PVAT1 GENE ;
12753	25935	31311	7.37	1.0E-03	BE760572.1	EST_HUMAN	AV759649 MDS Homo sapiens cDNA clone MDSDDF11 5'
5765	16857		1.76	9.0E-04	BE06727.1	SWISSPROT	2467609.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to
6398	18456		0.81	9.0E-04	AJ006345.1	NT	contains L1.H1.L1 repetitive element ;
6533	19891	32970	1.08	9.0E-04	P02381	SWISSPROT	60143508.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
10001	22928		1.39	9.0E-04	AB037203.1	NT	60143508.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu
1484	14517		1.04	8.0E-04	X66469.1	NT	60143508.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3872035 5'
3639	16979	28694	0.04	8.0E-04	P07008.1	EST_HUMAN	60143508.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3872035 5'
4209	17238		4.49	8.0E-04	P08547	SWISSPROT	60143508.F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3872035 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4788	17815	30709	2.7	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11480	24423		2.01	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Soares_fetal_NHH19W Homo sapiens cDNA clone IMAGE:377874 3'
11827	24665		2.02	8.0E-04	AJ571090.1	EST_HUMAN	tr85q03.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
1844	14870	27868	1.17	7.0E-04	U41825.1	NT	Homo sapiens CYP17 gene, 5' end
2408	15415	28439	1.01	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2726	16720	28737	1.22	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3293	16346	29266	1.13	7.0E-04	4895170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6215	19289	32522	1.02	7.0E-04	AA516212.1	EST_HUMAN	rs6q12.s1 NCI_CGAP_Lup2 Homo sapiens cDNA clone IMAGE:839718 similar to contains L1.53 L1.1
6862	19719		2.3	7.0E-04	AJ769331.1	EST_HUMAN	repetitive element;
7438	20405		0.78	7.0E-04	AK024445.1	NT	hg56109.x1 Soares_NSIF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10163	23089	36565	0.48	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00035 protein, partial cds
10163	23088	36566	0.48	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11892	24773		1.88	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
11920	24801	38392	2.41	7.0E-04	Z40561.1	EST_HUMAN	HSC9B4072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12921	25497		4.1	7.0E-04	R17356.1	EST_HUMAN	YF13C06.r1 Soares Infant brain N1B Homo sapiens cDNA clone IMAGE:32298 5'
12952	25527		3.97	7.0E-04	6005855	NT	Homo sapiens Rellike-derived POU-domain factor-1 (RPF-1) mRNA
2708	16701		1.03	6.0E-04	BF341380.1	EST_HUMAN	60201333BF1 NCI_CGAP_Bm54 Homo sapiens cDNA clone IMAGE:4149297 5'
3984	17024	29935	1.78	6.0E-04	AI862525.1	EST_HUMAN	W16a11.x1 NCI_CGAP_K4f2 Homo sapiens cDNA clone IMAGE:2402876 3'
4214	17243	30128	3.15	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7830	20778	34166	0.69	6.0E-04	Q16034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
8198	21108		3.16	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 8, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8349	21318		0.69	6.0E-04	H92947.1	EST_HUMAN	y94c11.s1 Soares_pitreal_gland_X38-PF9 Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element;
10339	23263		3.99	6.0E-04	AL046507.2	EST_HUMAN	DKFZp566M2024.1 f888 (synonym: hule1) Homo sapiens cDNA clone DKFZp566M2024
10440	23362	36852	2.19	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN01.20-250400-012-h11 BN01.20 Homo sapiens cDNA
10704	23628		0.65	6.0E-04	AF28478.1	NT	Lysichinus variegatus embryonic blastoderm extracellular matrix protein precursor (ECM3) mRNA, complete cds
11814	24659	38280	2.11	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11863	24774	38360	3.12	6.0E-04	AW013947.1	EST_HUMAN	UJH-BIC-aab-e-09-o-J1 s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708253 3'
12364	25920		5.73	6.0E-04	AW380519.1	EST_HUMAN	RG1-HT0269-281198-012-408 HT0269 Homo sapiens cDNA
652	13718	26640	8.71	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF62)
1501	14534		1.88	5.0E-04	AW851844.1	EST_HUMAN	QVC-CT0225-021098-030-a07 CT0225 Homo sapiens cDNA

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3424	16472	26391	1.28	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014784 3' similar to contains Alu repetitive element;	
3728	18770	26982	0.95	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)	
5549	18546	31588	2.37	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	
8784	19839	33124	5.64	5.0E-04	AA156080.1	EST_HUMAN	z333508.r1 Stragene clone (R637204) Homo sapiens cDNA clone IMAGE:598563 5'	
7802	20563	33924	10.72	5.0E-04	M23904.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds	
							qf1306.x1 Scarsa_placenta_BioWeeks_2NHPB05W Homo sapiens cDNA clone IMAGE:1726819 3' similar to gb:X61602_cde1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element	
8289	21258	34669	4.95	5.0E-04	AI188382.1	EST_HUMAN	op89602.s1 NCI_CGAP_GCB31 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element	
8546	21614	35036	0.92	5.0E-04	AA814519.1	EST_HUMAN	MER22 repetitive element;	
9532	22576	36028	1.97	5.0E-04	AA846545.1	EST_HUMAN	aj56003.s1 Scarsa_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'	
9726	22754	36207	0.92	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT	
9876	22829	36283	0.54	5.0E-04	P29129	SWISSPROT	BIJUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLX PRECURSOR	
9958	22893	36358	4.65	5.0E-04	AW270838.1	EST_HUMAN	x306e02.x1 NCI_CGAP_K411 Homo sapiens cDNA clone IMAGE:2768858 3'	
10640	23652		0.47	5.0E-04	U60871.1	NT	Human familial Alzheimer's disease (S1M2) gene, complete cds	
11320	24270		1.94	5.0E-04	AL048507.2	EST_HUMAN	DKFZp56862024_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp56862024	
12022	18246	31588	10.61	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds	
12295	25753	29753	4.4	5.0E-04	AA588513.1	EST_HUMAN	r11602.s1 NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:913875	
	674	13739	26695	1.46	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
							as170b08.x1 Barstead color HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825	
							Q13825 AL-BINDING PROTEINENYOYL-COA HYDRATASE. ;	
848	13904	26892	1.6	4.0E-04	AI720263.1	EST_HUMAN	as170b08.x1 Barstead color HPLR87 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825	
848	13904	26893	1.6	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AL-BINDING PROTEINENYOYL-COA HYDRATASE. ;	
1461	14494	27468	2.78	4.0E-04	AW763366.1	EST_HUMAN	RC3-C10294-130100-023-f01 C10294 Homo sapiens cDNA	
2095	15112	28133	1.57	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
2143	15160		0.99	4.0E-04	AL046704.1	EST_HUMAN	DKFZp430259_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp430259 5'	
2635	15304	28659	1.66	4.0E-04	O96816	SWISSPROT	SERINC-2 (SILK GUM PROTEIN 2)	
3178	16233	29150	1.8	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced	

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4351	17378	30257	3.23	4.0E-04	AA576831.1	EST_HUMAN	h104010.s1 NCL_CGAP_Cot Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4351	17378	30258	3.23	4.0E-04	AA576831.1	EST_HUMAN	h104010.s1 NCL_CGAP_Cot Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4588	17891	30484	1.4	4.0E-04	AA088324.1	EST_HUMAN	z061c08.s1 Stragene muscle 537209 Homo sapiens cDNA clone IMAGE:582670 3'
5124	18133	31010	4.37	4.0E-04	BE560680.1	EST_HUMAN	h01345895.f1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:387890 5'
5288	16921		1.02	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
7483	20449	33805	1.26	4.0E-04	P48442	SWISSPROT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
7780	20733		0.78	4.0E-04	AL161968.2	NT	A481d03a1 thallina DNA chromosome 4, contig fragment No. 66
7887	20929	34321	0.56	4.0E-04	AU122078.1	EST_HUMAN	AU122078 MAMMA1 Homo sapiens cDNA clone MAMMA1001620 5'
8881	21848	35269	1.07	4.0E-04	BF240712.1	EST_HUMAN	h01878985.f1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4089700 5'
8889	21855	35275	1.56	4.0E-04	N25507.1	EST_HUMAN	y339e12.f1 Soares melanocyte 2N9HM Homo sapiens cDNA clone IMAGE:284142 5'
100489	22878	36442	3.11	4.0E-04	AU255893.1	EST_HUMAN	ov67h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1844341 3'
10200	23125		1.11	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(g17) mRNA, alternatively spliced, complete cds
12864	25729		2.42	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
157	13260	26187	3.45	3.0E-04	AL118428.1	EST_HUMAN	DKFZp781J221.1 781 (synonym: henn2) Homo sapiens cDNA clone DKFZp781J221 5'
197	13268	28226	1.65	3.0E-04	P48259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
881	13838	28895	1.64	3.0E-04	U83997.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1858	14892	27878	1.65	3.0E-04	AI282100.1	EST_HUMAN	q228d03.y1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2028197 5'
1871	14899		1.43	3.0E-04	AI396674.1	EST_HUMAN	h23a02.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2118062 3'
3319	16371	26291	3.17	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3887	17027	28938	2.72	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4088	17120		1.21	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4120	17153		1.33	3.0E-04	BE140608.1	EST_HUMAN	PMO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4854	17871		5.29	3.0E-04	BE163778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5248	18268		1.02	3.0E-04	AL4271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6288	19339		5.73	3.0E-04	AL163291.2	NT	Homo sapiens chromosome 21 segment HS21C081
6863	20119	33432	1.62	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7183	18414	31216	0.71	3.0E-04	AW863881.1	EST_HUMAN	RC4-NN0027-080400-011-b08 NN0027 Homo sapiens cDNA
7847	20794		0.77	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8802	21670	34886	5.18	3.0E-04	P28607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10280	23205	36689	1.44	3.0E-04	AA454055.1	EST_HUMAN	z44608.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:796471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10538	23460	36957	0.58	3.0E-04	AI602139.1	EST_HUMAN	wf75a11.x1 Soares_thymus_NHFFth Homo sapiens cDNA clone IMAGE:2513276 3'
10825	23746	37247	7.72	3.0E-04	AA781201.1	EST_HUMAN	q24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072.609
12245	25957	31315	3.98	3.0E-04	AA228301.1	EST_HUMAN	nc39a04.r1 NCI CGAP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1 L2 L1 repetitive element:
12623	25802	31525	5.33	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
13014	25564		4.33	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: fibro1) Homo sapiens cDNA clone DKFZp547L185 5'
177	13276	26204	1.29	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
478	13551	26479	3.55	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001263 3'
908	13663	26919	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
908	13663	26920	4.01	2.0E-04	M86524.1	NT	Human dystrophin gene
1183	14224		2.52	2.0E-04	AI265021.1	EST_HUMAN	q18a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855032 3' similar to contains MER3 b2 MER3 repetitive element:
1190	14230		2.5	2.0E-04	AI169203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1848	14875		1.19	2.0E-04	AF224268.1	NT	Mus musculus 3' flanking region of Pib3 gene
2194	15209		1.03	2.0E-04	AA478960.1	EST_HUMAN	zu39b05.s1 Soares_ovary_tumor_NH0T Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element:
2381	15582	28601	4.05	2.0E-04	U66051.1	NT	Human granulosa T-cell receptor beta chain TORBV17S1A1T, TORBV2S1, TORBV10S1P, TORBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HV8 re1, TCRBV28S1P, TCRBV34S1, TCRBV14S1, amf8a09.x1 Johnson frontal cortex Homo sapiens cDNA clone IMAGE:1839760 3'
3000	16058	28977	1.13	2.0E-04	AI124529.1	EST_HUMAN	EST130550 IMAGE resequences, MAGP Homo sapiens cDNA
3449	16468	29413	2.44	2.0E-04	BE082317.1	EST_HUMAN	QV32.BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3932	16972	29888	1.21	2.0E-04	AW678441.1	EST_HUMAN	EST130550 IMAGE resequences, MAGP Homo sapiens cDNA
4197	17198		5.41	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PNR2) gene, complete cds
4698	17717	30612	1.21	2.0E-04	H99265.1	EST_HUMAN	yu07e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4698	17717	30613	1.21	2.0E-04	H99265.1	EST_HUMAN	yu07e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4834	17851		1.46	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5070	18080	30961	1.21	2.0E-04	H85683.1	EST_HUMAN	ya68b08.r1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:219927 5' similar to contains L1 repetitive element:
5098	18108	30981	1.85	2.0E-04	AB037697.1	NT	Danio rerio haemoglobin gene, exons 1 to 6, partial cds
5623	18719	31878	1.23	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLG Homo sapiens cDNA clone GLC0U10 3'
9536	19732	31894	1.78	2.0E-04	AI690862.1	EST_HUMAN	iq03b11.x1 NCI CGAP_U03 Homo sapiens cDNA clone IMAGE:2207709 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5843	19833	32117	1.15	2.0E-04	AA296652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6057	19138	32346	0.88	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6368	19435	32676	0.8	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7440	20407		2.84	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000769 5'
7546	20509		0.81	2.0E-04	AW860963.1	EST_HUMAN	QV0-C10387-180300-167-410 CT0387 Homo sapiens cDNA
7882	20828		15.1	2.0E-04	P08546	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7892	20836	34215	1.21	2.0E-04	P54286	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8170	21109	34508	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2023 5'
8170	21109	34509	0.53	2.0E-04	AL043272.2	EST_HUMAN	DKFZp434L2023.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2023 5'
8288	21257	34687	2.13	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8288	21257	34688	2.13	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8627	21595	35015	1.21	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8627	21595	35016	1.21	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8911	21677	35303	1.9	2.0E-04	AF020503.1	NT	Homo sapiens FRAS3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
9095	22081	35486	0.56	2.0E-04	X57931.1	NT	Human immunoglobulin C (mu) and C (delta) heavy chain genes (constant regions)
9889	22642	36100	0.51	2.0E-04	AA725700.1	EST_HUMAN	ai2a12.s1 Soares, Leslie, NHT Homo sapiens cDNA clone 1343578 3'
9774	22716	36170	0.65	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLOGF26.1
10334	23258	36755	1.21	2.0E-04	BE149303.1	EST_HUMAN	RC3-IT0254-151099-011-b05 HT0254 Homo sapiens cDNA
10377	23300	36776	2.74	2.0E-04	AA405777.1	EST_HUMAN	zid06c11.1 Soares, Leslie, NHT Homo sapiens cDNA clone IMAGE:742864 5'
11197	24152	37693	3.56	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01 5'
11510	24451		2.59	2.0E-04	AJ243213.1	NT	Homo sapiens partial E-H14 receptor gene, exons 2 to 5
11635	24872	38136	2.95	2.0E-04	AJ440282.1	EST_HUMAN	W0111.1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
11755	24983	39262	2.49	2.0E-04	AW136740.1	EST_HUMAN	U14-HB1-adm-c-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717180 3'
768	13827	26771	0.81	1.0E-04	H98646.1	EST_HUMAN	yz26c09.s1 Soares, melanocyte ZN0HM Homo sapiens cDNA clone IMAGE:262854 3' similar to contains L1.11 L1 repetitive element
951	14004	26855	2.93	1.0E-04	P48725	SWISSPROT	PERICENTRIN
1078	14121	27072	2.61	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE ;
1116	14160	27710	4.21	1.0E-04	AW013847.1	EST_HUMAN	U14-BIC-aab-e-09-0-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1116	14160	27111	4.21	1.0E-04	AJ013847.1	EST_HUMAN	U1H-B10-4tb-v-09-JUL1.1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1335	14369		3.08	1.0E-04	U62918.1*	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1632	14665		3.19	1.0E-04	AF148905.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds, and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1632	14665		3.19	1.0E-04	AF148905.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds, and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1878	14903	27641	2.37	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2698	15594	28710	1.05	1.0E-04	BE218833.1	EST_HUMAN	h45608.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176668 3'
2698	15594	28711	1.05	1.0E-04	BE218833.1	EST_HUMAN	h45608.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176668 3'
3297	16350	29270	1.14	1.0E-04	Q62203	SWISSPROT	SPIICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3748	16780	29702	0.93	1.0E-04	AI440282.1	EST_HUMAN	h0111.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4089	17123	30017	2.07	1.0E-04	M14042.1	NT	AV647727 GLC Homo sapiens cDNA clone GLOBDD04 3'
4109	17143	30037	1.04	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLOBDD04 3'
5132	18141	31019	1.87	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5132	18141	31020	1.87	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5137	18149	31028	0.92	1.0E-04	AI357166.1	EST_HUMAN	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5960	19045	32244	1.18	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6033	19116	32319	0.32	1.0E-04	T19815.1	EST_HUMAN	q68204.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005675 3'
6033	19116	32320	0.32	1.0E-04	T19816.1	EST_HUMAN	733F Heart Homo sapiens cDNA clone 733
6579	19639	32905	0.9	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.x1 NCL_CGAP_Fr3 Homo sapiens cDNA clone IMAGE:2582
7012	20139	33465	0.96	1.0E-04	AA684691.1	EST_HUMAN	q125a04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:393486 3' similar to gbM97252
7392	20361	33713	12.86	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7821	20361	33713	12.73	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
8328	21297	34712	0.89	1.0E-04	AA8304263.1	EST_HUMAN	q576710.x1 NCL_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985693 3'
8692	22645	36102	3.6102	1.0E-04	AI802620.1	EST_HUMAN	an9408.x1 Scarsene Lung (8637.21) Homo sapiens cDNA clone IMAGE:854654 3'
9703	22658	36111	1.47	1.0E-04	O88969	SWISSPROT	y126a08.x1 Scarsene, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9703	22658	36111	1.47	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
10004	22721		0.83	1.0E-04	T77153.1	EST_HUMAN	y172a08.r1 Scarsene fetal liver spleen 1MFLS Homo sapiens cDNA clone IMAGE:113774 5'
10004	22721	36394	1.89	1.0E-04	10863976	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10539	23461		0.91	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10576	23469	36900	0.91	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG



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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11987	24603		1.74	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11981	24840	38433	1.5	1.0E-04	AB032988.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11989	24870	38472	1.46	1.0E-04	AW269081.1	EST_HUMAN	xx49g12.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12032	24908	38502	1.81	1.0E-04	Q03668	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12032	24908	38503	1.81	1.0E-04	Q03668	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12413	25770		2.4	1.0E-04	BE076369.1	EST_HUMAN	7f29a10.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296088 3' similar to contains L1 L1
13061	25677		1.38	1.0E-04	BE700353.1	EST_HUMAN	repetitive element;
699	13761	26693	2.39	9.0E-06	AA116933.1	EST_HUMAN	PM44.NN0091-180700-004-f11 NN0091 Homo sapiens cDNA
2020	15041	28092	1.09	9.0E-06	AA116933.1	EST_HUMAN	af45c11.at Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
6074	19155	32367	1.58	9.0E-06	AW869218.1	EST_HUMAN	QV4-SN0023-070460-168-604 SN0023 Homo sapiens cDNA
7828	20776	34153	0.67	9.0E-06	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7828	20776	34154	0.67	9.0E-06	AW204958.1	EST_HUMAN	UJH-B11-aeer-4-05-Q-UJ.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9831	22680		2.89	9.0E-06	D89606.1	NT	Homo sapiens gene for cholestyramine type-A receptor, complete cds
9833	22682	36137	3.13	9.0E-06	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 1b5
11472	24415	37984	2.03	9.0E-06	AW073078.1	EST_HUMAN	xa34g05.x1 NCI CGAP_Br18 Homo sapiens cDNA clone IMAGE:2598728 3' similar to contains L1 L2 L1
11938	19155	32367	3.21	9.0E-06	Q60716	SWISSPROT	repetitive element;
							PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12465	25632		3.02	9.0E-06	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDH4, G6b, G6c, G6d, G6e, G6f, BATS, G5b,
822	13880	26831	1.70	8.0E-06	AJ251646.1	NT	CSK2B, BAT4, G4, ApoM, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
865	13921		7.38	8.0E-06	AJ251646.1	NT	Plasm sodium mRNA for beta-1,3 glucanase (gns2 gene)
2861	16019		0.81	8.0E-06	M83575.1	NT	Plasm sodium mRNA for beta-1,3 glucanase (gns2 gene)
4507	17532	30415	0.87	8.0E-06	AW044905.1	EST_HUMAN	Human placenta-derived growth factor A chain (PDGFA) gene, exons only
9101	22067	35493	0.48	8.0E-06	Y11693.1	NT	wy78d04.x1 Soares_NSIF_FR_gw_OT_PA_p_S1 Homo sapiens cDNA clone IMAGE:2564638 3'
11485	24428	37979	3.08	8.0E-06	M69197.1	NT	Mus musculus gene for hexokinase II, exon 1 (end joined CDS)
							Human hepatocellular and hepatoblastoma-related protein (HPR and HPR) genes, complete cds
							repetitive element; NCI CGAP_CCB1 Homo sapiens cDNA clone IMAGE:704563 3' similar to contains Alu
13050	26815		2.74	8.0E-06	AA276333.1	EST_HUMAN	288101.s1 NCI CGAP_CCB1 Homo sapiens cDNA clone IMAGE:704563 3' similar to contains Alu
347	13436	26358	6.11	7.0E-06	AW847445.1	EST_HUMAN	repetitive element; contains element MSK1 repetitive element;
347	13436	26359	6.11	7.0E-06	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
569	13639	26553	1	7.0E-06	L49075.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
569	13639	26554	1	7.0E-06	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
569	13639	26554	1	7.0E-06	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1058	14104	27055	1.47	7.0E-05	Q22949	SWISSPROT	PROBABLY GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2730	15724	28740	4.26	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3172	16227	28143	4.21	7.0E-05	AB009080.1	NT	Dickkopf1 discoidin domain gene for TRFA, complete cds
3714	18757	3714	0.9	7.0E-05	AI432413.1	EST_HUMAN	1q7308.k1 Soares NIH/NIHPU_S1 Homo sapiens cDNA clone IMAGE:2114416 3'
4400	17428	30313	1.53	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4982	17977	30987	0.69	7.0E-05	8945300	NT	Rat cytomegalovirus Maastricht, complete genome
8697	171635	34955	1.27	7.0E-05	AA505582.1	EST_HUMAN	h85g01.s1 NCI_GGAP_B2 Homo sapiens cDNA clone IMAGE:900098 3'
9911	22732	38187	3.34	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragapene (cat836206) Homo sapiens cDNA clone HFBED60
10982	23602	37415	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
10982	23602	37416	0.44	7.0E-05	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
11465	24438	37416	0.44	7.0E-05	10355048	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2041	15060	28080	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2041	15060	28081	1.6	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2594	15595	28613	1.05	6.0E-05	AI65241.1	EST_HUMAN	w54f106.k1 NCI_LGAP_G08 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:U03250 DNA TOPOISOMERASE I (HUMAN)
2894	15690	28707	1.3	6.0E-05	Z84506.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2894	15690	28708	1.3	6.0E-05	Z84506.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA28B10
2825	13743	28069	3.23	6.0E-05	AF058630.1	NT	Homo sapiens monocytic/neutrophil elastase inhibitor gene, complete cds
5107	18117	30690	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTB8ED12 5'
5107	18117	30691	0.93	6.0E-05	AV722942.1	EST_HUMAN	AV722942 HTB Homo sapiens cDNA clone HTB8ED12 5'
6019	19102	32303	3.08	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6019	19102	32304	3.08	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6543	19505	32887	1.45	6.0E-05	N72829.1	EST_HUMAN	w50g11.t1 Soares fetal liver spleen tINFs Homo sapiens cDNA clone IMAGE:246212 5'
7119	20053	33387	0.71	6.0E-05	AA897680.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8421	21930	34800	0.71	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-008 BT0311 Homo sapiens cDNA
8421	21930	34801	0.71	6.0E-05	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-008 BT0311 Homo sapiens cDNA
8789	21753	35175	0.98	6.0E-05	AA150482.1	EST_HUMAN	Z05c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:451726 3' similar to contains element MER28 repetitive element
8791	21753	35180	2.37	6.0E-05	AW809529.1	EST_HUMAN	PM4-NN0050-310300-001-470 NN0050 Homo sapiens cDNA
8927	21983	35321	0.61	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY ACCELERATING FACTOR PRECURSOR
9807	22811	36063	1.11	6.0E-05	P08807	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9807	22811	36064	1.11	6.0E-05	P08807	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9879	22832	36296	1.05	6.0E-05	T94149.1	EST_HUMAN	y628c12.t1 Stragapene lung (h837210) Homo sapiens cDNA clone IMAGE:118062 5'

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10079	23008	38477	0.71	6.0E-05	AW627985.1	EST_HUMAN	h37ad03.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
11100	24060	37584	2.27	6.0E-05	R75633.1	EST_HUMAN	yf59d08.s1 Scores: Placenta N52-IP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element/contains LTR7 repetitive element ;
11847	24720	38318	2.71	6.0E-05	AA044015.1	EST_HUMAN	z65802.r1 Scores: pregnant uterus Nbr1PU Homo sapiens cDNA
12670	25813	31529	16.08	6.0E-05	AW60110.1	EST_HUMAN	MR04T0038-250400-001-09 NT0039 Homo sapiens cDNA
1403	14436	27404	16.34	5.0E-05	AW392086.1	EST_HUMAN	QV4-S1T0234-241189-040-111 S10234 Homo sapiens cDNA
1800	14905	26951	1.15	5.0E-05	8923381	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC58589), mRNA
4004	17043	26951	3.54	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
6603	16669	31670	11.74	5.0E-05	X38555.1	NT	Human MLC1 emb gene for embryonic myosin alkaline light chain, 3'UTR
6107	18166	32405	3.22	5.0E-05	AW653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
6292	19364	32903	0.84	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7553	20516		1.18	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12462	23371		5.88	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12717	25371		4.8	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2818	13329		4.95	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4508	17533	30416	1.68	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4508	17533	30417	1.68	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4910	17627		0.99	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
7127	20060	33388	0.71	4.0E-05	U01947.1	NT	Maeaca mulatta haemoglobin (HP) gene, 5' region
9881	22634		8.43	4.0E-05	AF262635.1	NT	Homo sapiens PP1200 mRNA, complete cds
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10390	22293	36760	0.51	4.0E-05	P11369	SWISSPROT	ENDONUCLEASEI
10771	23662	37169	0.66	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11220	24080	37604	3.91	4.0E-05	AW627946.1	EST_HUMAN	h36d07.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'
12423	25162		2.48	4.0E-05	AW117590.1	EST_HUMAN	x095409.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:746252 3'
13081	25612		2.29	4.0E-05	AA417756.1	EST_HUMAN	z01611.s1 NCI CGAP GC61 Homo sapiens cDNA clone IMAGE:746252 3'
							contains Alu repetitive element/contains element KCR repetitive element ;
681	13744	26671	0.78	3.0E-05	AI249081.1	EST_HUMAN	qf64c10.x1 Scores: fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to
1061	14107	27057	1.89	3.0E-05	AW273851.1	EST_HUMAN	contains Alu repetitive element/contains element KCR repetitive element ;
1133	14176	27125	0.82	3.0E-05	BF037698.1	EST_HUMAN	xx24g03.x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1193	14178	27126	0.82	3.0E-05	BF037698.1	EST_HUMAN	601461463.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
4408	17437	30324	8.15	3.0E-05	BE169211.1	EST_HUMAN	601461463.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
							PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4409	17437	30325	8.15	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit SEQ ID Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4493	17519	30405	2.41	3.0E-05	AA308678.1	EST_HUMAN	EST779998 Placenta   Homo sapiens cDNA similar to p53-associated protein
4493	17518	30406	2.41	3.0E-05	AA308679.1	EST_HUMAN	EST779998 Placenta   Homo sapiens cDNA similar to p53-associated protein
4620	17641		0.7	3.0E-05	AL168302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5937	18733	31865	1.78	3.0E-05	11072102	NT	Mus muscula myosin light chain 2, precursor lymphocyte-specific (MyZb2), mRNA
5937	18971	33267	1.78	3.0E-05	AJ25762.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6921	16671	33268	1.18	3.0E-05	AJ25762.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8230	21199	34609	2.46	3.0E-05	BE793157.1	EST_HUMAN	6016874651 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842262 5'
8698	21663	35087	1.68	3.0E-05	AA238409.1	EST_HUMAN	36260605.61 Stratiagene scizto brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9244	22210	35641	1.64	3.0E-05	AW170682.1	EST_HUMAN	h94908.x1 NC1 CGAP L124 Homo sapiens cDNA clone IMAGE:3006838 3'
9248	22214	35644	1.37	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9252	22218	35649	0.89	3.0E-05	P43361	SWISSPROT	MELANO-ASSOCIATED ANTIGEN 8 (IMAGE-8 ANTIGEN)
9486	22450		0.51	3.0E-05	X03273.1	NT	Human A1u-family cluster 5' of alpha(1)-acid glycoprotein gene
9675	22528	36081	1.22	3.0E-05	AA317562.1	EST_HUMAN	EST784476 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end
10021	23249		3.24	3.0E-05	AJ769331.1	EST_HUMAN	wq36109.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367208 3'
10901	23621	37330	0.89	3.0E-05	G52918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10901	23621	37331	0.89	3.0E-05	G52918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10901	23621	37331	0.89	3.0E-05	G52918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12353	25147		1.49	3.0E-05	L71570.1	NT	Homo sapiens Dlgase syndrome critical region, centromeric end
2332	15943	28665	1.32	2.0E-05	AJ286021.1	EST_HUMAN	q968a11.x1 Soares, NFL_T1_GRC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
2587	15998	28665	1.22	2.0E-05	M131792.1	NT	HUMAN adenovirus desminase (ADA) gene, complete cds
2725	15719		7.98	2.0E-05	AA160562.1	EST_HUMAN	z446a12.r1 Stratiagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to
3154	16211	28728	1.15	2.0E-05	BE066038.1	EST_HUMAN	contains A1u repetitive element; contains element L1, repetitive element;;
3359	16409	29331	0.88	2.0E-05	AF184614.1	NT	RC5-BT03/6-120200-014-H08 BT0319 Homo sapiens cDNA
3362	16431	29350	1.35	2.0E-05	X89211.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3505	16552		0.7	2.0E-05	X95465.1	NT	H.sapiens DNA for endogenous retroviral like element
3620	16690		0.89	2.0E-05	AL039107.1	EST_HUMAN	S.cerevisiae 12.8 kbp fragment of the left arm of chromosome XV
4720	17740		1.1	2.0E-05	BE378471.1	EST_HUMAN	DKFZ566106M_41 666 (lynchpin: hfk22) Homo sapiens cDNA clone DKFZ566106M 5'
5952	18943	32128	1.57	2.0E-05	AJ011712.1	NT	6017238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3408653 5'
6024	19107		0.85	2.0E-05	AF029308.1	NT	Homo sapiens TNNI1 gene, exons 1-11 (and joined CDS)
6082	19162	32373	0.86	2.0E-05	Q13183	SWISSPROT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
							RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA+/DJICARBOXYLATE COTRANSPORTER)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6082	19162	32374	0.88	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6281	19353	32589	0.68	2.0E-05	A1149272.1	EST_HUMAN	q672a02.x1 Soares_placenta_8to9weeks_2NHBP8to9w Homo sapiens cDNA clone IMAGE:1716114 3'
8356	19425	32657	0.49	2.0E-05	P33085	SWISSPROT	similar to containe L1 (3 L1 repetitive element);
6778	19833	33116	2.32	2.0E-05	AA714330.1	EST_HUMAN	CALCIUM-BINDING PROTEIN
7086	20020	33322	1.52	2.0E-05	Y06926.1	NT	hw06012.s1 NCI CGAP SST Homo sapiens cDNA clone IMAGE:1238519 3'
7089	20033	33336	0.94	2.0E-05	A1492860.1	EST_HUMAN	P feliptum mRNA for AARP1 protein, partial
7108	20042		8.62	2.0E-06	A1891026.1	EST_HUMAN	Q02711 PRO-POL-DUTTPASE POLYPROTEIN:
7350	20330	33679	2.22	2.0E-05	AF224262.1	NT	w035107.x1 Soares_Dickgraff6_cdn_NHGD Homo sapiens cDNA clone IMAGE:2522077 3'
7360	20330	33680	2.22	2.0E-05	AF224262.1	NT	Heiderodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7592	20553		0.81	2.0E-05	AF128947.1	NT	Heiderodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
8157	21095	34494	0.5	2.0E-05	U66061.1	NT	Human gemline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV16S1T, TCRBV17S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TORBD1, TORBJ1S1, TORBJ1S2, >
8217	21189	34566	1.25	2.0E-05	A1391040.1	EST_HUMAN	q20h05.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109399 3'
9477	22441	35681	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCRAP2E1500 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCRAP1500
9477	22441	35682	0.52	2.0E-05	BE244840.1	EST_HUMAN	TCRAP2E1500 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCRAP1500
9822	22569	36015	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DEAC-ACCELERATING FACTOR (CD55)
9822	22569	36016	0.57	2.0E-05	P49457	SWISSPROT	COMPLEMENT DEAC-ACCELERATING FACTOR (CD55)
10283	23208	36693	0.57	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS210007
10484	23416	36914	0.87	2.0E-05	BF055693.1	EST_HUMAN	7175g09.y1 NCI CGAP Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10954	23874	37387	2.1	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NHBP8to9w Homo sapiens cDNA clone IMAGE:259570 5'
10954	23874	37388	2.1	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NHBP8to9w Homo sapiens cDNA clone IMAGE:259570 5'

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11006	20042		2.01	2.0E-05	AI391025.1	EST_HUMAN	WQ5507.x1 Soares_Dickgraefae_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11761	23536	37457	1.8	2.0E-05	BE175601.1	EST_HUMAN	HC5-HT0682-280300-072-E12 HT0592 Homo sapiens cDNA
12473	25740		6.5	2.0E-05	BE348228.1	EST_HUMAN	hw21603.x1 NCI_CGAP_Kd111 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:G12832
12826	25727		1.54	2.0E-05	AF275948.1	NT	Q12832 GLYOPHORIN HP22:
12768	25409	31789	1.48	2.0E-05	AF131513.1	EST_HUMAN	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2705	15902	28716	3.2	1.0E-05	AL163282.2	NT	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
3693	16709	28621	1.88	1.0E-05	AF088273.1	NT	Homo sapiens chromosome 21 segment HS21C082
3826	16886		1.17	1.0E-05	AF223391.1	NT	Drosophila melanogaster strain Lemto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3991	17031	29840	10.43	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4201	17232	30119	1.52	1.0E-05	AL163203.2	NT	MOSAIC PROTEIN LGN
4305	17335	30213	1.71	1.0E-05	AA431119.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4857	17304	30783	1.82	1.0E-05	AW419134.1	EST_HUMAN	zw5904.r Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
5005	18019	30807	0.94	1.0E-05	Z18943.1	NT	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856546 3'
5915	19967	33262	1.03	1.0E-05	AJ246003.1	NT	H sapiens repeat region
7023	18360	31281	0.52	1.0E-05	P06548	SWISSPROT	Homo sapiens Spast gene for spastin protein
7285	20063	33370	3.02	1.0E-05	AA841846.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7288	20260	33594	8.81	1.0E-05	4505844	NT	l1 repetitive element ;
7921	20984	34252	0.86	1.0E-05	BF222646.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
8067	20894		1.5	1.0E-05	P10474	SWISSPROT	7p57401.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3649545 3' similar to contains MER10.b3
8265	22232		2.45	1.0E-05	AL163227.2	NT	MER10 repetitive element ;
9415	22380	35818	2.22	1.0E-05	AA452578.1	EST_HUMAN	53KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9642	22566	36035	14.03	1.0E-05	AA236110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9721	22749	36201	0.82	1.0E-05	AV732180.1	EST_HUMAN	z35H12.x1 Soares_total_fetus_Nb24F9_3w Homo sapiens cDNA clone IMAGE:788519 3' similar to gbl02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10198	23123		0.79	1.0E-05	AW510502.1	EST_HUMAN	z40511.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element ;
10198	23123		0.79	1.0E-05	AW510502.1	EST_HUMAN	AV732180 HTF Homo sapiens cDNA clone HTFBIH01 5'
10198	23123		0.79	1.0E-05	AW510502.1	EST_HUMAN	h4d11002.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element ;
10198	23123		0.79	1.0E-05	AW510502.1	EST_HUMAN	h4d11002.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.11 OFR repetitive element ;
10278	23201	36685	1.11	1.0E-05	AW281521.1	EST_HUMAN	UHH-B12-egf-a-68-Q-U1.67 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724389 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10278	23201	36686	1.11	1.0E-06	AW291521.1	EST_HUMAN	UIH-H2-agk-a-08-0-Ui1.1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724358 3'
10544	23466		1.85	1.0E-06	AW468995.1	EST_HUMAN	ha07c10.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
11284	24216	37740	1.79	1.0E-06	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11284	24216	37741	1.79	1.0E-06	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12941	25900	31421	1.43	1.0E-06	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2680	15676	28697	6.9	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246366 3'
3112	16169	26079	4.25	9.0E-06	AI218933.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8tcdweeks_2N6HP8d9W Homo sapiens cDNA clone IMAGE:1759191 3'
3624	16987		2.82	9.0E-06	MB1755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6008	19091	32291	2.31	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7047	20089	33375	0.73	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-ao7 BT0313 Homo sapiens cDNA
7674	20632	33698	0.94	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8053	20990	34388	11.94	9.0E-06	AI034370.1	EST_HUMAN	cx20p01.x1 Soares_fetal_liver_inFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
8807	21774	35200	1.18	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9334	22296	35728	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9334	22299	35728	2.51	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9577	22339	35990	4.44	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11286	24236	37763	3.95	9.0E-06	Q10364	SWISSPROT	POTATIVE SERINE/THREONINE-PROTEIN KINASE C25E12.14C
2935	15906	28596	2.23	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201198-011-H11 CT0283 Homo sapiens cDNA
10998	23818	37326	0.64	8.0E-06	P34083	SWISSPROT	FASOCLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10998	23818	37327	0.64	8.0E-06	P34083	SWISSPROT	FASOCLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
980	14031		2.14	7.0E-06	AA695729.1	EST_HUMAN	ab50710 st Stragene lung (8937210) Homo sapiens cDNA clone IMAGE:354251 3' similar to contains MER20.1 MER20 repetitive element;
1433	14467	27444	3.05	7.0E-06	7682177	NT	Homo sapiens KIA00555 gene product (KIA00555), mRNA
2884	15943		7.04	7.0E-06	AI388252.1	EST_HUMAN	qiv16p09.x1 NCI CGAP_U03 Homo sapiens cDNA clone IMAGE:1981298 3' similar to contains Alu repetitive element;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3576	16621		0.78	7.0E-06	AA386542.1	EST_HUMAN	EST09205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5780	18972		5.16	7.0E-06	AW183141.1	EST_HUMAN	QV2-OT0062-250400-173-H01 OT0062 Homo sapiens cDNA
5902	18989	32179	0.81	7.0E-06	N98845.1	EST_HUMAN	Y65007.r1 Sources_multiple_sclerosis_2NbHNSIP Homo sapiens cDNA clone IMAGE:278412 5'
9141	22107	35533	0.7	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
10280	23185		0.54	7.0E-06	Q81147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	25927	31307	2.83	7.0E-06	BF215972.1	EST_HUMAN	607181522FT NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4093972 5'
2928	15988	28507	1.27	6.0E-06	BE069188.1	EST_HUMAN	QV3-BT0379-010300-105-dt11 BT0379 Homo sapiens cDNA
3708	16749	28564	1.08	6.0E-06	BE069188.1	EST_HUMAN	QV3-BT0379-010300-105-dt11 BT0379 Homo sapiens cDNA
4785	16010	28536	2.35	6.0E-06	Q01468	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
							ox08ed2.x1 Soares_fetal_liver_splice_1NFLS_31 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
4794	17811	30703	2.54	6.0E-06	A040099.1	EST_HUMAN	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5422	18526	31403	1.41	6.0E-06	AF167441.1	NT	PROTEIN XE7
5483	18583	31493	1.05	6.0E-06	Q02040	SWISSPROT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
10275	23140		1.52	6.0E-06	AW801912.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
13041	26582	31700	1.74	6.0E-06	11418167	NT	
6179	18254	32487	3.86	5.0E-06	AL103246.2	NT	
6471	18538	32784	3.98	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8504 Mel protein (M8504 Mel) gene, complete cds
7444	20410	33762	1.14	5.0E-06	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds
8803	21770	35165	0.49	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-H02 CT0302 Homo sapiens cDNA
8803	21770	35166	0.49	5.0E-06	AW856972.1	EST_HUMAN	RC1-CT0302-120200-013-H02 CT0302 Homo sapiens cDNA
10482	23384	35877	7.1	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
12101	24972	35569	2	5.0E-06	Q28039	SWISSPROT	SODIUM-AND CHLORIDE DEPENDENT GLYCINE TRANSPORTER 1 (GLYT-1)
12928	25512	31709	2.14	5.0E-06	A068046.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
							ye46d03.r1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element;
648	13714	26935	6.59	4.0E-06	R10297.1	EST_HUMAN	xc69g12.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu
847	13903	26961	6.33	4.0E-06	AW103554.1	EST_HUMAN	repetitive element; contains element MER21 repetitive element;
1337	14371	27340	4.22	4.0E-06	A0334928.1	EST_HUMAN	1633e06.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1337	14371	27341	4.22	4.0E-06	A0334928.1	EST_HUMAN	1633e06.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1470	14503	27477	2.68	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-H07 NT0046 Homo sapiens cDNA
2274	15287	28313	3.05	4.0E-06	AW015401.1	EST_HUMAN	U1H-B10-aak1-05-0-U1.x1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 5'
3076	16733	28046	0.94	4.0E-06	AF188349.1	NT	Callus gallus Dactyl protein (Dact2) mRNA, complete cds



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3909	16949	28980	1.1	4.0E-06	AJ848285.1	EST_HUMAN	IL3-CT0214-16020-074-B03 CT0214 Homo sapiens cDNA IMAGE:2432562 3' similar to contains element MER22 repetitive element;
4846	17863	30756	2.18	4.0E-06	AI885939.1	EST_HUMAN	W64C10.X1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8844	21811	35230	0.56	4.0E-06	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE SERINE 2
9152	22118	35545	3.18	4.0E-06	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S2A2 to TCRBV12S2 region
10059	22993	36462	1.14	4.0E-06	AJ27285.1	NT	Homo sapiens SP22 gene for secreted phosphoprotein 24 precursor, exons 1-8
11778	23633	37454	2.91	4.0E-06	AB007855.1	NT	Homo sapiens mRNAs, chromosome 1 specific transcript KIAA0486
2173	15189	28209	1.9	3.0E-06	AA700562.1	EST_HUMAN	234b08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2173	15189	28210	1.9	3.0E-06	AA700562.1	EST_HUMAN	234b08.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element;
2276	15288		1.88	3.0E-06	AF202635.1	NT	Homo sapiens PPT200 mRNA, complete cds
2833	15991	28911	0.95	3.0E-06	AA868218.1	EST_HUMAN	4k48g11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains L1.R1 L1 repetitive element;
3279	16333		2.92	3.0E-06	AI857779.1	EST_HUMAN	W122a03.X1 NCI CGAP_JU11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:060734 OG0734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3797	16837	29743	1.12	3.0E-06	BE047094.1	EST_HUMAN	h94412.x1 NCI CGAP_HNT3 Homo sapiens cDNA clone IMAGE:3124151 3'
3797	16837	29744	1.12	3.0E-06	BE047094.1	EST_HUMAN	h94412.x1 NCI CGAP_HNT3 Homo sapiens cDNA clone IMAGE:3124151 3'
4501	17529	30411	0.67	3.0E-06	T60288.1	EST_HUMAN	y67810.t1 Stratigene ovary (#837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4594	17815	30509	4.02	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus)
8284	19556	32592	0.74	3.0E-06	AU159412.1	EST_HUMAN	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
8974	20197	33525	0.56	3.0E-06	Z79478.1	NT	H.sapiens flow-sorted chromosome 6 T cell fragment, SC6A8E5
8974	20197	33526	0.56	3.0E-06	Z79478.1	NT	H.sapiens flow-sorted chromosome 6 T cell fragment, SC6A8E5
7439	20406		1.9	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8419	21388	34798	0.76	3.0E-06	BE562984.1	EST_HUMAN	601336213.F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3690314 5'
9032	21938	35417	0.64	3.0E-06	P07743	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
12931	25317		6.4	3.0E-06	AW385282.1	EST_HUMAN	RCOL10001-281189-011-A03 L10001 Homo sapiens cDNA
203	13304		3.24	2.0E-06	P64369	SWISSPROT	HOMEBOX PROTEIN G005600
1572	14605		5.6	2.0E-06	P21414	SWISSPROT	POLYPOXYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2387	16395	28420	2.84	2.0E-06	AI872198.1	EST_HUMAN	w604a03.x1 NCI CGAP_Ki611 Homo sapiens cDNA clone IMAGE:2287068 3' similar to contains MER30.b1 MER30 repetitive element;
2474	15478	28501	2.73	2.0E-06	P04626	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2673	15574	28594	1.94	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3531	16377	28600	1.29	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB03 3'
3774	16816	29726	1.95	2.0E-06	AA173518.1	EST_HUMAN	Z029205.t1 Stratiotes ovata cDNA clone IMAGE:595232 5'
3783	16824	29732	0.67	2.0E-06	AA173518.1	EST_HUMAN	UH-H83-ak-g-05-Q1.s1 NCI CGAP_S145 Homo sapiens cDNA clone IMAGE:2736176 3'
3789	16830	29736	1.74	2.0E-06	AB030886.1	NT	Mus musculus gene for odorant receptor A16, complete cds or3401.s1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568600 3' similar to contains Alu repetitive element;
6208	19282		0.9	2.0E-06	AA974932.1	EST_HUMAN	65105.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2060241 3' similar to TRQ13537
6241	19314	32544	0.93	2.0E-06	AI539448.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
6581	19841	32909	5.37	2.0E-06	AB1819424.1	EST_HUMAN	W95004.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410053 3'
8250	21219		0.81	2.0E-06	AW869223.1	EST_HUMAN	MR3-SN0067-120400-002-02 SN0067 Homo sapiens cDNA
8426	21395	34806	0.63	2.0E-06	T12238.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
			0.61	2.0E-06	AA772497.1	EST_HUMAN	2127611.s1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9188	22154		1.83	2.0E-06	H62051.1	EST_HUMAN	Y07404.t1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to Q0X74929
9200	22166	35596	0.87	2.0E-06	AF003529.1	NT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9571	22533	35983	0.87	2.0E-06	AF003529.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
9571	22533	35984	0.87	2.0E-06	AF003529.1	NT	Homo sapiens glycylalanine 3 (GPC3) gene, partial cds and flanking repeat regions
9591	22553		0.48	2.0E-06	AI473450.1	EST_HUMAN	J18g10.x1 NCI CGAP_Gask Homo sapiens cDNA clone IMAGE:2141730 3'
10059	22986	36454	0.92	2.0E-06	N30576.1	EST_HUMAN	Y06603.s1 Soares_placenta_8cbweeks_21bHP809W Homo sapiens cDNA clone IMAGE:25712 3'
10278	23204		0.61	2.0E-06	AV746969.1	EST_HUMAN	AV746969 NPC Homo sapiens cDNA clone NPCAXD05 5'
12111	24981	38581	2.21	2.0E-06	O15653	SWISSPROT	PYRIN (MARENOSTRIN)
12111	24981	38582	2.21	2.0E-06	O15653	SWISSPROT	PYRIN (MARENOSTRIN)
12540	26928	31308	2.97	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
			3.02	1.0E-06	O76092	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
36	13156	26557	1.96	1.0E-06	AF064394.1	NT	Mus musculus DMM45E protein (DMM45E) mRNA, complete cds
658	13724	26849	1.61	1.0E-06	P09126	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1445	14478	27454	1.67	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1527	14590	27631	1.22	1.0E-06	AA034141.1	EST_HUMAN	206a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1576	14609	27682	1.22	1.0E-06	AA034141.1	EST_HUMAN	206a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1576	14609	27683	1.22	1.0E-06	AA034141.1	EST_HUMAN	206a12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1587	14620		1.36	1.0E-06	P27925	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2010	15031	28040	5.53	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2010	15031	28041	5.53	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4397	17425	30309	13.21	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5146	18155	31034	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5146	18155	31035	1.23	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5383	18468	31339	4.63	1.0E-06	BF33015.1	EST_HUMAN	MR1-BT0800-330700-002-c08 BT0800 Homo sapiens cDNA
5388	18491	31387	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-c04 FN0004 Homo sapiens cDNA
5388	18491	31388	1.01	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-c04 FN0004 Homo sapiens cDNA
5582	18649	31592	1.24	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5892	18980		0.64	1.0E-06	BE06527.1	EST_HUMAN	GM0-BT0281-031196-087-k04 BT0281 Homo sapiens cDNA
7056	20078	33387	6.4	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA1(A) PHASE CHAIN PRECURSOR
8018	20095		0.50	1.0E-06	BE168330.1	EST_HUMAN	IL5-HT0730-020500-074-q01 HT0730 Homo sapiens cDNA
8334	21303		0.75	1.0E-06	AA912623.1	EST_HUMAN	q129-c08.at Soares_NFL_T_GBC_S1 Homo sapiens cDNA IMAGE:1624878 3'
8616	21584	35000	1.05	1.0E-06	AI847010.1	EST_HUMAN	q054-c02.x1 NCL_OGAP_C08 Homo sapiens cDNA IMAGE:1826842 3'
							q123-c06.x1 NCL_OGAP_Lyrb Homo sapiens cDNA IMAGE:1892435 3' similar to contains element
8833	21800	35219	1.26	1.0E-06	AI287878.1	EST_HUMAN	MIR repetitive element;
9659	22816	36270	1.15	1.0E-06	NT74695.1	EST_HUMAN	zaf55001.at Soares fetal liver spleen TNFIS Homo sapiens cDNA IMAGE:286472 3'
9734	22762	36217	0.85	1.0E-06	Q36576	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
10041	22968	36434	3.97	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10041	22968	36435	3.97	1.0E-06	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
10035	23012	36485	4.9	1.0E-06	AA132611.1	EST_HUMAN	zot17608.t1 Stralagene cdon (f837204) Homo sapiens cDNA IMAGE:587174 5'
10147	23073		3.89	1.0E-06	AA449257.1	EST_HUMAN	z04611.at Soares_biol_fetus_N82HF8_0w Homo sapiens cDNA IMAGE:785493 3' similar to
10854	23774		2.02	1.0E-06	AA163203.2	NT	g05D26128 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11980	24839		3.14	1.0E-06	AW890941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12672	15031	28040	1.71	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12672	15031	28041	1.71	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
360	13447	28374	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
360	13447	28375	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8750	21718		0.59	9.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C086
8838	21804		0.43	9.0E-07	AA448276.1	EST_HUMAN	z063101.at Soares_testis_NHT Homo sapiens cDNA IMAGE:782833 3'
11577	24515	38070	4.11	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4804	17821	30716	3.87	8.0E-07	AI288568.1	EST_HUMAN	q82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4804	17821	30716	3.87	8.0E-07	AI288568.1	EST_HUMAN	q82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5888	18073		8.55	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8335	21304		11.24	8.0E-07	AF136416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11843	24823		5.78	8.0E-07	T07770.1	EST_HUMAN	EST08680 Fetal brain, Stragelena (G4630206) Homo sapiens cDNA clone HFBN89
12183	25031		9.17	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C0880
5597	18593	31683	0.73	7.0E-07	6005700.NT	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5597	18593	31684	0.73	7.0E-07	6005700.NT	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1928	14952	27948	4.98	8.0E-07	AW865588.1	EST_HUMAN	CM8-CT0277-221090-024-e11 CT0277 Homo sapiens cDNA
2500	15503	29530	5.38	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tetrasin X (tetrasin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes. >
3598	17036		2.25	6.0E-07	P41479	SWISSPROT	HYPOPHYSICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
9487	22481	35902	2.17	6.0E-07	BF001867.1	EST_HUMAN	7g4f07.x1 NCL CGAP_C016 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR-075920 O75920 4FBL. ;
12442	25880		3.45	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-260300-121-h12 NN1028 Homo sapiens cDNA
328	13417		0.99	5.0E-07	AI831893.1	EST_HUMAN	wh4f10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1090	14108		2.45	5.0E-07	AA380680.1	EST_HUMAN	EST09315 Supr cells Homo sapiens cDNA 5' end
3044	16101		0.66	6.0E-07	AI831893.1	EST_HUMAN	wh4f10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4878	17697	30584	1.16	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6242	18915	32545	1.23	5.0E-07	U66067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7266	20001	33300	1.68	5.0E-07	AI393981.1	EST_HUMAN	ig06b05.x1 NCL CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7265	20001	33301	1.68	5.0E-07	AI393981.1	EST_HUMAN	ig06b05.x1 NCL CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element; contains element A3R repetitive element ;
7571	20584	33992	15.74	5.0E-07	AW070885.1	EST_HUMAN	xc371602.x1 NCL CGAP_Br18 Homo sapiens cDNA clone IMAGE:2668362 3' similar to gb-X16341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8618	21988	35002	0.87	5.0E-07	Q8WUQ1	SWISSPROT	ADAMTS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1) ;
8835	21988		1.86	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR ;
10732	23654	37147	5.39	5.0E-07	AI080587.1	EST_HUMAN	CM-BT176-220498-014 BT178 Homo sapiens cDNA
11845	24728	35314	3.52	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11906	24787		2.12	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
12842	25780		4.14	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0393-210400-204-b12 CT0393 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4024	17062	20984	1.81	4.0E-07	AW009602.1	EST_HUMAN	w84f05.x1 NCI_CGAP_Os3 Homo sapiens cDNA clone IMAGE:2504697 3'
7384	20354		0.81	4.0E-07	AL27265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7482	20448	33804	1.3	4.0E-07	Q8ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HDB) [HISTONE DEACETYLASE MHDAT1]
7482	20448	33805	1.3	4.0E-07	Q8ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HDB) [HISTONE DEACETYLASE MHDAT1]
8255	21224	34634	0.63	4.0E-07	AL169207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9408	22371	35806	5.82	4.0E-07	AW419134.1	EST_HUMAN	xy4g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2866548 3'
10488	23408	36904	0.46	4.0E-07	BE001975.1	EST_HUMAN	601670748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3659651 5'
10488	23408	36905	0.48	4.0E-07	BE001975.1	EST_HUMAN	601670748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3659651 5'
10688	23610	37105	0.47	4.0E-07	AL169218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11284	24234	37760	2.6	4.0E-07	AT65528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11284	24234	37761	2.6	4.0E-07	AT65528.1	EST_HUMAN	w81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
11555	24455		2.72	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
441	13515	28448	4.77	3.0E-07	U18719.1	NT	Human microtubulin-associated glycoprotein (MAP2) gene, putative promoter region and alternatively spliced untranslated exons
885	13553	26597	3.11	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1375	14409	27379	2.82	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1600	14663		2.45	3.0E-07	M64857.1	NT	Human Igk subgroup 1 germ-line gene, exons 1 and 2, V-region D18 allele
2092	15080		1.07	3.0E-07	AA529703.1	EST_HUMAN	n56b06.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1, L1 L1 repetitive element
2296	15308	28330	2.96	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2477	15481	28505	6.03	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2477	15481	28506	6.03	3.0E-07	BE005077.1	EST_HUMAN	MFO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3047	16104	29018	0.8	3.0E-07	T84704.1	EST_HUMAN	y45012.r1 Sources fetal liver spleen 1NF.L.S Homo sapiens cDNA clone IMAGE:111695 5'
3173	16228	29144	1.71	3.0E-07	P38739	SWISSPROT	HYPOPHOSPHATASE 63.8 KD PROTEIN IN GUTTI-RIMI INTERGENIC REGION PRECURSOR
4706	17727		0.74	3.0E-07	P20740	SWISSPROT	AV0502ATN1 PRECURSOR (OVONACROGLOBULIN)
4758	17778	30673	8.88	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLC0001 3'
4758	17778	30708	0.81	3.0E-07	AT97238.1	EST_HUMAN	w856b12.x1 Sources_NFL_T_GSG_S1 Homo sapiens cDNA clone IMAGE:2347567 3'
5103	18113	30885	2.02	3.0E-07	T57850.1	EST_HUMAN	yct14h03.e1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gbM402982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5103	18113	30886	2.02	3.0E-07	T57850.1	EST_HUMAN	yct14h03.e1 Striatagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gbM42952 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5749	18843	32026	9.02	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6085	19165	32377	0.73	3.0E-07	O42280	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6891	18914		5.12	3.0E-07	AA815176.1	EST_HUMAN	cc04c10.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7752	20705	34074	3.26	3.0E-07	AW787168.1	EST_HUMAN	QV1-LJM036-203030-115-02 UM0036 Homo sapiens cDNA
7925	20868		1.09	3.0E-07	AI591085.1	EST_HUMAN	W2811.1.x1 NCI CGAP_O435 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element;
13083	22614		7.27	3.0E-07	AJ13252.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
31	13161	28051	4.19	2.0E-07	AF262888.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
155	13258	28185	8.84	2.0E-07	L77688.1	NT	Homo sapiens D1Gec096 syndrome critical region, telomeric end
155	13258	28186	6.64	2.0E-07	L77688.1	NT	Homo sapiens D1Gec096 syndrome critical region, telomeric end
183	13283	28209	152.51	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vesicular) actin gene, complete cds
748	13810	28751	1.29	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
749	13810	28752	1.28	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
760	13820		0.87	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
942	13886	28947	3.12	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:650869 3' similar to cpl3.1860 GYOPHORIN A PRECURSOR (HUMAN) contains Alu repetitive element;
943	13996	28948	7.18	2.0E-07	T83042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (8837210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element;
1167	14208	27162	1.16	2.0E-07	Q28768	SWISSPROT	I16 AUTOANTIGEN
1604	14838	27613	2.35	2.0E-07	Q03701	SWISSPROT	HYPOHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3633	16876		0.88	2.0E-07	BF131397.1	EST_HUMAN	60181.60761 NIH MGCC 58 Homo sapiens cDNA clone IMAGE:404891 5'
3700	16743	28656	17.84	2.0E-07	AF126348.1	EST_HUMAN	Homo sapiens cavellin 1 (CAV1) gene, exon 3 and partial cds
4195	17226	30115	1.42	2.0E-07	AI873553.1	EST_HUMAN	wk20hp02.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2412919 3'
5417	18520	31397	1.71	2.0E-07	AW898099.1	EST_HUMAN	RC3-NN0066-280400-021-g11 NN0066 Homo sapiens cDNA
6702	25665	33037	0.9	2.0E-07	AW448968.1	EST_HUMAN	UJH-B15-aka-b-1-Q1-J1 s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:1839177 3'
6820	18874	33163	1.63	2.0E-07	AJ208716.1	EST_HUMAN	q56005.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1061938 similar to contains Alu repetitive element
6832	18885	33178	0.81	2.0E-07	AA572953.1	EST_HUMAN	nm33a06.s1 NCI CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061938 similar to contains Alu repetitive element
8813	21760		4.23	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8043	22009	35430	0.89	2.0E-07	AA035188.1	EST_HUMAN	2427609.s1 Soares, pregnant, uterus, NbhPU Homo sapiens cDNA clone IMAGE:471808 3'
10119	23045		1.8	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10630	23552	37052	6.11	2.0E-07	AW862507.1	EST_HUMAN	CN44-NN0063-280300-124-e08 NN0063 Homo sapiens cDNA
10855	23775	37272	0.92	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10855	23775	37273	0.82	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12138	25503		2.86	2.0E-07	BE153717.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
							PMO-H10339-260100-006-H07 H10339 Homo sapiens cDNA
12224	25781		1.86	2.0E-07	AI732462.1	EST_HUMAN	zn58h11.05 Stragarene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:655029 3' similar to contains THR-b2 THR repetitive element ;
1104	14148		1.46	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2838	14568	27629	2.95	1.0E-07	P09258	SWISSPROT	GLYCOPROTEIN GPV
3767	14148		1.25	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4321	17350	30234	3.01	1.0E-07	AV178662.1	EST_HUMAN	AV178662 GLC Homo sapiens cDNA clone GLCFNF04.5'
4321	17360	30235	3.01	1.0E-07	AV178662.1	EST_HUMAN	AV178662 GLC Homo sapiens cDNA clone GLCFNF04.5'
6652	19709	32886	0.82	1.0E-07	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathectin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
7050	20072	33376	4.44	1.0E-07	BE047871.1	EST_HUMAN	1243008.Y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7050	20072	33379	4.44	1.0E-07	BE047871.1	EST_HUMAN	1243008.Y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7735	20580	34054	9.42	1.0E-07	N55081.1	EST_HUMAN	W43007.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7910	20553	34240	0.99	1.0E-07	BF37609.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7910	20553	34241	0.98	1.0E-07	BF37609.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7940	20832	34272	1.27	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8558	21526	34944	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8558	21526	34945	2.28	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9306	22271	35702	2.83	1.0E-07	AA693578.1	EST_HUMAN	25110.S1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9306	22271	35702	2.83	1.0E-07	AA693578.1	EST_HUMAN	ADAMTS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9825	22559	36018	0.96	1.0E-07	P57110	SWISSPROT	h28h08.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
8975	22802	36868	0.53	1.0E-07	BE327843.1	EST_HUMAN	MER18 repetitive element ;
10296	23221	36705	2.5	1.0E-07	BF674524.1	EST_HUMAN	60713774.F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:4274426 5'
10304	23229	36712	1.26	1.0E-07	AA386311.1	EST_HUMAN	EST1186094 Brain IV Homo sapiens cDNA
10831	23752		2.53	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
							h53a11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR-095722 095722
12500	25766	31517	4.03	1.0E-07	BE048770.1	EST_HUMAN	DJ1163J1.1 ;
12634	25320		1.59	1.0E-07	X64467.1	NT	H1.sapiens ALAD gene for porphobilinogen synthase
12763	25423		1.89	1.0E-07	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
7498	20463	33623	0.84	8.0E-08	AI593622.1	EST_HUMAN	h51506.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23172	36661	2.18	9.0E-08	AF794819.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cDABF804 5'
11515	24456	38008	1.46	9.0E-08	AI891052.1	EST_HUMAN	w33907.x1 NCJ_GGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
11977	24654	38452	2.32	9.0E-08	AL163301.2	NT	OFR repetitive element;
12463	25212		3.51	9.0E-08	AJ251973.1	EST	Homo sapiens chromosome 21 segment HS21C101
609	15845		2.97	8.0E-08	AI911352.1	EST_HUMAN	wd1805.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
1052	14098		0.77	8.0E-08	BE705499.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
3555	16601		2.07	8.0E-08	BE765499.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
9091	22057	35482	3.38	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9091	22057	35483	3.38	8.0E-08	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9985	22812	36377	2.8	8.0E-08	AW970693.1	EST_HUMAN	EST362778 IMAGE reassesses, IMAGE Homo sapiens cDNA
10928	23848	37363	0.46	8.0E-08	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
11576	24513		2.93	8.0E-08	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
81	13187	26121	4.07	7.0E-08	Q02387	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1363	14397	27368	17.17	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3559	16634	29553	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3559	16634	29554	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3649	16989	29604	0.9	7.0E-08	P01608	SWISSPROT	IG KAPPA CHAIN VJ REGION OU
3949	16989	29605	0.9	7.0E-08	P01608	SWISSPROT	IG KAPPA CHAIN VJ REGION OU
11165	24123		2.33	7.0E-08	AI635743.1	EST_HUMAN	zong3.PT1.A3 contig Homo sapiens cDNA 3'
11982	24859	38454	4.32	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
12899	16634	29553	1.55	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12899	16634	29554	1.55	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16541		1.9	7.0E-08	AI131016.1	NT	Homo sapiens SCL gene locus
818	13876	26824	4.23	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
818	13876	26825	4.23	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2371	15379	28403	2.72	6.0E-08	BE144398.1	EST_HUMAN	MRO-HT1065-191165-004-g09 HT1066 Homo sapiens cDNA
4276	17305	30184	1.28	6.0E-08	AL165248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8162	21100	34469	0.49	6.0E-08	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene is glucose-6-phosphata dehydrogenase (G6PD) gene, complete cds s
8283	21262		0.74	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9683	22636		0.54	6.0E-08	AA827075.1	EST_HUMAN	ab56605.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains MER12 b3 MER12 repetitive element ;
11744	24629	38208	1.91	6.0E-08	P41359	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
85	13201	28125	3.22	5.0E-08	AL163303.2	NT	ENDONUCLEASE]
2245	15259	28286	1.95	6.0E-08	AA493951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
12185	25022		10.16	5.0E-08	P06981	SWISSPROT	h103309.51 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element
12982	25162	31614	1.63	5.0E-08	AW851878.1	EST_HUMAN	COMPLEMENT C2 PRECURSOR (C3/G5 CONVERTASE)
1775	14804	27769	1.07	4.0E-08	P25723	SWISSPROT	OYA-C10225-131099-0344-412 C10225 Homo sapiens cDNA
1775	14804	27790	1.07	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3077	16134		0.95	4.0E-08	AI078417.1	EST_HUMAN	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
3934	16974	29888	0.78	4.0E-08	U82668.1	NT	o205602.x1 Scores: fetal_liver, spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674498 3' similar to contains Alu repetitive element
6545	19608	32698	0.91	4.0E-08	P52824	SWISSPROT	Homo sapiens six3 gene, alternatively spliced products, complete cds
9150	22116	35542	0.6	4.0E-08	O15393	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
9494	22458	35898	1.32	4.0E-08	L42571.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
10003	22830		0.82	4.0E-08	P08547	SWISSPROT	Oricellulus griseus ribosomal transcription factor (UBP2) mRNA, complete cds
10693	23615		0.65	4.0E-08	AI016342.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10762	23674	37171	3.67	4.0E-08	AI050027.1	EST_HUMAN	q73812.51 Scores: total_fetus_N2ZH5_5w Homo sapiens cDNA clone IMAGE:1622903 3'
11411	24355	37869	1.51	4.0E-08	AA393827.1	EST_HUMAN	an22410.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1698411 3' similar to contains Alu repetitive element
11411	24355	37890	1.61	4.0E-08	AA393827.1	EST_HUMAN	repetitive element contains element MER22 repetitive element ;
11426	24370	37908	3.11	4.0E-08	BF692493.1	EST_HUMAN	G505579 NAICA-K-EXCHANGER ;
12190	25007		4.86	4.0E-08	W76158.1	EST_HUMAN	G505579 NAICA-K-EXCHANGER ;
12830	25448		1.84	4.0E-08	AI343353.1	EST_HUMAN	Z70608.1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
3438	16485	29404	0.84	3.0E-08	M83242.1	NT	G505579 NAICA-K-EXCHANGER ;
5592	18787	31658	3.06	3.0E-08	BE018348.1	EST_HUMAN	G605579 NAICA-K-EXCHANGER ;
							602248024F1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:4333300 5'
							602248024F1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:4333300 5'
							z46503.1 Scores: fetal_heart_NbH119W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
							tb95a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3
							MER18 MER18 repetitive element ;
							Macaca fascicularis apolipoprotein A-1 gene, complete cds
							b679a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q92158 Q92158
							SYNTAXIN 17 ;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7168	18399	31245	4.23	3.0E-08	AF192737.1	EST_HUMAN	q378f1.1;5 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:1944045 5'
7787	20740	34113	1.41	3.0E-08	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8025	20962		3.85	3.0E-08	AI436352.1	EST_HUMAN	hs3h09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TRC113337 Q13637 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
10259	23183		0.57	3.0E-08	AF065068.1	NT	Homo sapiens MHO class 1 region
12157	25013		2.76	3.0E-08	R18420.1	EST_HUMAN	XP0204.1.1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element
207	13308		10.84	2.0E-08	AW302988.1	EST_HUMAN	xs3708.x1 NCL CGAP_Luz8 Homo sapiens cDNA clone IMAGE:2767139 3'
230	13330		8.83	2.0E-08	AA425598.1	EST_HUMAN	zw4807.r1 Soares_tetua_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:779317 5' similar to contains Alu repetitive element/contains element MER15 repetitive element ;
497	13569	26402	1.3	2.0E-08	AF108349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
661	13727	28651	8.73	2.0E-08	AW88438.1	EST_HUMAN	MRO-OT0080-240200-001-q08 OT0080 Homo sapiens cDNA
681	13727	28652	8.73	2.0E-08	AW88438.1	EST_HUMAN	MRO-OT0080-240200-001-q08 OT0080 Homo sapiens cDNA
992	14044		17	2.0E-08	BE280477.1	EST_HUMAN	601165321.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1349	14381	27350	1.93	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1755	14784		1.87	2.0E-08	BE734871.1	EST_HUMAN	G01570493.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1872	14897		3.57	2.0E-08	AW270271.1	EST_HUMAN	xs43f1.1.x1 NCL CGAP_JN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2560	15552		1.7	2.0E-08	K00216.1	NT	Sheep Hic-RNA-GUG
3221	16276	29200	8.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3221	16276	29201	8.15	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3873	16512		1.62	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012403 ST0197 Homo sapiens cDNA
4104	17138	30033	0.88	2.0E-08	U32688.1	NT	Homo sapiens atox gene, alternatively spliced products, complete cds
4434	17481		1.2	2.0E-08	AA145940.1	EST_HUMAN	sa26607.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element ;
4994	18009		2.97	2.0E-08	AW572881.1	EST_HUMAN	hs7708.x2 NCL CGAP_QML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element
5719	18813	31892	1.25	2.0E-08	AA613204.1	EST_HUMAN	xs30204.x1 NCL CGAP_Ov28 Homo sapiens cDNA clone IMAGE:2565462 3' similar to contains MER18.b3
5332	19018	32213	0.99	2.0E-08	AW089024.1	EST_HUMAN	MER18 POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
6337	21306	34721	1.69	2.0E-08	P11072	SWISSPROT	POL R MLY18 repetitive element ;
8447	21416	34828	1.47	2.0E-08	AA480121.1	EST_HUMAN	ad0208.s1 Stragogene fetal retina 637202 Homo sapiens cDNA clone IMAGE:839674 3'
9440	22404		0.77	2.0E-08	AUT39978.1	EST_HUMAN	AUT39978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10886	23806	37310	0.8	2.0E-08	N78097.1	EST_HUMAN	yw7202.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.53 LTR1 repetitive element;
10889	23806	37311	0.8	2.0E-08	N78097.1	EST_HUMAN	yw7202.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.53 LTR1 repetitive element;
12472	25221		1.88	2.0E-08	AL163284.2	NT	LTR1.53 LTR1 repetitive element;
12082	25693		1.4	2.0E-08	11431676	NT	Homo sapiens chromosome 21 segment HS21C084
1510	15870	27613	1.42	1.0E-08	P31792	SWISSPROT	Homo sapiens hypodermal protein FLJ11342 (FLJ11342), mRNA
1750	14819	27804	2.12	1.0E-08	AF125348.1	NT	POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2067	15084		2.49	1.0E-08	BE141959.1	EST_HUMAN	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
3206	16281	29161	1.19	1.0E-08	BE246844.1	EST_HUMAN	PM2.H10130-160999-001-112 HT1030 Homo sapiens cDNA
3206	16281	29161	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Bay/ox-HGSC project=TCBA Homo sapiens cDNA clone TCBAP-5232
3206	16281	29161	1.19	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Bay/ox-HGSC project=TCBA Homo sapiens cDNA clone TCBAP-5232
5680	18775	31847	4.5	1.0E-08	AJ010770.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase, isoform 1-50
8046	20883	34380	0.98	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8359	21338	34748	0.47	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8466	21435	34852	0.56	1.0E-08	AF24659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8466	21435	34853	0.56	1.0E-08	AF24659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8892	21559	35280	1.89	1.0E-08	AJ015304.1	EST_HUMAN	033a05.s1 Soares: testis. NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9559	22521		0.46	1.0E-08	P08593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9560	22522	35970	0.68	1.0E-08	BE072572.1	EST_HUMAN	PM2.BT0546-210100-004-402 BT0546 Homo sapiens cDNA
10325	23249	36726	0.81	1.0E-08	P78110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10921	23841	37357	0.87	1.0E-08	P98063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11844	24591	38149	3.4	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1
12129	24998	38602	1.5	1.0E-08	P29315	SWISSPROT	Homo sapiens major histocompatibility locus class III region
12129	24998	38603	1.5	1.0E-08	P29315	SWISSPROT	RIBONUCLEASE INHIBITOR
12569	25291		3.12	1.0E-08	X57155.1	NT	RIBONUCLEASE INHIBITOR
12940	25520		1.88	1.0E-08	X57155.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4271	30779	30779	4.15	9.0E-09	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4271	17300	30180	4.15	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C076
10422	23344		0.53	9.0E-09	T97950.1	EST_HUMAN	yw8a12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121918 3'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6828	19688		1.59	8.0E-09	AI270615.1	EST_HUMAN	q880t1.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1978964 3' similar to contains L1.13 L1 repetitive element;
7479	20445	33801	7.91	8.0E-09	AI183500.1	EST_HUMAN	cd42607.x1 Scores_fetal heart NBH16W Homo sapiens cDNA clone IMAGE:132164 3' similar to contains MSR1.11 MSR1 repetitive element;
8333	21302	34719	3.04	8.0E-09	AI900189.1	EST_HUMAN	CMO-NT1004-103000-273-400 NT1004 Homo sapiens cDNA
9340	22305		2.64	8.0E-09	AA58892.1	EST_HUMAN	op74d03.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682576 3'
3821	16684		1.91	7.0E-09	D06842.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4034	17072		1.22	7.0E-09	U60871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8234	21203		0.56	7.0E-09	BF108765.1	EST_HUMAN	7145910.x1 Scores_NSIF_F8_3W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER23.b2 MER28 repetitive element;
8392	21351		0.91	7.0E-09	AA256220.1	EST_HUMAN	z80cd5.1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
9815	22559	36008	3.08	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10543	23465	36560	1.17	7.0E-09	BE254950.1	EST_HUMAN	60111173.F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10711	23633		0.59	7.0E-09	AA058826.1	EST_HUMAN	zf59a07.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:381196 3' similar to contains L1.12 L1 repetitive element;
11032	23988		3.85	7.0E-09	T07950.1	EST_HUMAN	x558a12.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2182	15178		0.98	6.0E-09	AL040439.1	EST_HUMAN	DKFZ49434C0514_r1 434 (synonym: Ites3) Homo sapiens cDNA clone DKFZ49434C0514 5'
4059	17095	29990	0.98	6.0E-09	AA557940.1	EST_HUMAN	nh7a1a1.s1 NCL CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.12 L1 repetitive element;
5017	18031	30917	5.44	6.0E-09	BE108421.1	EST_HUMAN	PM4-H10527-162200-001-H05 H10527 Homo sapiens cDNA
5464	18556	31467	9.55	8.0E-09	AW185784.1	EST_HUMAN	x885h08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8022	21888	38315	0.88	8.0E-09	BE161653.1	EST_HUMAN	MR3-H10446-260300-201-H12 H10446 Homo sapiens cDNA
8531	22494	35942	2.12	8.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10639	23551		4.42	6.0E-09	AF200423.2	NT	Homo sapiens testis-specific kinase substrate1 (TSKS) gene, complete cds
1413	14448	27418	4.43	5.0E-09	BE149284.1	EST_HUMAN	RC2-H10252-120200-014-H10 H10252 Homo sapiens cDNA
1870	14895	317894	1.02	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6550	19811	32872	2.31	5.0E-09	AA359454.1	EST_HUMAN	EST168746 Fetal lung II Homo sapiens cDNA 5' end
							Human geminins T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRCBV251P, TCRCBV2251A2N1T, TCRCBV951A1T, TCRCBV751A1N2T, TCRCBV551A1T, TCRCBV1353, TCRCBV65P, TCRCBV753A2T, TCRCBV1352A1T, TCRCBV652A3P1, TCRCBV752A1N4T, TCRCBV135913S>
7025	18357	31277	0.59	5.0E-09	U66059.1	NT	

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8832	21898	35328		0.5	5.0E-09/P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
10455	23371	36870	2.53	6.0E-09/AW769687.1	EST_HUMAN		PM2-UM0053-240300-005-009 UM0053 Homo sapiens cDNA
522	13933		1.81	4.0E-09/AL163282.2	NT		Homo sapiens chromosome 21 segment HS21Q082
966	14018		2.79	4.0E-09/AL163285.2	NT		Homo sapiens chromosome 21 segment HS21Q085
1465	14498	27472	2.79	4.0E-09/P558716	NT		Homo sapiens hypothetical protein (AF038169), mRNA
2038	15057	28075	1.63	4.0E-09/AF175325.1	NT		Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2038	15057	28076	1.63	4.0E-09/AF175325.1	NT		Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
2438	15443	28481	2.87	4.0E-09/AA350878.1	EST_HUMAN		EST58355 infant brain Homo sapiens cDNA 5' and similar to heat shock protein, 90 kDa
8179	21149	34556	0.68	4.0E-09/AA495747.1	EST_HUMAN		Zn04c06.01 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:788298 5'
8867	21834	33255	0.66	4.0E-09/T64942.1	EST_HUMAN		y011a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:56904 3'
2359	15867	28389	4.28	3.0E-09/BE222239.1	EST_HUMAN		h009e02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2560	15561	28579	1.39	3.0E-09/BE222239.1	EST_HUMAN		h009e03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2859	15596	28674	1.03	3.0E-09/P23249	SWISSPROT		MER18 repetitive element;
3940	16391	29312	1.15	3.0E-09/BE222239.1	EST_HUMAN		h009e02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3388	16437		0.78	3.0E-09/AA442272.1	EST_HUMAN		h009e03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
4124	17157		0.69	3.0E-09/X16874.1	NT		z054a04.r1 Soares testis_NHTT Homo sapiens cDNA clone IMAGE:757422 5'
4457	17483	30371	3.71	3.0E-09/AF175325.1	NT		H sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4540	17563	30450	3.44	3.0E-09/Q9Y3R5	SWISSPROT		Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
5225	18233		0.69	3.0E-09/D86842.1	NT		238.1 KDA PROTEIN C21ORF5 (K1AA0933)
8232	21201	34607	1.08	3.0E-09/BE465780.1	EST_HUMAN		Homo sapiens DNA for 3-hydroxy-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
10839	23531	37028	1.84	3.0E-09/AL163247.2	NT		h08d02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
11391	24310	37639	3.06	3.0E-09/BF103843.1	EST_HUMAN		O55091 IMPACT PROTEIN;
11391	24310	37637	3.06	3.0E-09/BF103843.1	EST_HUMAN		Homo sapiens chromosome 21 segment HS21Q047
813	13371		10.64	2.0E-09/X16874.1	NT		Homo sapiens chromosome 21 segment HS21Q084
1263	14298	27261	5.84	2.0E-09/AL163284.2	NT		H sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1697	14989		9.93	2.0E-09/AL16373.1	EST_HUMAN		Homo sapiens chromosome 21 segment HS21Q084
2334	15345	28366	2.58	2.0E-09/Q9Y3R5	SWISSPROT		DKFZp61B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp61B1710 5'
3958	16968	29913	3.67	2.0E-09/O60241	SWISSPROT		238.1 KDA PROTEIN C21ORF5 (K1AA0933)
4039	17077	29977	1.65	2.0E-09/AL283479.1	EST_HUMAN		BRIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
							Q107d09.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:165793 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5198	18207	31081	0.68	2.0E-09	M23161.1	NT	Human transposon-like element mRNA
5908	18898	32081	0.69	2.0E-09	A1004062.1	EST_HUMAN	044700.91 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1618987 3'
6273	19346		0.65	2.0E-09	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
6947	20171		0.8	2.0E-09	AA357407.1	EST_HUMAN	EST168142 Kidney/XY Homo sapiens cDNA 5' and similar to EST containing L1 repeat
7684	20642	34006	7.6	2.0E-09	AA461430.1	EST_HUMAN	z68306.01 Soares, total, testis, N52HF8, gw Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element
7768	20719	34092	0.63	2.0E-09	W26834.1	EST_HUMAN	524111 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8128	21063	34461	0.82	2.0E-09	AV1862128.1	EST_HUMAN	MR1-C10352-240200-105-b06 C10352 Homo sapiens cDNA
8062	22028	35452	2.25	2.0E-09	AJ271735.1	NT	Homo sapiens Xq1 pseudocentromeric region, segment 1/2
12705	13871		22.38	2.0E-09	X166974.1	NT	H1 sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12772	25675		1.67	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element
12778	25629		1.47	2.0E-09	AV301637.1	EST_HUMAN	x59a02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768234 3'
12813	25402		1.98	2.0E-09	U82968.1	NT	Homo sapiens sf10x gene, alternatively spliced products, complete cds
1111	14155	27105	1.1	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1111	14155	27106	1.1	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1638	14870		0.91	1.0E-09	AJ228041.1	NT	Homo sapiens 859 kb contig between AVL1 and CBR1 on chromosome 21q22; segment 1/3
2510	15513		1.16	1.0E-09	AI356088.1	EST_HUMAN	q64e11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER1212
2900	15559	28878	1.83	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (hlf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2937	15895	28915	4.07	1.0E-09	M26599.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2937	15995	28916	4.07	1.0E-09	M26599.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3051	16108	29022	0.89	1.0E-09	BE535440.1	EST_HUMAN	601058602FT NIH_IMGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4838	17853		5.63	1.0E-09	AA719287.1	EST_HUMAN	zh135b03.s1 Soares, pineal, gland, N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
5162	18171	31050	0.84	1.0E-09	T60216.1	EST_HUMAN	x22209.r1 StrataGene lung (8837210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu repetitive element; contains MER28 repetitive element
5391	18677	31640	0.82	1.0E-09	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
5630	19018	32211	1.35	1.0E-09	U07000.1	NT	Homo sapiens breakpoint cluster region (BQR) gene, complete cds
6267	19340	32572	3.11	1.0E-09	P26694	SWISSPROT	GIRKJUMPSOROZOITE PROTEIN PRECURSOR (GS)
8217	21050	34449	0.93	1.0E-09	AV728645.1	EST_HUMAN	AV728645 HTC Homo sapiens cDNA clone HTCBIG07 5'
8733	21701	35127	0.87	1.0E-09	AI698474.1	EST_HUMAN	wd98005.x1 Soares, NFP_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.11 MER25 repetitive element

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10877	23598		2.87	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12081	24063		1.53	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12018	25916	31425	2.01	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12781	25416		1.8	1.0E-09	T89176.1	EST_HUMAN	y24605.1 Statagene lung (#837210) Homo sapiens cDNA clone IMAGE:116838.5
1312	14348	27314	2.49	9.0E-10	AW867740.1	EST_HUMAN	MRO-SN0040-050500-002-507 SN0040 Homo sapiens cDNA
2845	15905	28830	6.64	9.0E-10	AB170071.1	EST_HUMAN	w81h03.x1 Soares Dieckgraefe colon_NHCO Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW-RL29, HUMAN P47814.60S RIBOSOMAL PROTEIN L29 ;contains element PTRS repetitive element ;
7008	20134	33449	4.22	9.0E-10	AI452982.1	EST_HUMAN	U46505.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
148	13251	29180	12.13	8.0E-10	U63530.2	NT	TR-000372 O00372 PUTATIVE P150 ;
3353	18404	26325	0.76	8.0E-10	BE080748.1	EST_HUMAN	Homo sapiens MCN4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
4228	17266	30142	3.69	8.0E-10	AA376832.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
10324	23248		2.48	8.0E-10	U36308.2	NT	EST80564 Small intestine   Homo sapiens cDNA 5' end
702	13764	26698	32.88	7.0E-10	T706225	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
702	13764	26699	32.88	7.0E-10	T706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1628	14659	27636	2.48	7.0E-10	Q13342	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
2668	15697		21.64	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3104	18161	29072	2.86	7.0E-10	X00958.1	NT	H. sapiens DHFR gene, exon 3
6309	19380	32619	3.72	7.0E-10	AA345220.1	EST_HUMAN	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
7647	20607	33973	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0618-110700-208-D12 HT0618 Homo sapiens cDNA
7918	23881		1.46	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8308	21277	34688	1.29	7.0E-10	AF026701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8308	21277	34689	1.29	7.0E-10	AF026701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10673	23595	37092	0.68	7.0E-10	L08956.1	NT	Homo sapiens MAD5/MEF2-family transcription factor (MEF2C) mRNA, complete cds
914	13650	26922	2.67	6.0E-10	AJ400871.1	NT	Homo sapiens ASCL3 gene, CEGF1 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2688	15692	28700	1.37	6.0E-10	AJ424405.1	EST_HUMAN	U02407.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4768	17785		2.72	6.0E-10	AW663718.1	EST_HUMAN	RC3-C10284-031066-012-g12 C10284 Homo sapiens cDNA
9135	22101	35527	0.89	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
9135	22101	35528	0.89	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
8992	22910	36388	0.43	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12221	25058		1.64	6.0E-10	AW971823.1	EST_HUMAN	EST3346712 MAGE resequences, MAGL Homo sapiens cDNA
761	13821		5.01	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219.1 J1 434 (synonym: Hhes3) Homo sapiens cDNA clone DKFZp434N219.5'
3469	16535	29460	1.63	5.0E-10	Q01033	SWISSPROT	HYPOPHYSICAL GENE 48 PROTEIN
5026	18040	30923	1.1	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
7844	20507		1.74	5.0E-10	AF181897.1	NT	HYPOPHYSICAL GENE 48 PROTEIN
9894	22847	36303	1.96	5.0E-10	BF105169.1	SWISSPROT	001822164F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4042413 5'
9894	22847	36304	1.95	5.0E-10	P34678	SWISSPROT	HYPOPHYSICAL GENE 48 PROTEIN
111	13222		1.27	4.0E-10	AI221083.1	EST_HUMAN	001822164F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4042413 5'
683	13851	28585	0.75	4.0E-10	AA516280.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
2012	15033	28043	1.4	4.0E-10	AW594709.1	EST_HUMAN	similar to contains LTRb2 LTR8 repetitive element:
2580	15581	28590	5.49	4.0E-10	AL163303.2	NT	HYPOPHYSICAL GENE 48 PROTEIN
7382	20352	33703	17.71	4.0E-10	AF224689.1	NT	HYPOPHYSICAL GENE 48 PROTEIN
10555	23477	36971	0.53	4.0E-10	AW293243.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
10812	23733	37235	0.87	4.0E-10	AI267342.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
10933	23853	37388	0.45	4.0E-10	BE166208.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
10933	23853	37369	0.46	4.0E-10	BE166208.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
916	13970	26924	1.8	3.0E-10	N36113.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
1353	14388		4.8	3.0E-10	AY05150.1	NT	HYPOPHYSICAL GENE 48 PROTEIN
4589	17589	30480	1.04	3.0E-10	AL163203.2	NT	HYPOPHYSICAL GENE 48 PROTEIN
4589	17589	30481	1.04	3.0E-10	AL163203.2	NT	HYPOPHYSICAL GENE 48 PROTEIN
5530	18528	31564	1.06	3.0E-10	N50109.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
6327	19397	32639	4.03	3.0E-10	P20350	SWISSPROT	HYPOPHYSICAL GENE 48 PROTEIN
6486	19551	32801	3.08	3.0E-10	BE302870.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
8036	20973	34367	1.42	3.0E-10	AV1743302.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
8036	20973	34368	1.42	3.0E-10	AV1743302.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
9082	22048	35471	1.04	3.0E-10	H87208.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
9404	22869	35803	1.8	3.0E-10	AW650731.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN
9404	22869	35804	1.8	3.0E-10	AW650731.1	EST_HUMAN	HYPOPHYSICAL GENE 48 PROTEIN



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9696	22649		0.73	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10828	23749		2.05	3.0E-10	T65891.1	EST_HUMAN	Y11612.1 Singapore lung (#637210) Homo sapiens cDNA clone IMAGE:80398 5'
10957	23877		1.76	3.0E-10	AA768294.1	EST_HUMAN	nc259303.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:126908 3'
12865	25458	31728	1.95	3.0E-10	BE179517.1	EST_HUMAN	IL3-H767818-170500-196-E07 H70618 Homo sapiens cDNA
37	13157	26058	1.55	2.0E-10	P48938	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	13167	26059	1.55	2.0E-10	P48938	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1913	14937		1.88	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b2p44) gene, partial cds, neuronal apoptosis inhibitor
2699	16057		0.68	2.0E-10	BF675047.1	EST_HUMAN	protein (help) and survival motor neuron protein (smn) genes, complete cds
5801	18988		3.12	2.0E-10	Q26840	SWISSPROT	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
							(HPRG)
6379	19447	32698	1.55	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds, cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7605	20566	33926	6.24	2.0E-10	BE781082.1	EST_HUMAN	601666208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8347	21319	34730	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: RIBONUCLEASE H]
8347	21316	34731	0.54	2.0E-10	P26809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: RIBONUCLEASE H]
9657	22600		0.85	2.0E-10	BF434565.1	EST_HUMAN	7678608.XT NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1, B L1 repetitive element
1509	14542		2.04	1.0E-10	AW687787.1	EST_HUMAN	MRO-SN00393-293030-001-701 SN0038 Homo sapiens cDNA
1611	14643	27619	3.27	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLC0X411 3'
2598	15587		1.92	1.0E-10	AW652123.1	EST_HUMAN	QVA-CT0225-191169-038-008 CT0225 Homo sapiens cDNA
3511	16599	29481	0.84	1.0E-10	AW832012.1	EST_HUMAN	QVZ-T10003-161169-013-G10 T10003 Homo sapiens cDNA
3550	16599		0.81	1.0E-10	AL041695.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3558	16596		0.94	1.0E-10	AL041695.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
4043	17081		6.46	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4154	17185	30072	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cag2/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4154	17185	30073	5.55	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cag2/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4160	17191	30080	2.48	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4199	17230		2.63	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5212	18221		0.92	1.0E-10	AJ797745.1	EST_HUMAN	wee2f04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains
6875	19928	33226	0.61	1.0E-10	AA631233.1	EST_HUMAN	MER31.11 MER31 repetitive element;
6931	20214	33543	0.49	1.0E-10	AF03523.1	NT	nr18a05.s1 NCL CGAP_C88 Homo sapiens cDNA clone IMAGE:1159704 3'
7716	20673		0.58	1.0E-10	P08548	SWISSPROT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7947	20888	34279	0.63	1.0E-10	AU128584.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8552	21550	34968	1.11	1.0E-10	AW408990.1	EST_HUMAN	AU128584 NT26P2 Homo sapiens cDNA clone NT26P2003751 5'
9002	21868		1.1	1.0E-10	AI268340.1	EST_HUMAN	1B_GA4 Fetal brain library Homo sapiens cDNA
10552	23484		3.95	1.0E-10	AA081668.1	EST_HUMAN	qm04610.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element;
11259	24211	37734	3.25	1.0E-10	AI038280.1	EST_HUMAN	zn23g06.l1 Stralagene neuroepithelium NT2RAMJ.837234 Homo sapiens cDNA clone IMAGE:648314 5'
12166	18354		2.46	1.0E-10	X87344.1	NT	0y65h03.x1 Scores_Total_liver_spleen_INF.LS_S1 Homo sapiens cDNA clone IMAGE:1672861 3'
261	13357	28232	0.98	9.0E-11	BE145600.1	EST_HUMAN	H sapiens DMA, DMB, HLA-Z1, IIP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2114	16131	28161	0.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbrt1) Homo sapiens cDNA clone DKFZp547D225 5'
2114	15131	28152	0.21	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbrt1) Homo sapiens cDNA clone DKFZp547D225 5'
3394	16443	29370	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbrt1) Homo sapiens cDNA clone DKFZp547D225 5'
3394	16443	26371	2.6	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hbrt1) Homo sapiens cDNA clone DKFZp547D225 5'
4528	17552	30440	0.72	9.0E-11	AA175955.1	EST_HUMAN	aa78i01.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5854	18750		3.89	9.0E-11	BE079780.1	EST_HUMAN	RCB-BT0627.140200-011-E06 BT0627 Homo sapiens cDNA
10514	23436	36934	1.22	9.0E-11	AA324660.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
10514	23436	36935	1.22	9.0E-11	AA324660.1	EST_HUMAN	EST127872 Cerebellum II Homo sapiens cDNA 5' end
12548	25289	31809	4.99	9.0E-11	CI16633.1	EST_HUMAN	C10635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone IMAGE:172173 3' similar to contains
3133	16190		8.85	8.0E-11	HI19971.1	EST_HUMAN	ym53f11.s1 Scores_adult brain N2b5H5557 Homo sapiens cDNA clone GEN-506808 5'
4073	17109	30003	4.35	8.0E-11	N23712.1	EST_HUMAN	L1 repetitive element;
5900	18078	32170	0.95	8.0E-11	AA1674316.1	EST_HUMAN	YW46G6.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
6829	19893		0.85	8.0E-11	AA168158.1	EST_HUMAN	ba80g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2300982 3'
1442	14475	27452	1.87	7.0E-11	AA330642.1	EST_HUMAN	X45h11.x1 NCL CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2821061 3' similar to contains MER10.11
						EST_HUMAN	MER10 repetitive element;
						EST_HUMAN	EST34392 Embryo 6 week 1 Homo sapiens cDNA 5' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3895	18925	29834	1.11	7.0E-11	AJ27546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8843	21810	33226	2.78	7.0E-11	AF163984.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10590	23512		1.19	7.0E-11	P11989	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
412	13485	28421	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
412	13485	28422	6.97	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6884	19836	33232	0.88	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from flamm (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
7957	20898	34281	3.22	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8707	21675	35100	7.37	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC09 5'
8668	22621	36072	0.42	6.0E-11	BE063509.1	EST_HUMAN	CMA-BT0281-031195-087-403 BT0281 Homo sapiens cDNA
12	13132	26030	0.75	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3377	13132	26030	1.31	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4256	17285	30167	1.51	6.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6865	19722	32987	1.91	5.0E-11	AL183213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7774	20727	34086	11.91	5.0E-11	11416769	NT	Homo sapiens prolactinadherin beta 3 (PCHB3), mRNA
1401	14434		1.88	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.11 Scarses, testis, NHT Homo sapiens cDNA clone IMAGE:730559 5'
2802	15794	28812	7.83	4.0E-11	BE86900.1	EST_HUMAN	601607831F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
2931	16039	29082	0.92	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4649	17670	30567	1.24	4.0E-11	D44668.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
5821	19879	32957	3.27	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
7107	20221	33552	0.54	4.0E-11	AA442630.1	EST_HUMAN	z68f10.11 Scarses, testis, NHT Homo sapiens cDNA clone IMAGE:737983 5' similar to TR:G1065260
7800	20561		3.97	4.0E-11	AF224669.1	NT	G1055250 PHEROMONE RECEPTOR VN4 ; Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
8750	22891		1.88	4.0E-11	BE148425.1	EST_HUMAN	(UBE2D3) genes, complete cds
10020	22947	36415	0.86	4.0E-11	AI608753.1	EST_HUMAN	RC1-HT0256-210100-013-103 HT0259 Homo sapiens cDNA
12736	25388	31752	1.56	4.0E-11	11545732	NT	162g12.11 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WIP:ZK353.1
1488	14521	27494	2.65	3.0E-11	6679077	NT	CE00388 ; Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4303	17334		1.37	3.0E-11	AA308248.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23) (Nme2), mRNA
981	14014	26087	1.48	2.0E-11	AI150502.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' and q36c04.X1 Scarses, testis, NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13 MER10 repetitive element ;

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1189	14229	27186	4.46	2.0E-11	R24807.1	EST_HUMAN	Y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1189	14229	27187	4.48	2.0E-11	R24807.1	EST_HUMAN	Y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1617	14649	27624	5.86	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and of olfactory receptor-like protein
1617	14649	27625	5.86	2.0E-11	L17432.1	NT	COR3beta (COR3beta) genes, complete cds
1620	14653	27629	1.25	2.0E-11	A1128371.1	EST_HUMAN	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
2775	15787	28787	1.04	2.0E-11	AF087913.1	NT	q651t10.x1 Soares, pregnant, uterus, NHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gbl:02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN) contains L1.11
3211	16286	29189	8.7	2.0E-11	P10263	SWISSPROT	L1 repetitive element;
3337	16388	29309	1	2.0E-11	A1478617.1	EST_HUMAN	Human endogenous retrovirus HERV-P-747D
3375	16425	29350	0.71	2.0E-11	Q10473	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3508	16554		1.09	2.0E-11	AF020503.1	NT	Im54g09.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2161836 3'
4472	17498		1.24	2.0E-11	BE065937.1	EST_HUMAN	POLYPEPTIDE N-ACETYL-GALACTOSAMINYLTRANSFERASE (PROTEIN LIDP)
4638	17657		0.98	2.0E-11	AL16327.2	NT	ACETYL-GALACTOSAMINYLTRANSFERASE (UDP-GALNAc:POLYPEPTIDE, N-ACETYL-GALACTOSAMINYLTRANSFERASE)(GALNAcT1)
4873	17686		2.36	2.0E-11	BE062568.1	EST_HUMAN	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
6268	18331	32562	1	2.0E-11	AW877806.1	EST_HUMAN	RC3-B1T0316-170200-014-a05 B1T0316 Homo sapiens cDNA
6443	19508	32758	1.71	2.0E-11	AA581028.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
7401	20369	33722	0.82	2.0E-11	BF562945.1	EST_HUMAN	QV2-B1T0288-261069-014-a01 B1T0288 Homo sapiens cDNA
8214	21183		0.51	2.0E-11	P37072	SWISSPROT	QV2-P1T0073-280300-109-h08 P1T0073 Homo sapiens cDNA
9378	22540		1.31	2.0E-11	AF026908.1	NT	nc83h05.r1 NCI CGAP GC1 Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR16_YEAST
10647	23560	37065	4.42	2.0E-11	Q13868	SWISSPROT	P16938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18 ;
10892	23602	37305	0.85	2.0E-11	AW885974.1	EST_HUMAN	7B76d03.x1 NCI CGAP G08 Homo sapiens cDNA clone IMAGE:3442565 3'
10982	23602	37306	0.85	2.0E-11	AW885974.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN COR6
11448	24391	37935	1.54	2.0E-11	AA035369.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
11448	24391	37936	1.54	2.0E-11	AA035369.1	EST_HUMAN	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
11477	24420	37969	2.14	2.0E-11	AA361693.1	EST_HUMAN	RC4-OT0072-170460-013-c11 OT0072 Homo sapiens cDNA
12326	25128		4.12	2.0E-11	AW842143.1	EST_HUMAN	RC4-OT0072-170460-013-c11 OT0072 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12354	25146	31854	2.14	2.0E-11	BF377859.1	EST_HUMAN	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12917	25313		1.49	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12754	25399		1.68	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13070	25604		3.68	2.0E-11	11417868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
677	13740	26687	0.83	1.0E-11	AL131016.1	NT	Homo sapiens SCL gene locus
784	13844	26789	1.89	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1221	14259	27216	4.66	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1498	14531		2.95	1.0E-11	AF118914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2053	16072	28091	1.41	1.0E-11	P16288	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2136	15153	28168	3.18	1.0E-11	AF000573.1	NT	Homo sapiens homotigritinase 1,2-dioxygenase gene, complete cds
2170	15186	28207	1.15	1.0E-11	AA309318.1	EST_HUMAN	EST180186 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3510	16558	29480	0.8	1.0E-11	BE004315.1	EST_HUMAN	GM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
4990	17975	30866	1.01	1.0E-11	A116825.1	EST_HUMAN	cd6106.s1 Soares_NHMPc.S1 Homo sapiens cDNA clone IMAGE:1661243 3'
6405	18508	31385	14.43	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5931	19017	32212	0.77	1.0E-11	BF222646.1	EST_HUMAN	7p67d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3646945 3' similar to contains MER10.b3
8112	21049		0.51	1.0E-11	AB042297.1	NT	MER10 repetitive element
8543	21511	34928	3.38	1.0E-11	4895546	NT	Homo sapiens PITS gene for 6-pyruvyltetrahydropyrimidin synthase, complete cds
8928	21894	35322	4.18	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9403	22368	35801	1.18	1.0E-11	BF365119.1	EST_HUMAN	QV4-NH1149-250900-423-e03 NN1149 Homo sapiens cDNA clone IMAGE:28166 5'
9403	22368	35802	1.18	1.0E-11	BF365119.1	EST_HUMAN	QV4-NH1149-250900-423-e03 NN1149 Homo sapiens cDNA
11819	24357	38120	1.48	1.0E-11	BF680078.1	EST_HUMAN	Q02154007F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295677 5'
2963	16021	28946	0.82	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10157	23092	36558	1.02	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10157	23092	36559	1.02	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12075	24947	38542	2.85	9.0E-12	AL046309.1	EST_HUMAN	DKFZp566i0417.J1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZp566i0417 5'
9993	25246		0.92	8.0E-12	BE074720.1	EST_HUMAN	IL5-B10578-103000-036-G12 B10578 Homo sapiens cDNA
12407	25180		3.22	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
4690	17711	30605	1.46	7.0E-12	Q08904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSN34)
11677	24543	38220	7.41	7.0E-12	AI704735.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_1NLSLS.S1 Homo sapiens cDNA clone IMAGE:451152 3'
3558	16904		0.95	6.0E-12	AV730594.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW106 5'
4375	17403	30283	9.29	6.0E-12	AA732618.1	EST_HUMAN	nz8811.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6528	19591	32851	0.65	5.0E-12	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
8347	22312	35736	0.68	6.0E-12	AF003246.1	NT	Macaca saxatilis myosin heavy chain FMA3 (FMA3) mRNA, complete cds
9829	22678		1.68	6.0E-12	AA847898.1	EST_HUMAN	cd010g11.t1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367888 similar to contains MER29.12
1044	14080	27043	3.57	5.0E-12	T06573.1	EST_HUMAN	MER29 repetitive element;
3401	14660	29376	1.17	5.0E-12	BE047770.1	EST_HUMAN	EST04462 Fetal brain, Stragelene (cat#936206) Homo sapiens cDNA clone HFB0V33
3740	18782	29694	6.8	5.0E-12	AJ271736.1	NT	324305.Y1 NCL CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291217 5'
6137	18214	32441	4.89	5.0E-12	AL163278.2	NT	Homo sapiens X4 pseudocentromeric region, segment 2/2
6137	18214	32442	4.89	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19897	32973	9.52	5.0E-12	AW874780.1	EST_HUMAN	EST386850 MAGC resequences, MAGN Homo sapiens cDNA
7232	19877	33274	1	5.0E-12	AL040739.1	EST_HUMAN	DKFZ43481615_s1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZ43481615 3'
7242	19877	33274	1.03	5.0E-12	AL040739.1	EST_HUMAN	DKFZ43481615_s1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZ43481615 3'
8571	21539	34980	1.14	5.0E-12	AA033745.1	EST_HUMAN	z01g12.e1 Scores_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:375716 3' similar to contains L1.8 L1 repetitive element;
9018	21981		0.7	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0086-220300-0711-007 OT0086 Homo sapiens cDNA
9348	22311		0.64	5.0E-12	AL079581.1	EST_HUMAN	DKFZ434J0426_1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZ434J0426 5'
9464	22428	36587	2.78	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
9778	22719	38173	1.38	5.0E-12	P34982	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E)(OLFACTORY RECEPTOR 17-4)(OR17-4)
10638	23660		4.14	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10729	23744		0.81	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
244	13342	28287	4.17	4.0E-12	AA700326.1	EST_HUMAN	274g11.s1 Scores_fetal_liver_spleen_INF1LS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
245	13342	28287	5.51	4.0E-12	AA700326.1	EST_HUMAN	274g11.s1 Scores_fetal_liver_spleen_INF1LS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4650	17671	30558	0.74	4.0E-12	AB98984.1	EST_HUMAN	h28h05.x1 NCL CGAP_Luz4 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
7881	20825		0.72	4.0E-12	BF445140.1	EST_HUMAN	nu21b03.x1 NCL CGAP_Luz4 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2
8585	21553		2.92	4.0E-12	AF109007.1	NT	MER7 repetitive element;
9036	22901	35422	0.76	4.0E-12	AB042815.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
11419	24363	37998	3.26	4.0E-12	AJ226043.1	NT	Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds
12688	25338		2.82	4.0E-12	U78027.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
616	13693	28600	3.08	3.0E-12	AW341683.1	EST_HUMAN	h13401.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR:Q14517
618	13693	28601	3.08	3.0E-12	AW341683.1	EST_HUMAN	O14517 SMRP. ;
5211	18220	31096	0.73	3.0E-12	AL163268.2	NT	O14517 SMRP. ;
5227	18228	31562	0.96	3.0E-12	AF111108.2	NT	Homo sapiens chromosome 21 segment HS21C068
7659	20619		0.84	3.0E-12	AB042297.1	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8030	20987		0.95	3.0E-12	AW654328.1	EST_HUMAN	Homo sapiens PTPS gene for 6-pyruvoylserinehydrolase synthase, complete cds
8718	21866	35114	0.48	3.0E-12	O35483	SWISSPROT	RC3-C10255-031089-011-02 C10255 Homo sapiens cDNA
9462	22428	38864	0.54	3.0E-12	O35483	SWISSPROT	SERINE PROTEASE HEPHSIN
11016	23981	37507	2.71	3.0E-12	U37872.1	NT	SERINE PROTEASE HEPHSIN
11018	23981	37508	2.71	3.0E-12	U37872.1	NT	Human prostate specific antigen gene, 5' flanking region
1691	14993	27658	2.41	2.0E-12	AW602181.1	EST_HUMAN	Human prostate specific antigen gene, 5' flanking region
3480	16526	28451	0.85	2.0E-12	675495	NT	IL5-UM0071-120400-065-05 UM0071 Homo sapiens cDNA
4141	17172	30060	1.09	2.0E-12	J01884.1	NT	Mus musculus keratin-associated protein 6.2 (Krap6.2), mRNA
4141	17172	30081	1.09	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4451	17477		1.97	2.0E-12	BE083509.1	EST_HUMAN	Rat U3A small nuclear RNA
5321	18427	31177	0.71	2.0E-12	P11369	SWISSPROT	CMO-BT0281-031199-087-403 BT0281 Homo sapiens cDNA
6922	19860		1.83	2.0E-12	AW971857.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
7381	20351	33702	3.22	2.0E-12	T08169.1	EST_HUMAN	ENDONUCLEASE
7567	20930	33989	1.18	2.0E-12	BE170035.1	EST_HUMAN	EST1383945 MAGC resources, MAGL Homo sapiens cDNA
7778	20731		0.97	2.0E-12	AW842798.1	EST_HUMAN	EST106050 Infant Brain, Bello Soares Homo sapiens cDNA clone HIBBA13 5' end
7922	20965	34253	2.1	2.0E-12	11422228	NT	MR0-HT0559-200400-015-008 HT0559 Homo sapiens cDNA
							MR2-CN0037-210200-101-502 CN0037 Homo sapiens cDNA
							Homo sapiens Ac-like transposable element (ALTE), mRNA
							POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP
							ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-
							ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
9077	22043	35466	0.43	2.0E-12	Q10473	SWISSPROT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
6653	22820		1.85	2.0E-12	AF198694.1	NT	MR3-HT0497-150200-113-g01 HT0497 Homo sapiens cDNA
10345	23269		14.41	2.0E-12	BE165960.1	EST_HUMAN	Q40702.x1 Soares, NHMPu_S1 Homo sapiens cDNA
							Q19538 ORF2: FUNCTION UNKNOWN. ;
10881	23801	37904	0.8	2.0E-12	AI334130.1	EST_HUMAN	940702.x1 Soares, NHMPu_S1 Homo sapiens cDNA clone IMAGE:1931835 3' similar to TR:Q13538
12308	25116		3.11	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12511	25245		1.69	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
123	13231	28159	2.83	1.0E-12	AW627674.1	EST_HUMAN	h80609.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11 MER18 repetitive element;
2004	15025						
3085	18142	29053	1.46	1.0E-12	AB171726.1	EST_HUMAN	hm5107.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439403 3' similar to contains L1.63 L1 repetitive element;
3085	18142	29053	0.78	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3085	18142	29054	0.78	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3888	16028	29836	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3888	16028	29837	31.6	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6078	18158		2.05	1.0E-12	U82828.1	NT	Homo sapiens aldoza telangiectasia (ATM) gene, complete cds
6159	19234		1.65	1.0E-12	O97237	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6277	18349	32582	0.57	1.0E-12	BF642800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847889 5'
6277	18349	32583	0.57	1.0E-12	BF642800.1	EST_HUMAN	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847889 5'
6882	19739	33014	0.76	1.0E-12	AF228943.1	NT	Mus musculus WNT-2 gene, partial cds; putative enkyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7323	20294	33637	1.9	1.0E-12	AF168894.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7357	20327	33675	11.35	1.0E-12	A1248533.1	EST_HUMAN	gb3M16503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
7357	20327	33676	11.35	1.0E-12	A1248533.1	EST_HUMAN	gb3M16503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10 repetitive element;
8834	21801	35220	0.48	1.0E-12	U65059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TORBV27S1P, TORBV221A2N1T, TORBV9S1A1T, TORBV7S1A1N2T, TORBV6S1A1T, TORBV13S3, TORBV6S7P, TORBV7S3A2T, TORBV13S2A1T, TORBV6S2A2P1, TORBV7S2A1N4T, TORBV13S9/13S9
9083	22019	35444	1.16	1.0E-12	AJ1782323.1	EST_HUMAN	ac3805.x1 Stragogene cmyb (#837217) Homo sapiens cDNA clone IMAGE:857677 3'
12213	25052	38628	2.92	1.0E-12	AW962164.1	EST_HUMAN	ES7374237 MACI9 ressequences, MAGG Homo sapiens cDNA
12434	25200		2.54	1.0E-12	AJ738592.1	EST_HUMAN	wb3308.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'
12682	25881		2.51	1.0E-12	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
1054	14100	27050	0.7	9.0E-13	AW082714.1	EST_HUMAN	xb3107.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2880805 3' similar to contains MER28.13 MER28 repetitive element;
3943	16886		1.01	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3967	17007	28623	0.96	8.0E-13	AB029600.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5



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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9960	22887		2.59	9.0E-13	N69553.1	EST_HUMAN	2a2b06.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:293651 3'
718	13780	28714	28714	8.0E-13	U25165.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
718	13780	28715	6.78	8.0E-13	U25165.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1855	14881	27877	3.1	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 P44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8449	21418	34831	0.75	8.0E-13	A1884398.1	EST_HUMAN	hm31109.x1 NC1_CGAP_UH Homo sapiens cDNA clone IMAGE:2437601 3'
8449	21418	34832	0.75	8.0E-13	A1884398.1	EST_HUMAN	hm31109.x1 NC1_CGAP_UH Homo sapiens cDNA clone IMAGE:2437601 3'
10505	23427		4	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTR3 (FTR3) genes, complete cds
8127	21064	34462	0.58	7.0E-13	A1884398.1	EST_HUMAN	hm31109.x1 NC1_CGAP_UH Homo sapiens cDNA clone IMAGE:2437601 3'
8127	21064	34463	0.58	7.0E-13	A1884398.1	EST_HUMAN	hm31109.x1 NC1_CGAP_UH Homo sapiens cDNA clone IMAGE:2437601 3'
8578	21544		0.49	7.0E-13	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12682	25350		5.56	7.0E-13	BE716223.1	EST_HUMAN	601453265.F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866613 5'
2111	15128	28148	3.56	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3333	16384		0.74	5.0E-13	R78338.1	EST_HUMAN	y8204.f1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu
3408	16457		1.35	6.0E-13	AA435773.1	EST_HUMAN	x177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:145799 5'
7060	20082	33360	0.7	6.0E-13	P08983	SWISSPROT	repetitive element/contains element MER22 repetitive element;
11209	24163	37693	2.07	5.0E-13	P07313	SWISSPROT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
1883	14908		6.02	4.0E-13	AW378914.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
2467	15471		2.44	4.0E-13	AF003529.1	NT	PM2-HT0224-221068-001-ct1 HT0224 Homo sapiens cDNA
4778	17798		0.89	4.0E-13	AA454054.1	EST_HUMAN	Homo sapiens dyx19c3 3 (GPC3) gene, partial cds and flanking repeat regions
5687	18762	31931	4.38	4.0E-13	BE769131.1	EST_HUMAN	zcd807.f1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:795459 5'
7413	20380	33731	1.05	4.0E-13	AB037750.1	NT	PI3-HT0520-220200-002-008 HT0520 Homo sapiens cDNA
7870	20814	34182	0.98	4.0E-13	AA431529.1	EST_HUMAN	Homo sapiens mRNA for KIAA1329 protein, partial cds
7958	20928		1.47	4.0E-13	AA4291.1	EST_HUMAN	zw76g12.f1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR-G452763
9193	22159	35537	1.2	4.0E-13	AL043810.1	EST_HUMAN	y93g05.f1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR-A32985
6860	22768	36249	0.59	4.0E-13	AA076607.1	EST_HUMAN	A32985 complex sterility protein - mouse;
10380	23303	36779	5.28	4.0E-13	A1288931.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A0128 5'
11502	24444	37595	1.9	4.0E-13	AA438819.1	EST_HUMAN	7804H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7804H11
11502	24444	37595	1.9	4.0E-13	AA438819.1	EST_HUMAN	hm32405.x1 NC1_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:189945 3' similar to contains Alu
11502	24444	37595	1.9	4.0E-13	AA438819.1	EST_HUMAN	repetitive element;
11502	24444	37595	1.9	4.0E-13	AA438819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
11502	24444	37595	1.9	4.0E-13	AA438819.1	EST_HUMAN	z178g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
181	13281		5.91	3.0E-13	AF005528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
866	13222		3.35	3.0E-13	AA430310.1	EST_HUMAN	zve8809.1 Sources, testis, NHT Homo sapiens cDNA clone IMAGE:781406 5'
2378	15386	28410	1.65	3.0E-13	AL271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2487	15491		2.11	3.0E-13	AL163210.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
2973	15670	28688	2.6	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT1000-140700-242-H08 FT10100 Homo sapiens cDNA
3201	16256		2.19	3.0E-13	AF474894.1	EST_HUMAN	dbt802.s1 NCL CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1324035 3'
3514	16560	29484	0.9	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3514	16560	29485	0.9	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5618	18714	31872	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn8810.1.r1 Straglene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
5618	18714	31873	0.64	3.0E-13	AA134017.1	EST_HUMAN	zn8810.1.r1 Straglene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR12 THR repetitive element;
6106	19185	32404	0.71	3.0E-13	AW005939.1	EST_HUMAN	wz86602.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565590 3' similar to TR:075139 075139 KIAA0844 PROTEIN.;
8215	21184	34594	8.24	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
8412	21331	34787	0.61	3.0E-13	AA352487.1	EST_HUMAN	EST160487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
8412	21331	34788	0.61	3.0E-13	AA352487.1	EST_HUMAN	EST160487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Reactive factor
10598	23480	36876	0.46	3.0E-13	AW1635487.1	EST_HUMAN	BC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
11038	24000		2.68	3.0E-13	AD64768.1	EST_HUMAN	HA0330 Human fetal liver cDNA library Homo sapiens cDNA
11385	24332	37851	3.32	3.0E-13	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-ad03 BT0281 Homo sapiens cDNA
11924	24805	38398	1.54	3.0E-13	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C048
151	13254	26183	3.93	2.0E-13	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
1275	14310	27271	7.14	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3234	16347	29287	1.08	2.0E-13	BF431809.1	EST_HUMAN	nal7816.s.x1 Sources, NSF_F8_SW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3518	16564	29489	1.25	2.0E-13	AF106607.1	NT	Homo sapiens S164 gene, partial cds, PS1 and hypothetical protein genes, complete cds, end S171 gene, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4135	17167		1.61	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS210278 CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6245	18318	32548	4.71	2.0E-13	Q0852	SWISSPROT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
6987	20210	33338	8.49	2.0E-13	X16912.1	NT	Homo sapiens N-myristoyltransferase 1 (NM1T1), mRNA
7255	18990	33287	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NM1T1), mRNA
7255	18990	33288	0.59	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NM1T1), mRNA
10824	23745	37248	4.53	2.0E-13	5031886	EST	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12387	23165		5.43	2.0E-13	AW082165.1	EST_HUMAN	GMO-NN0001-10300-274-e11 NN0001 Homo sapiens cDNA
291	13385	26312	1.48	1.0E-13	S74129.1	NT	FGF-1 fibroblast growth factor 1 (human, kidney, Genomic, 342 nt, segment 2 of 2)
889	13944	26502	4.85	1.0E-13	AJ007073.1	NT	Homo sapiens LGMD2B gene
1339	14373	27343	1.38	1.0E-13	X87344.1	NT	H sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2037	15069	28074	2.43	1.0E-13	AA720574.1	EST_HUMAN	hw21p02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element;
4823	17944	30532	2.2	1.0E-13	BF940987.1	EST_HUMAN	602038009FT NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:418586 5' y1635.ecq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
6586	18946	32815	0.91	1.0E-13	AA680732.1	EST_HUMAN	m24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8242	21211	34616	0.78	1.0E-13	AA577812.1	EST_HUMAN	m24401.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8242	21211	34617	0.78	1.0E-13	AA577812.1	EST_HUMAN	repetitive element; contains element MER24 repetitive element;
10450	23372		0.82	1.0E-13	Q15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (IMAGE-B4 ANTIGEN)
10884	23589	37084	0.49	1.0E-13	AF300701.1	NT	Mus musculus osteopontin protein tyrosine phosphatase mRNA, complete cds
11707	24872	38249	10.13	1.0E-13	BF108785.1	EST_HUMAN	745610.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER28.b2 MER29 repetitive element;
12206	25048		2.34	1.0E-13	AJ171637.1	EST_HUMAN	AV715377 DOB Homo sapiens cDNA clone DOBA1603 5'
12844	25454		3.21	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
333	13422	26345	3.14	9.0E-14	AA781159.1	EST_HUMAN	g24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1351222 3' similar to contains MER19.11 MER19 repetitive element;
334	13423	26346	2.37	9.0E-14	AA781159.1	EST_HUMAN	g24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1351222 3' similar to contains MER19.11 MER19 repetitive element;
2508	15511		4.8	9.0E-14	AA781157.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2597	15598	28617	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2597	15598	28618	1.03	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2794	15756	28777	6.84	9.0E-14	AB038182.1	NT	Homo sapiens TRF gene cluster for trefol factor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3128	16185	28084	5.43	9.0E-14	AW513296.1	EST_HUMAN	x54h05.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:2707833 3'
3252	13422	26345	0.67	9.0E-14	AA781169.1	EST_HUMAN	aj24c01.s1 Soares_ testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER181t MER19 repetitive element 1
3811	15851	29759	7.16	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4789	17807	30690	1.68	9.0E-14	AJ002153.1	NT	Sagittaria edulis gene for seminal vesicle secreted protein semenogelin I
3509	16555		1.44	8.0E-14	BE468283.1	EST_HUMAN	h271c09.x1 NCL_CGAP_L021 Homo sapiens cDNA clone IMAGE:3213424 3'
3978	17018		3.46	8.0E-14	R76289.1	EST_HUMAN	yf72c03.s1 Soares placentis N52HP Homo sapiens cDNA clone IMAGE:144796 3'
9803	21128	34530	21.45	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9918	22739	36192	3.1	8.0E-14	AA218316.1	EST_HUMAN	z17c10.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:829970 3'
11762	24690		1.92	8.0E-14	BEG62658.1	EST_HUMAN	CV22.B10288-261069-017-401 BT0258 Homo sapiens cDNA
12590	25294	31783	2.99	8.0E-14	AI688118.1	EST_HUMAN	wc92f08.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2326143 3'
1633	15873		3.99	7.0E-14	AV151673.1	EST_HUMAN	xi67e10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623149 3' similar to contains MER10.12 repetitive element 1
9272	22238		0.51	7.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
367	13453	20381	10.94	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
10181	23106	36587	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
10181	23106	36588	2.54	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
620	13685	26603	5.23	5.0E-14	O63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
3883	16726		0.95	5.0E-14	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5093	18103	30979	1.39	5.0E-14	AW073791.1	EST_HUMAN	x503a05.x1 NCL_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 repetitive element 1
5911	18707	31894	4.94	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1125	15859		1.95	4.0E-14	P04628	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1895	14920	27916	7	4.0E-14	AJ007973.1	EST_HUMAN	Homo sapiens LGM22B gene
3793	16907		1	4.0E-14	AA048502.1	NT	z67a04c.r1 Soares_pregnant uterus_NH-FU Homo sapiens cDNA clone IMAGE:487859 5'
4320	17349	30233	0.66	4.0E-14	N46328.1	EST_HUMAN	yf73c12.s1 Soares_multiple_sclerosis_2NHMSHP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element 1
8291	21280		0.6	4.0E-14	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12905	25988		6.38	4.0E-14	AI866224.1	EST_HUMAN	wr08c03.x1 NCI_CGAP_UK4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
950	14003	26055	4.69	3.0E-14	X95468.1	NT	R. norvegicus mRNA for CFG2 protein
4963	17978	30868	1.16	3.0E-14	7658844	NT	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), mRNA
6998	19950	33246	0.06	3.0E-14	AI207868.1	EST_HUMAN	fa91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE. ;
6998	19950	33247	0.06	3.0E-14	AI207868.1	EST_HUMAN	fa91c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:000519 O00519 FATTY ACID AMIDE HYDROLASE. ;
7021	25976		0.51	3.0E-14	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7229	20251	33586	0.57	3.0E-14	AA396311.1	EST_HUMAN	EST186054 Brain IV Homo sapiens cDNA
9139	22105	35531	0.93	3.0E-14	N42165.1	EST_HUMAN	yo7b10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270523 5'
11337	24287	37811	2.63	3.0E-14	BE888016.1	EST_HUMAN	60151530.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3973087 5'
11568	18347	31293	6.06	3.0E-14	AW263354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HK11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element ;
12824	25854		1.88	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
390	13465	26395	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
390	13465	26396	2.76	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
691	15947	26882	0.98	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2397	15404		1.99	2.0E-14	AW372868.1	EST_HUMAN	RC5-B10377-091.29-031-D12 B10377 Homo sapiens cDNA
2472	15476		1.4	2.0E-14	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDRT), mRNA
2531	15534	28554	2.2	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2547	15548		1.03	2.0E-14	BE222492.1	EST_HUMAN	h9d0g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738 3' similar to contains Alu repetitive element; contains OFR.11 OFR repetitive element ;
2883	15579		1.48	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5602	18598	31669	0.91	2.0E-14	BF380691.1	EST_HUMAN	IL2-UT0072-240800-142-007 UT0072 Homo sapiens cDNA
5702	18797	31972	0.81	2.0E-14	AB12351.1	EST_HUMAN	9a78M1.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element ;
5809	18898	32082	3.16	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7097	20039		0.92	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-071-a08 BN0072 Homo sapiens cDNA
7260	20262	33596	0.57	2.0E-14	4685709	NT	Homo sapiens a disintegrin and metalloproteinase domain 11 (ADAM11), mRNA
7502	20467	33628	0.87	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7751	20704	34072	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071.289-024-004 HT0397 Homo sapiens cDNA
7751	20704	34073	21.51	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071.289-024-004 HT0397 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10277	23202	36697	0.52	2.0E-14	AI978195.1	EST_HUMAN	wf5g10.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2462034 3' similar to contains Alu repetitive element
10763	23704	37203	0.53	2.0E-14	AF741648.1	EST_HUMAN	AF741648 CB Homo sapiens cDNA clone CBFBBF04 5'
11133	24093	37622	3.94	2.0E-14	AW138600.1	EST_HUMAN	U14H311 active-10-0.U1 at NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12822	25857		1.71	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (G6P) gene, complete cds
1068	14113	27063	2.09	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1405	14438	27406	8.16	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1405	14438	27407	8.16	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2017	15038	28049	15.42	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
2195	15210	28228	5.71	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2419	15426	28449	5.29	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2555	16013	28640	1.05	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-4)
3182	16237	29154	6.2	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-3:10700-013-409_1 CT0432 Homo sapiens cDNA
3182	16237	29156	6.2	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-3:10700-013-409_1 CT0432 Homo sapiens cDNA
3901	16841	29852	1.75	1.0E-14	AA682594.1	EST_HUMAN	es6b2.12 Stragene schizo brain 31T Homo sapiens cDNA clone IMAGE:971350 3'
4500	17525	30410	2.07	1.0E-14	AW275852.1	EST_HUMAN	xc39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2763059 3'
5907	18993	32184	2.1	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/mid-chain fatty acid-CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6831	25659	33176	11.02	1.0E-14	11437160	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6831	25659	33177	11.02	1.0E-14	11437160	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
1579	14812	27584	1.78	9.0E-15	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2163	15198		1.37	9.0E-15	AF166770.1	NT	Homo sapiens transcription factor (GHM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 0, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha$
7738	20493	34056	4.26	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8350	21319	34733	1.17	9.0E-15	BE03559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960159 5'
2822	13653		1.42	8.0E-15	BE281462.1	EST_HUMAN	601148832F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7387	20356	33706	1.55	7.0E-15	BF035327.1	EST_HUMAN	601148833F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:362086 5'
10801	23722		2.45	7.0E-15	AW241958.1	EST_HUMAN	x177602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element
596	14047	27001	6.55	6.0E-15	AJ277356.1	NT	Homo sapiens Xq pseudocautosomal region; segment 2/2
6027	19110	32311	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6027	19110	32312	1.11	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
410	13483	28418	5.24	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2771	15763	28784	2.05	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
3482	16528		1.08	5.0E-15	AW296817.1	EST_HUMAN	U1H-BWG-4p-p-10c-U1.s1 NCI_CGAP_S1088 Homo sapiens cDNA clone IMAGE:2731218.3'
11035	23959		2.27	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06.5'
427	13122	26520	3.54	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6822	10878	33166	0.98	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0501
11401	21088	34487	1.79	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11401	21088	34488	1.78	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4246	17274		6.64	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142.5' similar to ANFCARDIODILATIN
5067	18077	30958	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5067	18077	30959	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6988	20209		1.27	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2DT PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7495	20460	33819	3.66	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7495	20460	33820	3.66	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
10285	23210		2.66	3.0E-15	AA4807128.1	EST_HUMAN	cd3807.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:1351784.3' similar to contains MER19.11
11146	24108	37633	3.42	3.0E-15	AB028898.1	NT	MER19 repetitive element ; Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL4 genes, complete cds)
260	13347	28273	4.45	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
388	13454	28382	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
388	13454	28383	4.01	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2381	15388	28413	1.02	2.0E-15	BE350127.1	EST_HUMAN	h09001.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256.3' similar to contains MER29.53
2381	15389	28414	1.02	2.0E-15	BE350127.1	EST_HUMAN	h09001.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256.3' similar to contains MER29.53
4095	17129	30023	1.21	2.0E-15	AW238499.1	EST_HUMAN	h09001.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741521.3' similar to contains L1.13 L1

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4853	17674		2.73	2.0E-15	AI80335.1	EST_HUMAN	w70708.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN.1
6308	19377	32618	1.02	2.0E-15	BE62352.1	EST_HUMAN	G0134233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6306	19377	32617	1.02	2.0E-15	BE62352.1	EST_HUMAN	G0134233F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7321	20292		1.42	2.0E-15	AI40087.1	NT	Homo sapiens ASC13 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
7486	20451	33810	2.84	2.0E-15	AA704195.1	EST_HUMAN	Z177643.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7625	20585	33948	4.75	2.0E-16	W05094.1	EST_HUMAN	Z177643.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
8117	21054	34451	0.97	2.0E-16	AL163247.2	NT	WP:14474.8 CE02227 TRANSPOSASE.1
8257	22223	35653	2.73	2.0E-16	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C047
9427	22391	35829	0.74	2.0E-15	AA397758.1	EST_HUMAN	Human DNA, SINE repetitive element
9427	22391	35830	0.74	2.0E-15	AA397758.1	EST_HUMAN	Z177608.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9759	22700	36157	1.18	2.0E-15	AA397758.1	EST_HUMAN	Z177608.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9759	22700	36156	1.19	2.0E-15	AA397758.1	EST_HUMAN	CMQ-HT0244-201095-078-at12 HT0244 Homo sapiens cDNA
11187	24143		4.15	2.0E-15	AL271735.1	NT	CMQ-HT0244-201095-078-at12 HT0244 Homo sapiens cDNA
12834	18339	31288	3.19	2.0E-15	AF223391.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12834	18338	31289	3.19	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
2785	15777		2.95	1.0E-15	AI698984.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
3025	16092	29005	1.83	1.0E-15	BE043584.1	EST_HUMAN	X25605.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.1
3158	16214	29028	1.2	1.0E-15	P08647	SWISSPROT	INR4002.Y1 NCI CGAP_Ox34 Homo sapiens cDNA clone IMAGE:2999162 5'
5189	18198	31071	1.11	1.0E-15	AI894928.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6508	19572	32925	1.63	1.0E-16	T05763.1	EST_HUMAN	wf8604.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494860 3'
7205	19979		1.83	1.0E-15	BE074217.1	EST_HUMAN	Z177610.x1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MERS repetitive element.1
7209	19974	33272	0.76	1.0E-15	P39057	SWISSPROT	QV3-B1 10569-270700-074-g05 BT0569 Homo sapiens cDNA
8574	21542	34982	1.04	1.0E-15	AL163280.2	NT	DYNEIN BETA CHAIN, CILIARY
8793	21730	35152	4.51	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8793	21730	35153	4.51	1.0E-15	AI200976.1	EST_HUMAN	q168006.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8394	22359	35789	0.49	1.0E-15	AL163207.2	NT	q168006.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9397	22362	35793	1.5	1.0E-15	4507208.NT	NT	Homo sapiens chromosome 21 segment HS21C007



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6802	22806	36055	0.79	1.0E-15	Q38575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
6890	22817	36883	0.95	1.0E-15	AA664653.1	EST_HUMAN	chr37a03.s1 NC1_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1456972 3' similar to contains L1 L3 L1
11169	24127	37657	4.18	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
13008	25720	37612	9.25	1.0E-16	AI763944.1	EST_HUMAN	131-r05.x1 NO_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive
4532	17555	30443	1.15	9.0E-16	4503168	NT	repetitive element;
11338	24286	37812	1.94	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Discepolia)-like 1 (CCAA1 displacement protein) (CUTL1) mRNA
5766	18878	32060	0.78	7.0E-16	4885120	NT	HSC2F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
7564	20527	33885	1.46	7.0E-16	O88807	SWISSPROT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7664	20527	33886	1.45	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
12957	25509		1.88	7.0E-16	I784149.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
2151	15167		7.77	6.0E-16	AW672611.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
1489	14522	27495	1.28	5.0E-16	AL251154.1	NT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2889	15885	25702	2.52	5.0E-16	AA992178.1	EST_HUMAN	ye26-12.r1 Stragane lung (6537210) Homo sapiens cDNA clone IMAGE:118052 5'
10414	23336	35821	0.48	5.0E-16	AL163246.2	NT	EST3384702 IMAGE: resequences, MAGL Homo sapiens cDNA
11849	24732	38319	2.54	5.0E-16	BF217368.1	EST_HUMAN	mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
13044	25535		10.68	5.0E-16	11418127	NT	chr02a4.s1 Scovex_total_fetus_Nb2H-F8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
2249	15283		1.64	4.0E-16	AB001523.1	NT	contains element L1 repetitive element;
2388	15396	28421	2.21	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
2398	15396	28422	2.21	4.0E-16	AW797168.1	EST_HUMAN	601885734.F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
3471	15517	29436	3.94	4.0E-16	Q16653	SWISSPROT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4168	17197	30083	4.74	4.0E-16	BE083875.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PVP2, complete and partial cds
7980	20919	34310	37.37	4.0E-16	BE083875.1	EST_HUMAN	QV1-UM00036-200300-115-g02 UM0038 Homo sapiens cDNA
6650	22594	36042	0.67	4.0E-16	AL163284.2	NT	QV1-UM00036-200300-115-g02 UM0038 Homo sapiens cDNA
12290	25106		2.41	4.0E-16	P08548	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
12392	25169	31818	2.11	4.0E-16	6812456	NT	PM4-BT10650-010400-002-g09 BT10650 Homo sapiens cDNA
12656	25336		1.38	4.0E-16	AW022892.1	EST_HUMAN	PM4-BT10650-010400-002-g09 BT10650 Homo sapiens cDNA
133	13238	28169	1.24	3.0E-16	AW022892.1	EST_HUMAN	PM4-BT10650-010400-002-g09 BT10650 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
133	13238	26170	1.24	3.0E-16	AW022892.1	EST_HUMAN	d145c01.y1 Merton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2468376 5'
466	13339		1.91	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
476	13548		3.08	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1446	14479	27455	1.33	3.0E-16	Q25893	SWISSPROT	ZONADHESIN PRECURSOR
2998	16046	28966	3.84	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (NA) [CONTAINS: GLYCOPROTEIN GP220]
3953	16993	29909	0.96	3.0E-16	T08169.1	EST_HUMAN	EST00600 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
3980	17020		0.77	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3981	17021		1.06	3.0E-16	U03887.1	NT	Human BXP20 gene
5350	18455		1.11	3.0E-16	AA077225.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5698	18793	31986	1.2	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8005	21971	35392	4.92	3.0E-16	A002836.1	EST_HUMAN	am98h05.x1 Stragene schizo train S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR12 THR repetitive element ;
10250	23175		0.9	3.0E-16	BF60617.1	EST_HUMAN	602246538FT NIH_MGC 82 Homo sapiens cDNA clone IMAGE:4332032 5'
10478	23400	36997	5.77	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13079	25951	31317	1.4	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L1623 5'
873	14025		1.04	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2395	15402		1.32	2.0E-16	AA621761.1	EST_HUMAN	ad08b04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2699	15595		1.25	2.0E-16	J03061.1	NT	Human SNAV-related endogenous retroviral LTR-like element
4207	17236	30123	1.14	2.0E-16	X69211.1	NT	H sapiens DNA for endogenous retroviral like element
6905	19957	33254	0.83	2.0E-16	Q31125	SWISSPROT	HISTIDINE-RICH PROTEIN KE4
7884	20923	34316	1.4	2.0E-16	AI470723.1	EST_HUMAN	H16611.x1 NCI CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element ;
8300	21269	34681	1.86	2.0E-16	AI732837.1	EST_HUMAN	nz47063.x5 NCI CGAP_P112 Homo sapiens cDNA clone IMAGE:1200947 similar to TR:O54849 O54849 HYPOPHYSICAL 42.8 KD PROTEIN [2] TR:O08005 contains MER7 t1 MER7 repetitive element ;
8498	21466	34882	0.73	2.0E-16	BE568026.1	EST_HUMAN	782h09.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3'
8498	21466	34883	0.73	2.0E-16	BE568026.1	EST_HUMAN	782h09.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3'
8872	21939	35281	0.76	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-601 PT0034 Homo sapiens cDNA
8872	21939	35282	0.75	2.0E-16	AW877214.1	EST_HUMAN	GM4-PT0034-180200-506-601 PT0034 Homo sapiens cDNA
11274	24226	37752	1.88	2.0E-16	5802145	NT	Homo sapiens ubiquitin carrier protein E2-C (UBCH10), mRNA
186	13286	28210	2.97	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
382	13495		37.96	1.0E-16	AAG28592.1	EST_HUMAN	af3911.1.1 Soares, total, fetus, NB2H8, sw Homo sapiens cDNA clone IMAGE:1034084.3 similar to contains OFR 12 OFR repetitive element:
1988	15009	28014	2.22	1.0E-16	BF327942.1	EST_HUMAN	QV4-BN0148-070700-283-at10 EN0148 Homo sapiens cDNA
5810	18900	32083	0.88	1.0E-16	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6574	19834		25.8	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (GMR8R) gene, complete cds
6726	19782	33061	3.06	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7802	19834		6.75	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (GMR8R) gene, complete cds
9638	22882	36031	1.08	1.0E-16	AW676651.1	EST_HUMAN	QV2.PT0012-040400-124-e05 P10012 Homo sapiens cDNA
3751	19793	29704	2.77	9.0E-17	AW800048.1	EST_HUMAN	CM1-KN1003-200300-163-401 NN1003 Homo sapiens cDNA
6868	19938		2.35	9.0E-17	AI392964.1	EST_HUMAN	ig2211.x1 NCL_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2109524.3 similar to contains MER28.12 MER28 repetitive element:
8445	21414		5.47	9.0E-17	AF150287.1	EST_HUMAN	xg6g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950.3 similar to contains OFR 12 OFR repetitive element:
10584	23506		2.3	9.0E-17	AF220719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1020	14066		2.01	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-401 OT0032 Homo sapiens cDNA
3807	16347		0.88	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C030
5863	25842	31927	3.24	8.0E-17	BE17281.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7480	20455		1.82	8.0E-17	AV730769.1	EST_HUMAN	AV730769 HTF Homo sapiens cDNA clone HTFAB07.5
8018	20956	34349	0.54	8.0E-17	6753951	NT	Mus musculus dynein, axon, heavy chain 11 (Dnaht11), mRNA
1452	14485		2.63	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBc2), mRNA
5395	18499		3.14	7.0E-17	AF216550.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6845	19598	33183	7.34	7.0E-17	AF228943.1	NT	Mus musculus WNT-2 gene, partial cds; putative enkyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
204	13305	28234	6.82	6.0E-17	AW683880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
8446	19511	32761	1.8	6.0E-17	AW652722.1	EST_HUMAN	h81d04.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695.3 similar to contains L1.12 L1 repetitive element:
10655	23577	37074	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
10926	23846		0.46	6.0E-17	W92331.1	EST_HUMAN	ze15h03.at1 Soares, fetal, heart, N9HHT9W Homo sapiens cDNA clone IMAGE:359093.3
421	13116	26014	3.22	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stragelene lung (8537210) Homo sapiens cDNA clone IMAGE:79839.5
7840	20787	34182	1.78	5.0E-17	T81043.1	EST_HUMAN	x2b04.r1 Soares, fetal, liver, spleen, INFLS Homo sapiens cDNA clone IMAGE:109327.5
9717	22745	36198	1.24	4.0E-17	AW129165.1	EST_HUMAN	x2b04.x1 NCL_CGAP_Ki68 Homo sapiens cDNA clone IMAGE:2618622.3 similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element:

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11821	24704	38286	1.66	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12303	25114		2.02	4.0E-17	A0173546.1	EST_HUMAN	Q16530 PMS3 mRNA, testis. NIH Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR-Q16530
1490	14523		1.72	3.0E-17	D14547.1	NT	Q16530 PMS3 mRNA, testis. NIH Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR-Q16530
2108	15125	28144	1.22	3.0E-17	AW118123.1	EST_HUMAN	Human DNA, SINE repetitive element
3208	16263		1.68	3.0E-17	P35410	SWISSPROT	x88609.x1 Soares_NFL1_GBC_S1 Homo sapiens cDNA clone IMAGE:2804784 3'
3658	16689	28614	1.33	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3659	16689	28615	1.33	3.0E-17	BE326522.1	EST_HUMAN	h04504.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181699 3'
5088	18078		1.17	3.0E-17	BF811266.1	EST_HUMAN	h04504.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181699 3'
			1.17	3.0E-17	BF811266.1	EST_HUMAN	UIH814-c9 c-06-C-UT1a1 NCL CGAP_Su8a Homo sapiens cDNA clone IMAGE:3065043 3'
8811	21579	34995	1.16	3.0E-17	N88461.1	EST_HUMAN	z14b02.s1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:292491 3' similar to contains P1R5.13 P1R5 repetitive element
10060	22987	36455	4.94	3.0E-17	AB028688.1	NT	Homo sapiens DNA, DLEC1 to ORG1L4 gene region, section 1/2 (DLEC1, ORG1L3, ORG1L4 genes, complete cds)
10749	23663	37164	0.73	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-at2 BN0047 Homo sapiens cDNA
10746	23663	37166	0.73	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-at2 BN0047 Homo sapiens cDNA
12268	25088		3.31	3.0E-17	11417668	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
353	13442	26387	3.4	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCL CGAP_E602 Homo sapiens cDNA clone IMAGE:1959222 3' similar to contains Aliu repetitive element
354	13442	26387	3.97	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCL CGAP_E602 Homo sapiens cDNA clone IMAGE:1959222 3' similar to contains Aliu repetitive element
880	14042		2.04	2.0E-17	AA122832.1	EST_HUMAN	z861d04.s1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:399751 3'
2483	15458	28478	2.3	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2453	15458	28480	2.3	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2941	15939	28922	6.23	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5440	18542	31452	1.8	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5440	18542	31453	1.8	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6395	18463		1.99	2.0E-17	AF055066.1	NT	Homo sapiens MHC class I region
6838	19696		1.68	2.0E-17	AL134881.1	EST_HUMAN	DKFZ27620610.1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZ27620610 5'
8133	21070	34489	0.85	2.0E-17	AB037639.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8420	21389	34789	1.47	2.0E-17	Q88166	SWISSPROT	OL FACTORY RECEPTOR-LIKE PROTEIN OLF3
8900	21767	35191	1.26	2.0E-17	AA300640.1	EST_HUMAN	EST13304 Testis tumor Homo sapiens cDNA 5' and similar to similar to glycogenin
10228	23153	36943	2.35	2.0E-17	BE236888.1	EST_HUMAN	800944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2840615 5'
10284	23189	36973	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10264	23169	36674	2.83	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10622	23544	37044	5.23	2.0E-17	D13361.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10745	23667	37162	0.68	2.0E-17	P68063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10745	23667	37163	0.68	2.0E-17	P68063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10772	23693	37190	0.57	2.0E-17	AI168902.1	EST_HUMAN	w64b04.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10772	23693	37191	0.57	2.0E-17	AI168902.1	EST_HUMAN	w64b04.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
12368	25153		1.31	2.0E-17	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1721	13812	28755	3.24	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1721	14761		1.36	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1782	14811	27787	4.94	1.0E-17	AL160207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2124	15141	28168	1.96	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2343	15353	28374	2.43	1.0E-17	U75410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3581	16626		1.05	1.0E-17	AF224603.1	NT	Homo sapiens thymosin, beta A, (yeastoma) (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4162	17163		8.5	1.0E-17	R09942.1	EST_HUMAN	X60407.11 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128388 5'
6900	19650		0.88	1.0E-17	AW468498.1	EST_HUMAN	h63605.x1 NCI_CGAP_OML1 Homo sapiens cDNA clone IMAGE:2821312 3' similar to contains Alu repetitive element/contains LTRs, 11 LTR8 repetitive element, 1
6909	19863	33151	1.73	1.0E-17	AI185642.1	EST_HUMAN	q64505.x1 Soares_fetal_lung_NH-L18W Homo sapiens cDNA clone IMAGE:1743825 3'
6909	19863	33152	1.73	1.0E-17	AI185642.1	EST_HUMAN	q64505.x1 Soares_fetal_lung_NH-L18W Homo sapiens cDNA clone IMAGE:1743825 3'
7298	20288	33603	0.96	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8939	21605	35329	1.7	1.0E-17	BE062744.1	EST_HUMAN	QV0-B10283-101289-072-d07 B10283 Homo sapiens cDNA
10366	23239	36768	1.97	1.0E-17	AW966538.1	EST_HUMAN	QV3-BK0048-229300-129-c10 BK0048 Homo sapiens cDNA
11747	24632	38212	1.64	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLOK) [CONTAINS: TETRAKIN]
13104	25825		1.63	1.0E-17	BE221470.1	EST_HUMAN	h62565.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1
9856	22792		2.98	8.0E-18	AI472167.1	EST_HUMAN	h62565.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1
3800	16840	29747	1.87	8.0E-18	4758977	NT	h62565.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1
3889	16839	28650	3.75	8.0E-18	Q07537	SWISSPROT	h62565.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1
349	13438		23.15	7.0E-18	AW316076.1	EST_HUMAN	h62565.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171104 3' similar to contains MER13.b1

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
349	13438	26392	23.15	7.0E-18	AW316976.1	EST_HUMAN	xx10604.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S
7677	20835	33997	0.95	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); RC3-O-OT0091-170300-011-003 OT0091 Homo sapiens cDNA
12769	13438	26391	2.67	7.0E-18	AW316976.1	EST_HUMAN	xx10604.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S
12769	13438	26392	2.67	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN); xx10604.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbL20868 60S
3306	16359	28278	1.29	6.0E-18	X71791.2	NT	Rattus norvegicus partial GdhP2-1 gene for dila-derived neuroprotease neslin I, enhancer region
4777	17797		4.3	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8593	21561		2.84	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8891	21659	35082	0.57	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11469	24412	37681	1.54	6.0E-18	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
11657	24593	38166	2.06	6.0E-18	X97344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IIP2, LIMP2, TAP1, LIMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12627	25256	31805	2.95	6.0E-18	U87628.1	NT	Human acollitase hydrolase (AC02) gene, exon 4
1150	14192	27144	17.6	5.0E-18	AI280214.1	EST_HUMAN	gms911.x1 Scores, placenta, 8to2weeks, 2NbpHP8b9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
5345	18450	31321	0.99	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-1747D
9070	22036	35456	5.53	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221088-002-c06 HT0161 Homo sapiens cDNA
11323	24273	37800	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11923	24273	37801	3.26	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12849	25332	37801	6.26	5.0E-18	AW887182.1	EST_HUMAN	MRT1-SN0333-000400-001-g11 SN0333 Homo sapiens cDNA
12980	25544		3.2	5.0E-18	AV850547.1	EST_HUMAN	AV850547 GLC Homo sapiens cDNA clone GLC0402 3'
125	13232	28160	1.04	4.0E-18	BE044076.1	EST_HUMAN	xx36104.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29.b3
125	13232	28161	1.04	4.0E-18	BE044076.1	EST_HUMAN	xx36104.x1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:3038511 3' similar to contains MER29.b3
1729	14759	27744	1.81	4.0E-18	AA821814.1	EST_HUMAN	ng2411.at NCL CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gbM28529
1808	14630		0.95	4.0E-18	AI73592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN); xx33108.x1 NCL CGAP_Cot0 Homo sapiens cDNA clone IMAGE:2392095 3'
2211	15226	28247	1.1	4.0E-18	Q08430	SWISSPROT	N-ACETYL-LACTOSAMINIDE BETA-1-6-N-ACETYL-GLUCOSAMINYL TRANSFERASE (N-ACETYL-GLUCOSAMINYL TRANSFERASE) (C-BRANCHING ENZYME) (IGNT)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2211	15226	28248	1.1	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (GNNT)
3808	18648	29753	0.78	4.0E-18	A1581585.1	EST_HUMAN	ar3b08.x1 Barleas colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element.
5437	18539	31447	2.29	4.0E-18	A1017565.1	EST_HUMAN	0023a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5437	18539	31448	2.28	4.0E-18	A1017566.1	EST_HUMAN	0023a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8178	21148		0.67	4.0E-18	AA74681.1	EST_HUMAN	nc84a08.s1 NCI_CGAP_ALM1 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1,12 L1 repetitive element.
11348	24298	37826	4.22	4.0E-18	AA371807.1	EST_HUMAN	EST16353 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
850	13006	26885	24.86	3.0E-18	AA814195.1	EST_HUMAN	0b23h11.s1 NCI_CGAP_JK68 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SWR56_HUMAN
530	13883	26886	3.54	3.0E-18	BE06834.1	EST_HUMAN	P-48782 40S RIBOSOMAL PROTEIN S6.
3972	17012	26926	1.31	3.0E-18	AL163247.2	NT	QAC0-B10690-210300-288-007 B10690 Homo sapiens cDNA
7003	20129	33444	6.43	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
11271	24223	37746	1.78	3.0E-18	BF218650.1	EST_HUMAN	PNC-BN0061-100300-001-508 BN0081 Homo sapiens cDNA
12774	25412		5.15	3.0E-18	AW02015.1	EST_HUMAN	601884856FT NIH_MGC_S7 Homo sapiens cDNA clone IMAGE:4103652 5'
251	13348	28274	5.97	2.0E-18	AW838620.1	EST_HUMAN	d131h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
1155	14197		67.85	2.0E-18	BE266097.1	EST_HUMAN	QV14-L10039-150200-070-007 L10039 Homo sapiens cDNA
3140	16197	29107	1.27	2.0E-18	Q35975	SWISSPROT	60114352F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
5485	16585		3.85	2.0E-18	AA868610.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5394	16890	31644	3.38	2.0E-18	D14547.1	NT	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408652 3' similar to TR:014577
5594	16890	31645	3.38	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM TQ31. COMPLETE SEQUENCE. ;
5978	19093		1.67	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6289	19351	32598	1	2.0E-18	X60459.1	NT	Human DNA, SINE repetitive element
6289	19351	32599	1	2.0E-18	X60459.1	NT	602021164FT NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
6409	19477	32724	0.75	2.0E-18	BF352640.1	EST_HUMAN	Human FNAR gene for Interferon alpha/beta receptor
6451	19516	32767	4.42	2.0E-18	AW665953.1	EST_HUMAN	Human FNAR gene for Interferon alpha/beta receptor
7870	20029	33893	0.72	2.0E-18	AA457618.1	EST_HUMAN	IL3-H10619-220700-222-012 H10619 Homo sapiens cDNA
8487	21455	34872	0.52	2.0E-18	BE439524.1	EST_HUMAN	ribAgp01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.12 MER19 repetitive element
							aa8911.1 Stragapene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to
							TR-G61634.061634 POLYPEPTIDE PR77 ;
							HTM1-160F1 HTM1 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10407	23329	36813	1.31	2.0E-18	AW151673.1	EST_HUMAN	x87a10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
10407	23329	36814	1.31	2.0E-18	AW151673.1	EST_HUMAN	x87a10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12 MER10 repetitive element;
11319	24289	37797	3.07	2.0E-18	AW470791.1	EST_HUMAN	h33d06.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875409 3' similar to contains THR.b3 THR repetitive element;
12039	24914	38508	2.88	2.0E-18	AW151299.1	EST_HUMAN	xq47c09.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element;
12461	14197		3.97	2.0E-18	BE256097.1	EST_HUMAN	601114322F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5' L1 repetitive element;
4445	17471		0.93	1.0E-18	T85408.1	EST_HUMAN	y43g05.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:120358 5' similar to contains L1 repetitive element;
5429	18532	31412	2.71	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLOCHE11 3'
5850	18746	31914	1.87	1.0E-18	D000581	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5850	18746	31915	1.87	1.0E-18	D000581	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6597	18657	32929	1.33	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HSZ1C080
8785	21752	36174	1.13	1.0E-18	AI146288.1	EST_HUMAN	cc6b09.x1 Soares, senescent, fibroblasts_NBHSF Homo sapiens cDNA clone IMAGE:1880583 3' similar to contains L1.L1 L1 repetitive element;
10259	23184	36699	4.28	1.0E-18	U81328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorA gene, and sodium phosphate transporter (NPT3) gene, complete cds
12412	25184	31821	6.49	1.0E-18	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
547	19818	26540	5.55	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
548	19818	26540	4.1	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
8181	21151		5.71	9.0E-19	F08688.1	EST_HUMAN	HSC29F057 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8036	22002	35423	2.84	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HSZ1C003
9038	22002	35424	2.84	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HSZ1C003
11462	24405	37653	3.37	9.0E-19	AB032959.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12172	13618	26540	1.94	9.0E-19	AA281961.1	EST_HUMAN	z111d06.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element;
1050	14066		1.31	8.0E-19	AW674902.1	EST_HUMAN	EST387007 MAGC resequences, MAGN Homo sapiens cDNA
4433	17460		0.96	8.0E-19	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8488	21456	34873	1.04	8.0E-19	BE156836.1	EST_HUMAN	MRQ-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2257	15271	28286	1.43	7.0E-16	4759139	NT	Homo sapiens DEAD(H) (Asp-Glu-Ala-Asp-His) box polypeptide 6 (RNA helicase, 54kD) (DDX9) mRNA
6598	19658	32930	1.95	7.0E-19	AF092090.1	NT	Rattus norvegicus opt151 mRNA, partial cds
7519	20484	33845	1.02	7.0E-16	P28444	SWISSPROT	BETA CRYSTALLIN A2
10372	23295	38771	0.43	7.0E-19	AI344851.1	EST_HUMAN	IGFBP3-01.NC1 CGAP Lu28 Homo sapiens cDNA clone IMAGE:2062302.3'
12313	25669		3.28	7.0E-19	AA705894.1	EST_HUMAN	zif600.1.1 Scores: fetal liver, spleen, 1NRLS_S1 Homo sapiens cDNA clone IMAGE:435145.3'
3782	16833		1.6	8.0E-19	AW852300.1	EST_HUMAN	PMD-C10248-131099-001-p01 C10248 Homo sapiens cDNA
4490	17515	30403	1.44	8.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4490	17515	30404	1.44	8.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4837	17854		1.47	8.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5084	18074	30954	1.28	8.0E-19	AL120817.1	EST_HUMAN	DKF-Zp762F192.1 782 (synonym: hmel2) Homo sapiens cDNA clone DKF-Zp762F192.5'
5958	19043	32242	4.88	5.0E-19	Q00193	SWISSPROT	ZP-X (RC95)
5342	19411	32652	0.99	5.0E-19	AW683302.1	EST_HUMAN	h177606.YT NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2985787.5'
10760	23711	37213	0.78	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL12RB1 gene for IL-12 receptor beta1 chain, exon 14
11805	24747	38329	4.78	5.0E-19	AW183725.1	EST_HUMAN	X187002.x1 Scores: NFL_T GBC S1 Homo sapiens cDNA clone IMAGE:2664171.3' similar to contains element MSR1 repetitive element
556	13628	26544	0.89	4.0E-19	AB007870.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2981	15687	28704	1.69	4.0E-19	BF687382.1	EST_HUMAN	602130810F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287874.5'
5470	18571	31481	1.05	4.0E-19	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
3956	16905	29812	1.4	3.0E-19	Q28987	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3956	16905	29813	1.4	3.0E-19	Q28987	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4315	17344	30227	0.99	3.0E-19	Q43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4315	17344	30228	0.99	3.0E-19	Q43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4475	17501	30385	1.79	3.0E-19	AV708138.1	EST_HUMAN	AV708138 ADC Homo sapiens cDNA clone ADCAMA11.5'
5352	18457		0.63	3.0E-19	AF229467.1	NT	Homo sapiens NP0003 protein (NP0003) mRNA, complete cds
7612	20572		1.81	3.0E-19	11432214	NT	Homo sapiens similar to aldol-keto reductase family 1, member 811 (aldose reductase-like) (H. sapiens) (LOC83222) mRNA
8814	21137	34539	1.11	3.0E-19	X86695.1	NT	M. musculus mRNA for TPCRC33 protein
12552	26275		10.28	3.0E-19	AF165520.1	NT	Homo sapiens ribonin 1 protein (PBI) mRNA, complete cds
2587	15688	28589	27.04	2.0E-19	AL165201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4474	17500		1.23	2.0E-19	AI311783.1	EST_HUMAN	qs01602.x1 NCL_OGAP_Kid3 Homo sapiens cDNA clone IMAGE:1915898.3' similar to TR-Q69588 Q69586 POJENV GENE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6172	19247	32480	0.61	2.0E-19	AV731982.1	EST_HUMAN	AV731982 HTF Homo sapiens cDNA clone HTFAZC08 5'
7551	20524	33882	0.72	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8673	21841	35088	9.35	2.0E-19	AA012854.1	EST_HUMAN	3634c09.r1 Soares online N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10269	23194	36682	0.66	2.0E-19	Q65155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OL2
482	13565		2.11	1.0E-19	BE408811.1	EST_HUMAN	601304125F.1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							y07907.r1 Soares adult brain N2b4HB557 Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2174	15190	29211	1.68	1.0E-19	H30795.1	EST_HUMAN	Human gene for Ah-receptor, exon 1-9
2729	15723		2.48	1.0E-19	D38044.1	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
2860	15920		4.28	1.0E-19	4765977	NT	el49b12.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.2
3412	16460	29381	1.18	1.0E-19	AA834687.1	EST_HUMAN	MER37 repetitive element;
							xc88h10.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604739 3' similar to contains L1.1 L1
5186	18195		0.8	1.0E-19	AW117377.1	EST_HUMAN	ryc2d03.st NOI_CGAP_P1 Homo sapiens cDNA clone IMAGE:953083 similar to contains L1.1 L1
6193	19297	32502	2.73	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
6333	25095		0.63	1.0E-19	AA595527.1	EST_HUMAN	repetitive element;
7890	20934	34213	0.98	1.0E-19	U08913.1	NT	Oryctolagus cuniculus Nsr/glucose cotransporter-related protein mRNA, complete cds
7890	20934	34214	0.99	1.0E-19	U08913.1	NT	Oryctolagus cuniculus Nsr/glucose cotransporter-related protein mRNA, complete cds
8085	25694		0.71	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
8793	21760	35182	1.72	1.0E-19	M84657.1	NT	Rabbit phosphotyrase kinase beta subunit mRNA, complete cds
							y072002.r1 Soares fetal liver spleen, 1NFLS Homo sapiens cDNA clone IMAGE:123249 5' similar to contains OFR repetitive element;
8093	22059		2.74	1.0E-19	T9620.1	EST_HUMAN	Human tyrosophin (OHD) gene, exons 7, 8 and 9, and partial cds
10108	23032		0.97	1.0E-19	U060822.1	NT	RCO-ST0174-191099-031-505 ST0174 Homo sapiens cDNA
10547	23489	36984	27.33	1.0E-19	AW812259.1	EST_HUMAN	Y918109.r1 Soares melanocyte SNHMM Homo sapiens cDNA clone IMAGE:272872 5'
10557	23479	36974	2.1	1.0E-19	AA44631.1	EST_HUMAN	d14901.Y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5'
11809	24694		3.69	1.0E-19	AW023137.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6903	19857	33143	2.46	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6903	19857	33144	2.45	8.0E-20	7657286	NT	q98609.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7761	20714	34084	1.31	8.0E-20	A1221371.1	EST_HUMAN	q98609.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7761	20714	34085	0.71	8.0E-20	A1221371.1	EST_HUMAN	PM4-AN00065-03000-003-ae04 AN00065 Homo sapiens cDNA
3289	16342	29263	1.32	7.0E-20	BF22455.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D092 5'
7188	18419	31220	5.66	7.0E-20	AL138120.1	EST_HUMAN	m46604.st NOI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.82
8841	21808	35227	9.11	7.0E-20	AA597657.1	EST_HUMAN	MER29 repetitive element;

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Table 4  
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	21808	35228	9.11	7.0E-20	AA57657.1	EST_HUMAN	n146604.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 b2
12023	24899		6.31	7.0E-20	6A12633	NT	MER29 repetitive element;
3668	15613	29535	3.93	6.0E-20	P38188	SWISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4301	17930	30210	2.88	6.0E-20	BE622434.1	EST_HUMAN	ALU SUBFAMILY J1 SEQUENCE CONTAMINATION WARNING ENTRY
4926	17647		1.06	5.0E-20	AV725123.1	EST_HUMAN	801441231 F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7322	20283	33836	1.19	5.0E-20	AF075301.1	EST_HUMAN	AA728123 H7C Homo sapiens cDNA clone HTCBTA01 5'
8277	21246	34657	5	5.0E-20	W90525.1	EST_HUMAN	AF076301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8277	21246	34657	5	5.0E-20	W90525.1	EST_HUMAN	2178608.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8440	21409	34822	0.79	5.0E-20	BE163860.1	EST_HUMAN	2178608.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8187	22153	35582	1.24	5.0E-20	AB028174.1	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9187	22153	35582	1.24	5.0E-20	AB028174.1	NT	Mus musculus IMAN-g mRNA, complete cds
9800	22123		0.93	5.0E-20	O60809	SWISSPROT	Mus musculus IMAN-g mRNA, complete cds
1624	14657	27635	1.73	4.0E-20	AL163247.2	NT	HYPOTHETICAL PROTEIN DJ845024.1
5732	18526		0.89	4.0E-20	Q98880	SWISSPROT	Homo sapiens chromosome 21 segment HS210047
8298	21227		6.27	4.0E-20	A1874352.1	EST_HUMAN	HISTONE H2B C (H2B/C)
10895	23785	37266	1.8	4.0E-20	AW637466.1	EST_HUMAN	554403.x1 NCI_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:22583386 3'
2149	15165	28181	0.91	3.0E-20	U03888.1	NT	QY3-DT0043-090200-000-c04 DT0043 Homo sapiens cDNA
4237	17266	30153	1.63	3.0E-20	P23273	SWISSPROT	Human EXP21 gene
4655	17676	35582	1.43	3.0E-20	AA037616.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 114
9287	22253		3.32	3.0E-20	D14547.1	NT	z35b12.s1 Soares pregnant uterus_NhpPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.481.1 repetitive element;
10684	23906	37096	0.88	3.0E-20	BF185264.1	EST_HUMAN	Human DNA, SINE repetitive element;
11024	23989		1.59	3.0E-20	P11369	SWISSPROT	601843861 F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4064943 5'
11840	24723	38306	8.22	3.0E-20	A128424.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11840	24723	38306	8.22	3.0E-20	A128424.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Ki03 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
12329	25130	31849	4.15	3.0E-20	BE888422.1	EST_HUMAN	q70d02.x1 NCI_CGAP_Ki03 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
831	13888		33.91	2.0E-20	AW303868.1	EST_HUMAN	801514180 F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
							x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761068 3' similar to SW:RS5_MOUSE
							P87461 40S RIBOSOMAL PROTEIN S5.;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1113	14157	27107	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.;
1113	14157	27108	3.88	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN.;
2828	13888		13.67	2.0E-20	AW303868.1	EST_HUMAN	x224e10.s1 NCL CGAP_Lip2 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW:RSE_MOUSE
4983	17989	30886	4.76	2.0E-20	Q28983	SWISSPROT	ZONADIESIN PRECURSOR
4983	17989	30887	4.78	2.0E-20	Q28983	SWISSPROT	ZONADIESIN PRECURSOR
8455	21424	34840	0.8	2.0E-20	AA306457.1	EST_HUMAN	EST180328 Liver III Homo sapiens cDNA 5' end
8545	22508	35957	7.66	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8545	22508	35958	7.66	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12703	25714	31611	3.98	2.0E-20	H55371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
2029	15622	29063	4.32	1.0E-20	AA281961.1	EST_HUMAN	Z1106.r1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element.;
4467	17493	30380	1.04	1.0E-20	BF115158.1	EST_HUMAN	hr84b06.s1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element.;
7079	20100	33411	1.04	1.0E-20	AF049567.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
8518	22481	35926	2.24	1.0E-20	11418461	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP) mRNA
11879	24761	38346	2.11	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12458	25216		3.08	1.0E-20	AA420453.1	EST_HUMAN	nc69g08.r1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:745594 similar to contains L1.13 L1 repetitive element.;
2923	15981		1	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-BJ21
12175	25023		3.77	9.0E-21	AW808189.1	EST_HUMAN	RC3-NN0069-090300-021-503 NN0068 Homo sapiens cDNA
9463	22129		1.13	8.0E-21	AW674891.1	EST_HUMAN	b53062.y1 NIH_LMG_C 10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR.;
11868	24748	38330	4.38	8.0E-21	AJ008411.1	EST_HUMAN	q671606.s1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:1336835 3'
12342	25140		2.84	8.0E-21	O21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2082	15099	28115	1.59	7.0E-21	P16900	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
2082	15099	28116	1.59	7.0E-21	P16900	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
3716	16769	29571	0.83	7.0E-21	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4283	17312		5.22	7.0E-21	AA045502.1	EST_HUMAN	3467a06.r1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:487898 5'
6573	16833	32900	0.81	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8731	21089	35124	1.42	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
9024	21090	35411	11.21	7.0E-21	D14718.1	NT	Human chromosomal protein HMGT related gene
10472	23394	36891	0.82	7.0E-21	AW86922.1	EST_HUMAN	RCO-CT0301-271192-031-F03 CT0301 Homo sapiens cDNA
11054	24017	37540	1.69	7.0E-21	AA728404.1	EST_HUMAN	zq73003.s1 Soares_fetal_NKH1816/Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:U14338 VITAMIN K-DEPENDENT PROTEIN 5' PRECURSOR (HUMAN); contains THR18 OFR repetitive element;
11599	24537	39094	1.97	7.0E-21	7708698	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4130	17163	30052	1.68	8.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3938310 5'
9491	22455	30052	0.98	8.0E-21	BE162737.1	EST_HUMAN	PM1-HT0464-080100-002109 HT0454 Homo sapiens cDNA
4390	17418	30302	3.16	5.0E-21	BE968939.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4839	17856	30753	8.18	5.0E-21	4895474	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
8927	20151		0.92	5.0E-21	AW440864.1	EST_HUMAN	he05610.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
7213	20266	33570	0.98	5.0E-21	BE665605.1	EST_HUMAN	7683411.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11 OFR repetitive element;
10839	23859	37374	0.43	5.0E-21	Q97690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10839	23859	37375	0.43	5.0E-21	Q97690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
12255	25081		5.38	5.0E-21	AA393574.1	EST_HUMAN	z12204.1 Soares_Ieslie_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1748	14777	27782	1.95	4.0E-21	AA970713.1	EST_HUMAN	oa89608.s1 NCI_CGAP_K465 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TRQ16530 Q16530 PMS3 mRNA; contains OFR.11 OFR repetitive element;
7055	20077	33386	3.35	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for RTM, complete cds
10139	22065	36541	0.59	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
1834	14880	27876	1.05	3.0E-21	AA218891.1	EST_HUMAN	zq75006.s1 Stratagene fetal retina g37202 Homo sapiens cDNA clone IMAGE:629771 3'
2282	15295	29319	1.48	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3096	16153	29066	4.17	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5577	18673	31836	0.93	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5577	18673	31837	0.93	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5828	18518		0.74	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLC0A10 3'
6303	10274		1.86	3.0E-21	BF184730.1	EST_HUMAN	60184465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4054945 5'
7271	20006	33306	7.18	3.0E-21	BF367093.1	EST_HUMAN	RC1-OT0063-100800-019-g08 OT0063 Homo sapiens cDNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10561	22978	36445	0.77	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280403-203-H8 NN0063 Homo sapiens cDNA
147	13250		28.46	2.0E-21	BE103247.1	EST_HUMAN	QV9-HT0498-170200-090-G12 HT0498 Homo sapiens cDNA
1219	12957		3.29	2.0E-21	BE084410.1	EST_HUMAN	IC4-BT0311-141198-011-H06 BT0311 Homo sapiens cDNA
2646	15643	28687	2.26	2.0E-21	Q26983	SWISSPROT	ZONADHESIN PRECURSOR
2646	15643	28688	2.28	2.0E-21	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
5661	18658	31604	1.54	2.0E-21	AI624682.1	EST_HUMAN	ts30103.x1 NCI_CGAP_P41 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5669	18752	31818	0.81	2.0E-21	AA027211.1	EST_HUMAN	HYPOPHYSICAL 51.1 KD PROTEIN
5669	18752	31919	0.81	2.0E-21	AA027211.1	EST_HUMAN	z697a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6149	19224	32454	0.81	2.0E-21	W44493.1	EST_HUMAN	z697a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8615	21593	34899	0.48	2.0E-21	AJ010770.1	NT	z228102.r1 Soares_senescent_fibroblasts_NH-ISF Homo sapiens cDNA clone IMAGE:326667 5'
8706	21874	35099	0.64	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
9175	22141	35597	3.96	2.0E-21	AU136779.1	EST_HUMAN	QVQ-HT0103-091199-050-G11 HT0103 Homo sapiens cDNA
11647	24584	38152	1.72	2.0E-21	BE073829.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1003032 5'
11647	24584	38153	1.72	2.0E-21	BE073829.1	EST_HUMAN	60168036FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12560	25279		17.51	2.0E-21	AF176815.1	NT	60168036FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1260	14295	27259	2.06	1.0E-21	AA557657.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1402	14435		7.77	1.0E-21	AJ001284.1	EST_HUMAN	ri46c04.g1 NCI_CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
8834	19692		2.6	1.0E-21	AL076762.1	EST_HUMAN	MER29 repetitive element
7398	20366	33719	4.83	1.0E-21	AI223104.1	EST_HUMAN	608812.x1 Bastedad colon_HPLR17 Homo sapiens cDNA clone IMAGE:2152343 3'
10803	23525	37021	0.46	1.0E-21	AL163203.2	NT	DKFZP4340830_r1 434 (synonym: h3a3) Homo sapiens cDNA clone DKFZP4340830 5'
10803	23525	37022	0.46	1.0E-21	AL163203.2	NT	ig97a05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838338 3' similar to gb:M64241 QM
10949	23959		1.37	1.0E-21	57300338	NT	PROTEIN (HUMAN)
12632	25514		1.82	1.0E-21	AF046133.1	NT	Homo sapiens chromosome 21 segment HS21C003
4439	17495	30355	2.03	9.0E-22	AJ702438.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8951	21917	35341	1.29	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8951	21917	35342	1.29	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11144	24104	37631	3.13	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSOCG05 5'
949	14002		7.03	8.0E-22	BE144748.1	EST_HUMAN	CM0-HT0176-281058-076-H05 HT0176 Homo sapiens cDNA
8228	21197		3.82	8.0E-22	AA045502.1	EST_HUMAN	z687a06.r1 Soares_pregnet_uterus_NH-FPU Homo sapiens cDNA clone IMAGE:487868 5'
968	13731	28656	0.78	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4312	17341	30221	2.36	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5076	18086	30956	0.97	7.0E-22	AB006981.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
6038	22004		2.48	7.0E-22	AF11054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9184	2150	35578	3.66	7.0E-22	AF178500.1	EST_HUMAN	EST 100738 fetal brain, Sitagliptine (cat#363208) Homo sapiens cDNA clone HFBOF07
9881	22898	36349	1.82	7.0E-22	AF095660.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TORBV/TS2A2 to TORBV12S2 region
8584	21562		1.88	6.0E-22	AW026123.1	EST_HUMAN	w03507.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
5285	18291		0.72	5.0E-22	D14647.1	NT	Human DNA, SINE repetitive element
6966	19723	32968	3.05	5.0E-22	AL103503.2	NT	Homo sapiens chromosome 21 segment HS21G103
10682	23604	37098	7.82	5.0E-22	U60622.1	NT	Human dystrophin (DMD) gene, exon 7, 8 and 9, and partial cds naa27006.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:3259698 3' similar to contains Alu repetitive element;
12775	25413		2.76	5.0E-22	BF476511.4	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3650	16693		0.83	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8442	21411	34824	0.42	4.0E-22	AF0703223.1	EST_HUMAN	AF0703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8766	29008		9.38	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11077	24039	37563	2.15	4.0E-22	BF216030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12538	25518		2.74	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
960	14013		1.06	3.0E-22	AI469079.1	EST_HUMAN	hm14h10.x1 NCI CGAP C014 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gpl.19593 HIGH AFFINITY INTERLEUKIN-3 RECEPTOR B (HUMAN); contains L1, L1.1 repetitive element;
2576	15577	26596	2.16	3.0E-22	AI859038.1	EST_HUMAN	w06604.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SV:RL21_HUMAN
3688	19729		1.35	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21 : Human chromosomal protein HMGI related gene
4838	17855	30752	2.88	3.0E-22	AI090125.1	EST_HUMAN	q28c07.x1 Soares_pregnant_Uterus_NH-P1 Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8572	21540		1.21	3.0E-22	BE159813.1	EST_HUMAN	QVQ-HT0388-090200-099412 HT0388 Homo sapiens cDNA
8577	21645	34984	3.4	3.0E-22	BE089841.1	EST_HUMAN	RC5-BT0707-150300-021-HT0 BT0707 Homo sapiens cDNA
8703	21671	35093	0.77	3.0E-22	X60660.1	NT	R ratius RY265 mRNA for a potential ligand-binding protein
8703	21671	35094	0.77	3.0E-22	X60660.1	NT	R ratius RY265 mRNA for a potential ligand-binding protein
1970	14991		4.79	2.0E-22	N24942.1	EST_HUMAN	yx78405.st Soares melanocyte 2N0HM Homo sapiens cDNA clone IMAGE:267359 3'
2528	15531	28552	1.82	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3431	16478	29398	4.76	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4263	17282	30163	1.26	2.0E-22	AW617794.1	EST_HUMAN	FM1-S10282-261199-001-d12 S10282 Homo sapiens cDNA
5951	25648	32232	1.34	2.0E-22	W39456.1	EST_HUMAN	zcc2001.1 Soares_sensory_fibroblasts_NHSE Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:272308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
6301	16372	32611	3.57	2.0E-22	BF092116.1	EST_HUMAN	RQ0-TN0076-150300-025-h12 TN0076 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10061	22988	36456	1.61	2.0E-22	AI276522.1	EST_HUMAN	q16h08.x1 Soares_NHIMP_u_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains
10156	23081	36566	0.65	2.0E-22	AA715315.1	EST_HUMAN	MER29.13 MER29 repetitive element;
10156	23081	36567	0.65	2.0E-22	AA715315.1	EST_HUMAN	in04H11.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219269 3'
10391	23911	37426	0.55	2.0E-22	PI5209.1	EST_HUMAN	in04H11.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219269 3'
10391	23911	37426	0.55	2.0E-22	PI5209.1	EST_HUMAN	YB8609.r1 Soares Infant brain T1NB Homo sapiens cDNA clone IMAGE:28740 5'
12054	24927	38525	1.58	2.0E-22	AW418960.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_K1412 Homo sapiens cDNA clone IMAGE:2874655 3'
12139	25504	37705	1.92	2.0E-22	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21O80
1696	14921	27917	1.78	1.0E-22	AW96517.1	EST_HUMAN	PMA-SN0070.016400-009-R02 SN0020 Homo sapiens cDNA
2588	15589	28606	1.82	1.0E-22	U90871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3422	16470	29390	1.46	1.0E-22	D14647.1	NT	Human DNA, SINE repetitive element
5295	18900		1.5	1.0E-22	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
8016	20953	34347	0.95	1.0E-22	BE084687.1	EST_HUMAN	topons
10918	23638	37354	0.8	1.0E-22	A1365435.1	EST_HUMAN	MRD-BT0659-220200-002-R07 BT0659 Homo sapiens cDNA
10918	23638	37355	0.8	1.0E-22	A1365435.1	EST_HUMAN	q209007.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER25.b2
12991	25551		9.05	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3385	16630	29548	0.73	8.0E-23	AF198349.1	NT	q209007.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER25.b2
3322	16373		1.98	7.0E-23	AV647246.1	EST_HUMAN	MER29 repetitive element;
11376	24523	37852	4.11	7.0E-23	5031952	NT	q209007.x1 NCI_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER25.b2
3447	16494		1.68	8.0E-23	AF168333.1	NT	MER29 repetitive element;
4297	17526	30206	1.73	6.0E-23	AL163249.2	NT	MER29 repetitive element;
12281	25009	31834	4.64	6.0E-23	AF224669.1	NT	MER29 repetitive element;
12281	25009	31835	4.64	6.0E-23	AF224669.1	NT	MER29 repetitive element;
12480	25228	31795	3.03	6.0E-23	AI209130.1	EST_HUMAN	MER29 repetitive element;
5519	18818	31552	4	5.0E-23	U82871.2	NT	MER29 repetitive element;
6357	25559	32579	3.85	6.0E-23	AF179818.1	NT	MER29 repetitive element;
7671	25559	32579	3.25	5.0E-23	AF179818.1	NT	MER29 repetitive element;



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	16940	32908	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6580	16940	32907	1.07	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8171	21141	34547	4.18	3.0E-23	AA130165.1	EST_HUMAN	z35g09.r1 Soares, pregnant uterus, Nih-PU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element;
6604	22903	30059	2.74	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
6604	22903	30059	2.74	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
10880	23602	30059	1.27	3.0E-23	AW897827.1	EST_HUMAN	RCS-KN00066-270400-011-011 NN0066 Homo sapiens cDNA
667	13732	28657	3.76	2.0E-23	AJ298880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1145	15917	28657	3.02	2.0E-23	M55270.1	NT	Human milk Gla protein (MGP) gene, complete cds
2807	15799	28817	2.08	2.0E-23	P22105	SWISSPROT	TEXASIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2807	15799	28818	2.08	2.0E-23	P22105	SWISSPROT	TEXASIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3384	18433		1.5	2.0E-23	AI201458.1	EST_HUMAN	q57311.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:1943767 3' similar to TRQ13537 Q13537
3729	16771		2.97	2.0E-23	BE165680.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
4001	17040	29947	2.99	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-113-901 HT0487 Homo sapiens cDNA
4001	17040	29948	2.99	2.0E-23	H59931.1	EST_HUMAN	Y18a02.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:205418 5'
5062	18072	30952	8.49	2.0E-23	D14547.1	NT	Y18a02.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:205418 5'
8205	21175		4.28	2.0E-23	AF260107.1	NT	Human DNA, SINE repetitive element
9195	22161	35589	1.12	2.0E-23	AL168303.2	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
12262	25086		3.91	2.0E-23	M32658.1	NT	Homo sapiens chromosome 21 segment HS21C103
12787	25419		2.65	2.0E-23	AF009860.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
4558	17581	30472	1.44	1.0E-23	AL163252.2	NT	Homo sapiens T cell receptor beta locus, TCRBV7/TS3A2 to TCRBV12S2 region
4789	17916		4.78	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C052
6882	19934		3.11	1.0E-23	BE378471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C070
6889	21987	35080	4.73	1.0E-23	AA448057.1	EST_HUMAN	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606653 5'
							zw62006.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:782688 5' similar to contains PTR5.12 PTR5 repetitive element;
							ab75608.s1 Strabagena fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
554	13824		3.05	9.0E-24	AA663213.1	EST_HUMAN	TR1E19822 P19822 CA PROTEIN ;
4678	17659	30586	1.16	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4678	17659	30587	1.16	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
6891	16851	32922	1.34	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA3), mRNA
8155	21083	34492	0.77	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3886	16926		1.36	7.0E-24	AW937894.1	EST_HUMAN	QVQ-DT047-170200-122-08 DT047 Homo sapiens cDNA
707	13769		2.31	8.0E-24	AB001421.1	NT	Macaca fascicularis mRNA for Testis-Specific Protein Y (TSPY), complete cds
839	13596	28351	15.68	8.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3894	17034	28942	8.31	5.0E-24	AJ22043.1	NT	Homo sapiens 959 kb contig between AXL1 and CBR1 on chromosome 21q22, segment 3/8
8034	20571	34366	1.34	5.0E-24	AF22391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6039	19121	33326	3.63	4.0E-24	AA594178.1	EST_HUMAN	m311h05.s1 NCL CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085629 3' similar to SW_P0L_MLVK
9028	21865	35415	1.29	4.0E-24	AW813711.1	EST_HUMAN	P31785 POL POLYPROTEIN 1
11514	24455	38005	1.52	4.0E-24	BE644922.1	EST_HUMAN	RC3-ST0197/130100-014-08 ST0197 Homo sapiens cDNA
12644	25328	31780	5.56	4.0E-24	AB028016.1	NT	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464468 5'
12807	25713	31610	9.62	4.0E-24	M20707.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12878	25509	31708	1.88	4.0E-24	T1418316	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
7285	20052	33388	0.6	3.0E-24	U66061.1	NT	Homo sapiens G-2 and S-phase expressed 1 (G7SE1), mRNA
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
7285	20082	33360	0.6	3.0E-24	U66061.1	NT	m3808.s1 NCL CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2687660 3' similar to contains MER28 b2
							MER28 repetitive element ;
8766	21733		2.89	3.0E-24	AW614871.1	EST_HUMAN	EST374149 IMAGE resequences, MAGG Homo sapiens cDNA
8822	21789		1.25	3.0E-24	AW62076.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
9820	22669	38126	4.11	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12715	25369	31772	2.16	3.0E-24	BF127762.1	EST_HUMAN	30181049F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2354	15563	28385	2.8	2.0E-24	AA187539.1	EST_HUMAN	zp1109.r1 Stralogen fetal retina 93702 Homo sapiens cDNA clone IMAGE:603161 5'
3812	16681		0.89	2.0E-24	AW898189.1	EST_HUMAN	RC3-NN0068-00500-021-503 NN0068 Homo sapiens cDNA
7583	26011		0.61	2.0E-24	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C069
7715	20672	34039	1.12	2.0E-24	AF08824.1	NT	Mus musculus rho/rac-interacting cation kinase (Crik) mRNA, complete cds
7720	20877	34042	0.55	2.0E-24	AJ003536.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MP1p12-5H13
8092	22058	35484	3.09	2.0E-24	AL161193.1	EST_HUMAN	DKFZp781L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781L1712 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9130	22086		0.96	2.0E-24	H69214.1	EST_HUMAN	y92b09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER23 repetitive element;
10213	23138	36628	0.98	2.0E-24	A1521756.1	EST_HUMAN	U77409.X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
10213	23138	36627	0.98	2.0E-24	A1521756.1	EST_HUMAN	U77409.X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12568	25947		10.03	2.0E-24	M2897.1	NT	Homo O family dispersed repeat element
1705	14735	27717	2.63	1.0E-24	T706340	NT	Homo sapiens CGH127 protein (LOC61649), mRNA
2881	15077		1.52	1.0E-24	AW820164.1	EST_HUMAN	Q1A-ST0284-100400-185-c10 ST0284 Homo sapiens cDNA
3033	16091	29008	0.78	1.0E-24	D66423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4289	17328		2	1.0E-24	AF143313.1	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
6541	19603	32665	0.68	1.0E-24	T106336	NT	Homo sapiens PTEN (PTEN) gene, exon 2
7796	20748	34123	3.98	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8002	20941	34334	0.68	1.0E-24	BE144526.1	EST_HUMAN	MRQ-HT0166-271189-005-d08 HT0168 Homo sapiens cDNA
8276	21245	34656	1.81	1.0E-24	AW801184.1	EST_HUMAN	OMD-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
6623	16683	32981	0.32	9.0E-25	11420402	NT	Homo sapiens helicase-like protein NHL (LOC87750), mRNA
12008	24885	38480	1.53	9.0E-25	T706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5031	18045	30627	2.85	7.0E-25	AA48944.1	EST_HUMAN	MEF1 repetitive element;
8561	21529	34049	6.83	7.0E-25	AA468946.1	EST_HUMAN	MEF1 repetitive element;
12012	24889	38486	3.24	7.0E-25	AA583540.1	EST_HUMAN	repulsive element;
7184	18415		4.41	8.0E-25	W87623.1	EST_HUMAN	P25H08.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
7992	20931	34326	10.26	8.0E-25	7305360	NT	P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA;
1559	14891	27697	1.97	5.0E-25	AW850271.1	EST_HUMAN	z6507.r1 Soares fetal_liver_spleen_1NFLS_s1 Homo sapiens cDNA clone IMAGE:416989 5'
5183	18192		0.92	5.0E-25	AA994228.1	EST_HUMAN	Mus musculus obagelin (Oag), mRNA
11645	24932	38150	3.16	5.0E-25	AW979107.1	EST_HUMAN	IL3-CT0210-181199-031-D04 CT0219 Homo sapiens cDNA
1441	14474	27451	2.3	4.0E-25	T86107.1	EST_HUMAN	044901.s1 NCI CGAP_B2 Homo sapiens cDNA clone IMAGE:1631161 3' similar to contains Alu repetitive element;
3413	16461		2.68	4.0E-25	AW887671.1	EST_HUMAN	EST1391217 IMAGE ressequencas, IMAGE Homo sapiens cDNA
3923	16983	28876	0.93	4.0E-25	AF000368.1	NT	y65804.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
4345	17372		3.13	4.0E-25	BE170957.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
3331	16392	29303	2.77	3.0E-25	8623321	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
3331	16392	29304	2.77	3.0E-25	8623321	NT	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
5877	18068	32157	0.64	3.0E-25	U53212.1	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
							Human degenerin channel MDEG mRNA, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8769	19824	33107	0.66	3.0E-26	AA603590.1	EST_HUMAN	np27602.st NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:U81866 ZINC FINGER PROTEIN 85 (HUMAN);
8860	21048	33070	4.08	3.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1350	14385	27354	2.6	2.0E-26	5032168	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2317	15328	28351	7.52	2.0E-26	BE688016.1	EST_HUMAN	601611630FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2842	15551	28572	3.35	2.0E-26	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4218	17247	30131	1.98	2.0E-26	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4218	17247	30132	1.96	2.0E-26	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
10123	23049	36528	2.03	2.0E-26	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Starckes GS) Homo sapiens cDNA
384	13450	26378	1.4	1.0E-26	AL040229.1	EST_HUMAN	DKFZp434H0313.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0313 5'
1253	14289	28466	1.34	1.0E-26	8635487	NT	Human endogenous retrovirus, complete genome
2441	16448	30802	1.04	1.0E-26	Q08055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4895	17912	30802	2.33	1.0E-26	BE162737.1	EST_HUMAN	PM1-HT0454-030100-002-R99 HT0454 Homo sapiens cDNA
6719	16775	33516	0.83	1.0E-26	AA185080.1	EST_HUMAN	zq4506.e1 Stragene nNT neuron (NS37233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
6905	25076	33516	3.22	1.0E-26	AA582690.1	EST_HUMAN	ms4h11.at NCL_CGAP_Kid9 Homo sapiens cDNA clone IMAGE:1087749 3'
8246	21215	34623	4.36	1.0E-26	AA709078.1	EST_HUMAN	206p04.e1 Scores_fetal_heart_NSHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains P1R13 P1R5 repetitive element;
5904	22853	36317	0.69	1.0E-26	X60660.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
5904	22853	36318	0.69	1.0E-26	X60660.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
11316	24269	37764	2.91	1.0E-26	U83163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12278	25097	38180	1.47	1.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
12278	25097	38181	1.47	1.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
13053	25691	28519	1.83	1.0E-26	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2491	15494	28519	1.47	8.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
5778	18870		1.56	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1580	14613	27595	2.88	7.0E-26	AF003528.1	NT	Homo sapiens X-linked and/or endometrial dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4008	17044	28952	1.21	7.0E-26	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4196	17217	30103	1.69	7.0E-26	AY340163.1	EST_HUMAN	hd0261.2.x1 Scores_NFL_I_GGC_S1 Homo sapiens cDNA clone IMAGE:29083868 3'
5721	18816	31984	0.72	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11976	24855		8.08	7.0E-26	AA115893.1	EST_HUMAN	zr30408.t1 Stragene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2234	15248	28272	2.28	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3357	16407	28329	1.03	6.0E-26	AA220613.1	EST_HUMAN	z552h04.r1 Stratagene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:645271 5'
11590	24887	38482	1.91	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment H621C010
1181	14222	27178	1.86	5.0E-26	AI708235.1	EST_HUMAN	as33h08.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2310519 3' similar to WPF:FA9C12.11 CE03371 ;
1181	14222	27178	1.88	5.0E-26	AI708235.1	EST_HUMAN	as33h08.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2310519 3' similar to
1546	14579	33334	0.86	4.0E-26	AA328948.1	EST_HUMAN	WP:FA9C12.11 CE03371 ;
9787	22708	33334	3.71	4.0E-26	7657670	NT	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
11022	23887	37514	2.93	4.0E-26	BE265187.1	EST_HUMAN	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
1773	14802	27787	2.15	3.0E-26	D14547.1	NT	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:333210 5'
2019	15040	28051	1.27	3.0E-26	AL048653.2	EST_HUMAN	Human DNA, SINE repetitive element
2047	15066		3.59	3.0E-26	AA116805.1	EST_HUMAN	DKFZ434056_r1.434 (synonym: itas3) Homo sapiens cDNA clone DKFZ4341066 5'
3791	16832	29738	1.12	3.0E-26	AA152464.1	EST_HUMAN	z330d08.r1 Stratagene neuroepithelium NT72RAM1 637234 Homo sapiens cDNA clone IMAGE:548943 5'
3791	16832	29738	1.12	3.0E-26	AA152464.1	EST_HUMAN	z330f0.r1 Stratagene cdon (#637204) Homo sapiens cDNA clone IMAGE:388427 5' similar to TR:G695374
7096	20030	33334	6.22	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11894	24776	38381	2.03	3.0E-26	AW875651.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11894	24776	38382	2.03	3.0E-26	AW875651.1	EST_HUMAN	6011864963F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4083278 5'
11828	24809	38404	4.91	3.0E-26	AA983173.1	EST_HUMAN	QV2-PT0012-04040-124-e05 PT0012 Homo sapiens cDNA
13101	25024	31678	1.37	3.0E-26	AF165520.1	NT	QV2-PT0012-04040-124-e05 PT0012 Homo sapiens cDNA
682	13745	26872	10.08	2.0E-26	AL163282.2	NT	m37d05.s1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.lt
1884	14800	29225	3.56	2.0E-26	AL038099.2	EST_HUMAN	OFR repetitive element ;
3245	16300		4.62	2.0E-26	X86894.1	NT	Homo sapiens phospholipase 21 segment HS21C082
11105	24055		2.38	2.0E-26	D87675.1	NT	DKFZ566L171.s1 566 (synonym: htkd2) Homo sapiens cDNA clone DKFZ566L171 3'
11553	24493	38049	2.55	2.0E-26	AI801412.1	EST_HUMAN	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
11748	24633		1.78	2.0E-26	AF055068.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12007	24968	38565	1.64	2.0E-26	M32788.1	NT	ts8a01.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element ;
12388	25169		1.7	2.0E-26	AB037859.1	NT	Homo sapiens MHC class 1 region
							Homo sapiens endogenous retroviral element S71
							Homo sapiens mRNA for KIAA1438 protein, partial cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
137	13242	28172	37.48	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0638-020300-129-402 HT0538 Homo sapiens cDNA
2083	10081	28100	1.33	1.0E-26	AL039363.2	EST_HUMAN	DKFZp434H1910.1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2897	16693		11.4	1.0E-26	AF231083.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
7016	20142		2.78	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-162000-113-901 HT0487 Homo sapiens cDNA
11239	24192		2.12	1.0E-26	AL038487.1	EST_HUMAN	DKFZp688c2146.J1_368 (synonym: htk42) Homo sapiens cDNA clone DKFZp688c2146 5'
12630	25066		2.65	1.0E-26	H95093.1	EST_HUMAN	CHP220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
7637	20784		1.24	9.0E-27	BF371227.1	EST_HUMAN	RC6-FNG138-110800-022-402 FNG138 Homo sapiens cDNA
9658	22815		4.04	9.0E-27	U83183.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
12142	25006		5.65	9.0E-27	BF445558.1	EST_HUMAN	hna03507.x1 NCL CGAP_P228 Homo sapiens cDNA clone IMAGE:3263644 3' similar to contains OFR.L1
11	13131	28029	4.71	8.0E-27	AI831462.1	EST_HUMAN	w49d04.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.L2
559	13529		4.61	8.0E-27	AL163227.2	NT	THFR repetitive element;
1414	14447	27419	30.06	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HSZ1C027
1414	14447	27420	30.06	8.0E-27	AW162737.1	EST_HUMAN	au87H08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558
2177	15192	28214	1.1	8.0E-27	AW864776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
3199	18254	28174	1.17	8.0E-27	P12238	SWISSPROT	au87H08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00558
3384	16414	26339	0.84	8.0E-27	AF181887.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
5778	18871	32053	0.97	8.0E-27	AV73214.1	EST_HUMAN	PM2-SN0018-220300-002-407 SN0018 Homo sapiens cDNA
7170	18401		2.12	8.0E-27	BE926590.1	EST_HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
7248	19893	33280	2.41	8.0E-27	N84970.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
9594	22528	39976	1.41	8.0E-27	AW857579.1	EST_HUMAN	AV73214.1 HTF Homo sapiens cDNA clone HTFBCB08 5'
9564	22526	39976	1.41	8.0E-27	AW857579.1	EST_HUMAN	MR4-BT0398-280300-204-408 BT0398 Homo sapiens cDNA
684	13747		1.65	7.0E-27	Z70664.1	NT	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to
5126	18135		2.05	7.0E-27	AW629172.1	EST_HUMAN	REPETITIVE ELEMENT L1
9209	22175		0.88	7.0E-27	D86884.1	NT	GM1-CT0315-091298-063-407 CT0315 Homo sapiens cDNA
11101	24051		3.24	7.0E-27	AJ271735.1	NT	GM1-CT0315-091298-063-407 CT0315 Homo sapiens cDNA
12759	25402		1.54	7.0E-27	AV723365.1	EST_HUMAN	h51h12.x1 Scores_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2876879 3' similar to TR:O76040
							Human endogenous retroviral element HC2
							ORF540 ORF2: FUNCTION UNKNOWN.
							Human mRNA for KIAA0231 gene, partial cds
							Human sapiens Xq pseudocentromeric region, segment 1/2
							AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11080	24042	37665	10.71	8.0E-27	M26897.1	NT	Human nuclear protein (B23) mRNA, complete cds
8055	20992		0.78	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10597	23519	37010	3.37	5.0E-27	BF686814.1	EST_HUMAN	602121491F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4278527 5'
10597	23519	37011	3.37	5.0E-27	BF686814.1	EST_HUMAN	602121491F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4278527 5'
6908	19890	33256	1.72	4.0E-27	9510569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8271	21240		1.22	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8316	21285		1.25	4.0E-27	AF078179.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10101	23027	36504	0.72	4.0E-27	AW680859.1	EST_HUMAN	QVQ-010033-073900-152-b10 OT0033 Homo sapiens cDNA
11929	24810	38405	1.98	4.0E-27	X80211.1	NT	H. sapiens DNA for endogenous retroiral like element
2057	16078	28096	4.38	3.0E-27	X60658.1	NT	R. rattus RY3 mRNA for a potential ligand-binding protein
4300	17929	30209	1.08	3.0E-27	BE071924.1	EST_HUMAN	PMO-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5419	18522	31400	5.65	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
8089	21025	34424	0.67	3.0E-27	BE670351.1	EST_HUMAN	743302.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284283 3'
9680	22817	36271	4.46	3.0E-27	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3652068 5'
43	13183	26066	8.25	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1911	14935		24.32	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.at NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:U17886 60S
3126	16183		10.81	2.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Scavenging_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975579 3' similar to TR:076040
3238	16293	29215	1.61	2.0E-27	AF111167.2	NT	076040 ORF2: FUNCTION UNKNOWN. ;
3238	16293	29216	1.61	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6833	16986	33179	0.72	2.0E-27	H02655.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
8427	21395	34807	1.44	2.0E-27	AI896347.1	EST_HUMAN	SP-HMGC_MOUSE_Q02591 HOMEOBOX PROTEIN ;
9824	22658		2.61	2.0E-27	AA551527.1	EST_HUMAN	w28g07.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2425258 3'
10151	23076	36552	0.78	2.0E-27	X60658.1	NT	nk01b10.at NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:U17886 60S
10395	23177	36797	1.32	2.0E-27	M78590.1	EST_HUMAN	replicative element ;
10395	23317	36798	1.32	2.0E-27	M78590.1	EST_HUMAN	R. rattus RY3 mRNA for a potential ligand-binding protein
11302	24252	37778	2.97	2.0E-27	AU121695.1	EST_HUMAN	EST107038 Fetal brain, Striatum (cat#639206) Homo sapiens cDNA clone HFB07
11816	14935		19.93	2.0E-27	AA565345.1	EST_HUMAN	EST107038 Fetal brain, Striatum (cat#639206) Homo sapiens cDNA clone HFB07
							AU121695 MAMMA1 Homo sapiens cDNA clone MAMMA100746 5'
							nk01b10.at NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:U17886 60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
436	13510		2.28	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21046
998	14049	27002	1.58	1.0E-27	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
1707	14738	27720	0.95	1.0E-27	4827059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XylB) mRNA
4108	17142		1.08	1.0E-27	BE350127.1	EST_HUMAN	h009g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3 MER29 repetitive element;
6094	19751	33028	5.21	1.0E-27	6005655	NT	Homo sapiens Raf-like domain factor-1 (RPF-1), mRNA
7054	20076	33394	2.01	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000066C10
7054	20076	33385	2.01	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000066C10
8957	21923	35351	0.71	1.0E-27	AB07923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9537	22302	36478	2.33	1.0E-27	BE079780.1	EST_HUMAN	RC8-B10827-140200-011-506 B10827 Homo sapiens cDNA
10080	23007	38478	2.7	1.0E-27	DB7449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12016	24693	38490	3.73	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant b3b mRNA, complete cds
143	13245		2.16	9.0E-28	BE348399.1	EST_HUMAN	hwt7c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR-Q07314 Q07314
311	13403	28329	2.64	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR, [3] TR-Q07280 TR-Q07313;
4817	17634	30732	1.08	9.0E-28	P60447	SWISSPROT	AU126260 NT25P1 Homo sapiens cDNA clone NT2RP1000443 5'
12222	25056		3.71	9.0E-28	BF377859.1	EST_HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) PROTEASE INHIBITOR (ALPHA-1-ANTITRYPSIN)
12553	25817		1.9	8.0E-28	AW157571.1	EST_HUMAN	CNA2-TN014P-070900-372-g01 TN0140 Homo sapiens cDNA
1185	14226	27182	8.08	7.0E-28	AU142780.1	EST_HUMAN	au83108.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR-Q0302 Q0302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
11520	24461	38012	2.43	7.0E-28	11417866	NT	AU142780 Y78A11 Homo sapiens cDNA clone Y78A11000824 5'
12181	25029		2.98	7.0E-28	AV735348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9271	22237		1.09	6.0E-28	AF016052.1	NT	AV735348 CB Homo sapiens cDNA clone CBFAK12 5'
12806	26433		3.82	6.0E-28	AA504662.1	EST_HUMAN	aa50463.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:625340 5' similar to contains Alu repetitive element/contains element P1TR5 repetitive element;
318	13410		3.1	5.0E-28	AI921003.1	EST_HUMAN	wt18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element;
4035	17073	29973	1.52	5.0E-28	R70762.1	EST_HUMAN	y8310.1.1 Soares placenta N82HP Homo sapiens cDNA clone IMAGE:148443 5'
2633	15632	29857	1.48	4.0E-28	AW195066.1	EST_HUMAN	x03309.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2685504 3' similar to SW:GG95_HUMAN
2869	16047	28687	1.18	4.0E-28	4505316	NT	Q08379 GOLGIN-95;
3125	16182	28082	1.93	4.0E-28	BE409100.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
							B01300703FT NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3935305 5'



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7551	20514	33872	2.45	4.0E-28	AI108941.1	EST_HUMAN	qf6810.x1 Soares_testa_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
11213	24166		3.61	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 8 duplication of the T cell receptor beta locus and tyrosinogen gene families
11349	24298		39.65	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11964	20514	33872	3.87	4.0E-28	AI108941.1	EST_HUMAN	qf6810.x1 Soares_testa_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12999	25301		1.86	4.0E-28	AW854244.1	EST_HUMAN	RC3-C10254-240400-210-112 CT0254 Homo sapiens cDNA
1288	14323		2.61	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
9179	22145	35572	1.64	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-109 HT0713 Homo sapiens cDNA
11282	24232	37758	2.14	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12628	25316		2.92	3.0E-28	AI811991.1	EST_HUMAN	w9807.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element/contains element HCR repetitive element;
89	13205	29129	11.64	2.0E-28	BE082167.1	EST_HUMAN	RC1-B10264-220300-019-c05 B10254 Homo sapiens cDNA
1047	14093	27045	4.14	2.0E-28	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
1168	14210	27184	12.37	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2485	15489	28513	2.27	2.0E-28	AI348834.1	EST_HUMAN	q35006.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3373	16423	29346	0.76	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment H6210009
8440	19005	32756	1.48	2.0E-28	BF224402.1	EST_HUMAN	h7f6c03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
8494	19526		6.48	2.0E-28	BF212605.1	EST_HUMAN	601814166F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8379	21348	34760	0.76	2.0E-28	AF005273.1	NT	Sus scrofa domestica submandibular apomucin mRNA, complete cds
9943	22870		8.83	2.0E-28	AW972305.1	EST_HUMAN	EST7384394 IMAGE resequences, MAGL Homo sapiens cDNA
11636	24817	38414	1.92	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12609	26308		2.06	2.0E-28	H06376.1	EST_HUMAN	y7f6c09.1 Soares Infant brain 1N18 Homo sapiens cDNA clone IMAGE:44300 5'
1474	14507	27481	3.15	1.0E-28	D38044.1	NT	Human gene for Ahr-receptor, exon 7-9
2229	15243	28268	1.84	1.0E-28	BF333236.1	EST_HUMAN	QV1-B10821-120800-350-403 B10821 Homo sapiens cDNA
2862	15883	28703	0.92	1.0E-28	AF000605.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
4885	18000	30889	0.64	1.0E-28	AV732184.1	EST_HUMAN	AV732184 HTF Homo sapiens cDNA clone HTF-BH05 5'
8193	21763		8.03	1.0E-28	11429886	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
6332	21321		3.37	1.0E-28	8622703	NT	Homo sapiens hypothetical protein FLJ10688 (FLJ10688), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9833	22577	39027	4.47	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HOC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10235	23160	36648	6.47	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
10235	23160	36648	6.47	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
12186	25033		4.36	1.0E-28	AA054182.1	EST_HUMAN	Zf557c01.1f1 Soares retina N24-HR Homo sapiens cDNA clone IMAGE:380448 5'
12631	25716		2.58	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS210047
13037	25918	31302	3.46	9.0E-29	AW663987.1	EST_HUMAN	hT769.6.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12713	25367		3.12	8.0E-29	Q00130	SWISSPROT	HYPOPHYSICAL GENE 50 PROTEIN
1606	14638	27615	1.04	7.0E-29	AW966447.1	EST_HUMAN	EST178521 IMAGE resequences, MAGI Homo sapiens cDNA
3564	16510		0.9	7.0E-29	BE254708.1	EST_HUMAN	60114990FT NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355367 5'
13086	25616		9.37	7.0E-29	AJ132952.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
597	13664	26578	6.87	6.0E-29	AI938748.1	EST_HUMAN	w69801.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2465985 3' similar to TR.O15475
12469	25234		8.12	6.0E-29	BE64038.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN :contains LTR.b1 LTR7 repetitive element ;
12574	25284		1.97	6.0E-29	BF660097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0052 Homo sapiens cDNA
5033	18047		1.34	5.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
9083	22049		8.5	5.0E-29	AW687541.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3246	16301		1.33	4.0E-29	AI752387.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
6125	18203		5.91	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
8417	21086	34794	0.92	4.0E-29	AI678101.1	EST_HUMAN	QV1-H170471-280300-121-ad05 HT0471 Homo sapiens cDNA
8417	21396	34795	0.92	4.0E-29	AI678101.1	EST_HUMAN	w435906.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
9097	22053	35488	0.94	3.0E-29	J04988.1	NT	MER29.12 MER29 repetitive element ;
2379	15597	28411	2.97	4.0E-29	U167847.1	NT	w45905.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
4444	17470	30369	1.61	3.0E-29	AB042297.1	NT	MER29.12 MER29 repetitive element ;
4764	17784	30880	0.94	3.0E-29	BF332286.1	EST_HUMAN	Human 80 kD heat shock protein gene, complete cds
6040	19122	32327	0.77	3.0E-29	BE1314018.1	EST_HUMAN	Human beta-galactoside alpha2,6-sialyltransferase (SIAT1) mRNA, exon U
9085	22051	35473	2.19	3.0E-29	D38044.1	NT	Homo sapiens P17S gene for 6-pyruvoylhistidinol synthase, complete cds
9655	22598	36047	1.97	3.0E-29	AW303317.1	EST_HUMAN	QV1-H18267F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
9889	22842		2.2	3.0E-29	AL163246.2	NT	601152857F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
							Human gene for Ahr-receptor, exon 7-9
							xm1703.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Ahr
							repetitive element;contains MER19.12 MER19 repetitive element ;
							Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10318	23242		0.73	3.0E-29	BE50127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
12385	25163		2.34	3.0E-29	D63882.1	NT	HUMAN HAI1M13 mRNA for Hsi1m15, complete cds
483	13555	29487	1.08	2.0E-29	AF094689.1	NT	Homo sapiens envelope protein RIC-5 (env) gene, complete cds
483	13555	29488	1.08	2.0E-29	AF094689.1	NT	Homo sapiens envelope protein RIC-5 (env) gene, complete cds
1535	14568	27538	7.19	2.0E-29	A1963904.1	EST_HUMAN	w65d10.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR.O15546 O15546
1535	14568	27539	7.19	2.0E-29	A1963904.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
4308	17337	30215	2.4	2.0E-29	AL163288.2	NT	HERV-E ENVELOPE GLYCOPROTEIN ;
5251	18259	31128	0.99	2.0E-29	O54827	SWISSPROT	Homo sapiens chromosome 21 segment HS21C088
5824	19010	32203	1.08	2.0E-29	A082459.1	EST_HUMAN	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA
6304	19375	32613	1.22	2.0E-29	A1806418.1	EST_HUMAN	os71e04.x1 NCL CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.L2.L1
7808	19375	32613	1.18	2.0E-29	A1806418.1	EST_HUMAN	repetitive element ;
8309	21278	34590	1.04	2.0E-29	BE807157.1	EST_HUMAN	w27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains
8924	21890	35317	0.63	2.0E-29	-10597821	NT	element MER6 repetitive element ;
8924	21890	35318	0.63	2.0E-29	10597821	NT	601442206FT.NIH.MGC.65 Homo sapiens cDNA clone IMAGE:3846945 5'
8965	22802	39255	3.5	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC86242), mRNA
9868	23521	37013	3.27	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC86242), mRNA
10589	23521	37014	3.27	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11806	24922		4.13	2.0E-29	11425108	NT	Homo sapiens chromosome 21 segment HS21C048
11844	24727		2.03	2.0E-29	AW880701.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
9144	22110	35536	10.17	1.0E-29	AW198380.1	EST_HUMAN	Homo sapiens splicing factor similar to drsJ (SPF31), mRNA
10966	23006	37420	0.59	1.0E-29	X60558.1	NT	QV0-OT0032-050300-155-d01 OT0032 Homo sapiens cDNA
6734	19790	33070	3.20	9.0E-30	AA761215.1	EST_HUMAN	RYA33 mRNA for a potential ligand-binding protein
12263	25087		2.14	9.0E-30	11422745	NT	nz20d7.st NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.57
6452	19517		0.62	8.0E-30	F08698.1	EST_HUMAN	MER4 repetitive element ;
8913	21951	34997	3.18	8.0E-30	AA363873.1	EST_HUMAN	Homo sapiens zinc/finger regulated transporter-like (ZIRTL), mRNA
9031	21997	35416	3.9	8.0E-30	AB57072.1	EST_HUMAN	HSC2337051 normalized infant brain cDNA Homo sapiens cDNA clone c-2305

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1518	14550		1.02	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1571	14604		1.4	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
1788	14817	27802	1.8	6.0E-30	D28303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3204	16259	29178	2.81	6.0E-30	BE080028.1	EST_HUMAN	QV6-BN0147-200400-214-112 BN0147 Homo sapiens cDNA
4781	18259	29178	1.02	6.0E-30	BE080028.1	EST_HUMAN	QV6-BN0147-200400-214-112 BN0147 Homo sapiens cDNA
10505	23826	37337	0.74	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen scz0-10 mRNA, partial cds
13054	14804		4.36	6.0E-30	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4041	17079		32.98	5.0E-30	AI399992.1	EST_HUMAN	ig92d03.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116278 3' similar to contains Alu repetitive element
5510	25746		4.98	5.0E-30	U87631.1	NT	Human acetylase hydratase (ACO2) gene, exon 7
11233	24186		2.21	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11489	24432	37681	2.03	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C070
11489	24432	37682	2.03	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C070
2153	15169	28185	1.78	4.0E-30	AW837471.1	EST_HUMAN	QV6-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2153	15169	28185	1.79	4.0E-30	AW837471.1	EST_HUMAN	QV6-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
7035	18387	31254	0.85	4.0E-30	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9259	22222	35652	2.5	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-008 ST0181 Homo sapiens cDNA
1154	14186		4.51	3.0E-30	AI338851.1	EST_HUMAN	q493-05.x1 Scores_Total_fetus_Nk2Hf9_5w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
3770	15912	28721	1.03	3.0E-30	AF128983.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
7470	20436	33763	0.5	3.0E-30	T18982.1	EST_HUMAN	b1205961 Testis 1 Homo sapiens cDNA clone b120596
8284	21253		0.52	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8831	21768		0.44	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10800	23721	37224	2.18	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER28.b3 MER29 repetitive element;
10932	23652	37366	0.62	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
10932	23652	37367	0.62	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11541	24482	38034	5.89	3.0E-30	P34058	SWISSPROT	TRANSCRIPTION FACTOR AP-2
678	13739	26666	1.87	2.0E-30	AW857315.1	EST_HUMAN	CM2-CT0307-310100-158-H03 CT0307 Homo sapiens cDNA
1068	14130		3.03	2.0E-30	F08988.1	EST_HUMAN	HSC-D231057 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
1475	14508	27482	6.38	2.0E-30	BE175877.1	EST_HUMAN	RC3-H10582-110400-013-H08 HT0582 Homo sapiens cDNA
2727	15721	28738	11.19	2.0E-30	BE165232.1	EST_HUMAN	IL2-NT101-280700-116-E04 NT101 Homo sapiens cDNA
2830	15088	28909	6.11	2.0E-30	AF114159.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3803	16943	29751	2.1	2.0E-30	AW206581.1	EST_HUMAN	UI-HB1-af6-c-124.U1.x1 NCI CGAP_SuL3 Homo sapiens cDNA clone IMAGE:272558 3'
4812	17529	30726	1.76	2.0E-30	BE268945.1	EST_HUMAN	60111980F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029439 5'
4812	17529	30727	1.76	2.0E-30	BE268945.1	EST_HUMAN	60111980F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029439 5'
6922	18972	33269	0.71	2.0E-30	BF050337.1	EST_HUMAN	60189208F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138993 5'
8820	21787	35211	0.98	2.0E-30	AA019103.1	EST_HUMAN	z658c10.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:563166 5'
8892	21649	35270	7.02	2.0E-30	C16939.1	EST_HUMAN	C16939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN:570C01 5'
8892	21648	35371	3.99	2.0E-30	BE670617.1	EST_HUMAN	7a37c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8892	21948	35372	3.99	2.0E-30	BE670617.1	EST_HUMAN	7a37c12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
10355	23280	35756	3.98	2.0E-30	AW971588.1	EST_HUMAN	EST336357 MAGE resequences, MAGEL Homo sapiens cDNA
10442	23364	36854	8.55	2.0E-30	AW470701.1	EST_HUMAN	ha33d06.x1 NCI CGAP_Kid2 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.L3 THR repetitive element ;
289	13381	28309	18.55	1.0E-30	C16939.1	EST_HUMAN	C16939 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains MER.13 MER1 repetitive element ;
539	13610	28529	7.04	1.0E-30	AW458897.1	EST_HUMAN	h33b004.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone GEN:570C01 5'
717	13779	28713	1.23	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2222	15236	28260	3.82	1.0E-30	AA064377.1	EST_HUMAN	ac77b08.st Stratagene lung (H937210) Homo sapiens cDNA clone IMAGE:865599 3'
2469	15473	28406	2.39	1.0E-30	BF347728.1	EST_HUMAN	60202250F1 NCI CGAP_Bms7 Homo sapiens cDNA clone IMAGE:4167891 5'
3067	16124	29037	1.12	1.0E-30	AA316045.1	EST_HUMAN	EST1165868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7695	20934	34328	2.08	1.0E-30	BF18230.1	EST_HUMAN	60180993F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 6'
12862	25841		11.93	1.0E-30	H65563.1	EST_HUMAN	CHR22D0532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
8667	21635	35056	0.92	9.0E-31	R18214.1	EST_HUMAN	Y09908.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30556 5' similar to gb:X12853 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8667	21635	35057	0.92	9.0E-31	R18214.1	EST_HUMAN	Y09908.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30556 5' similar to gb:X12853 RAS- RELATED PROTEIN RAB-2 (HUMAN);
8971	21937	35384	1.79	9.0E-31	Z39293.1	EST_HUMAN	HS029F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05503 3'
8973	21939	35384	0.49	9.0E-31	AF07879.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
1078	14123	27076	1.82	8.0E-31	AL163208.2	NT	Homo sapiens hypophyseal protein FLJ20420 (FLJ20420), mRNA
2423	15430	30890	5.94	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C003
4955	17970	30891	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4955	17970	30891	1.12	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
712	1374		1.99	7.0E-31	AA372837.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2878	15672	28891	2.38	7.0E-31	BE326517.1	EST_HUMAN	hw054111.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2878	15672	28892	2.38	7.0E-31	BE326517.1	EST_HUMAN	hw054111.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8744	21712	35133	0.99	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8744	21712	35134	0.99	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9821	22866		0.82	7.0E-31	BE408811.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12711	23366	31771	5.68	7.0E-31	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3691	16734		3.06	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8493	21461		7.57	6.0E-31	AF050068.1	NT	Homo sapiens MHC class I region
8874	21942	35087	0.7	6.0E-31	BE350127.1	EST_HUMAN	hw0901.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146255 3' similar to contains MER20.b3
11090	24050	37573	1.86	6.0E-31	AU119105.1	EST_HUMAN	MER29 repetitive element:
12325	25127	31848	2.27	6.0E-31	AW372868.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA:1005050 5'
12458	25784		2.08	6.0E-31	BE694488.1	EST_HUMAN	RC5-BT0377-091289-031-012 BT0377 Homo sapiens cDNA
184	13295	26222	2.83	5.0E-31	M60894.1	NT	601433037 F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
184	13295	26223	2.83	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8768	21755		1.46	5.0E-31	BF056540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
598	13665		3.45	4.0E-31	AZ71735.1	NT	7K0604.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537
							SIMILAR TO POGO ELEMENT, contains L1 L1 repetitive element;
							Homo sapiens Xq pseudautosomal region, segment 1/2
1615	14647	27622	1.01	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-LUDP
1834	14861		2.09	4.0E-31	AL163280.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNA4POLYPEPTIDE, N-
2800	15782		1.98	4.0E-31	5730338	NT	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
10900	23920	37329	0.43	4.0E-31	AF084484.1	NT	Homo sapiens SET domain and murine transposase fusion gene (SETMAR) mRNA
2603	15503	28625	0.98	3.0E-31	6005871	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
7662	20525	33883	6.73	3.0E-31	4828853	NT	Homo sapiens SEC63, endoplasmic reticulum translocan component (S. cerevisiae) like (SEC63L), mRNA
7736	20891	34055	1.28	3.0E-31	11420329	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (18kD, ASH) (NDUFB8) mRNA
8501	21469		2.35	3.0E-31	AL163208.2	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
9939	22866	36328	4.66	3.0E-31	D14523.1	NT	Homo sapiens chromosome 21 segment HS21C006
10061	23891	37594	0.82	3.0E-31	AA421242.1	EST_HUMAN	Horse mRNA for ferritin L-chain, complete cds
							2106004.r1 Scores_NHT Homo sapiens cDNA clone IMAGE:731047 5'

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Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10995	23861	37486	3.17	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
11487	24430		6.94	3.0E-31	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3802088 5'
1932	14859	27953	1.33	2.0E-31	AW838171.1	EST_HUMAN	QV2-L1T0051-260300-111-03 L1T0051 Homo sapiens cDNA
2224	15238	28282	0.98	2.0E-31	A133358.1	EST_HUMAN	194405.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:211672 3'
2347	15366	28379	2.53	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513.J1 761 (synonym: haryn2) Homo sapiens cDNA clone DKFZp761G1513 5'
2447	15452	28473	6.97	2.0E-31	AA45824.1	EST_HUMAN	aa88f11.s1 Stragelns fetal retina 937202 Homo sapiens cDNA clone IMAGE:6394173 3' similar to contains THR 12 THR repetitive element ;
5347	18462	31323	0.72	2.0E-31	AW444698.1	EST_HUMAN	U1-HB13-ab07-09-CU1.s1 NCL CGAP_S165 Homo sapiens cDNA clone IMAGE:2733833 3'
5768	18860	32072	2.89	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
9431	22395		2.71	2.0E-31	AA67764.1	EST_HUMAN	m08104.s1 NCL CGAP_Cor10 Homo sapiens cDNA clone IMAGE:1181065 3' similar to TR:Q13537 Q13537
9562	22524	35973	4.13	2.0E-31	7661535	NT	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
10266	23191	36677	1.13	2.0E-31	AV710948.1	EST_HUMAN	Homo sapiens B9 protein (B9), mRNA
10268	23191	36678	1.13	2.0E-31	AV710948.1	EST_HUMAN	AV710948.C1 Homo sapiens cDNA clone CUAALB07 5'
10435	23357	36844	2.57	2.0E-31	BE408611.1	EST_HUMAN	AV710948.C1 Homo sapiens cDNA clone CUAALB07 5'
10435	23357	36845	2.57	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688310 5'
12427	25195		1.91	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase I gene, promoter region
12568	25987		3.94	2.0E-31	AF114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
17	13137	26036	11.03	1.0E-31	U95163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1671	14703	27678	3.34	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1671	14703	27679	3.34	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1671	14703	27680	3.34	1.0E-31	O98371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4666	17997	30571	1.35	1.0E-31	AL134378.1	EST_HUMAN	DKFZp547B235.J1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
4666	17997	30572	1.35	1.0E-31	AL134378.1	EST_HUMAN	DKFZp547B235.J1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
5365	18470	31341	3.75	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151298-028-a08.1 ST0220 Homo sapiens cDNA
6256	19529	32659	2.31	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite cb51 repeat region
7506	20471	33831	1.08	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
8132	21069	34468	0.76	1.0E-31	BE972818.1	EST_HUMAN	60165205F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
10596	23518	37009	0.88	1.0E-31	U95163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11261	24213	37737	4.66	1.0E-31	AI086434.1	EST_HUMAN	q12h03.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR-Q16595 Q16595 FRATAXIN. ;
12103	24874	39571	1.5	1.0E-31	U66051.1	NT	Human germline T-cell receptor beta chain TORBV17S1A1T, TORBV2S1, TORBV10S1P, TORBV29S1P, TORBV16S1P, TORBV15S1, TORBV15S1A1T, HVB relic, TORBV28S1P, TORBV34S1, TORBV14S1, TORBV3S1, TORBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TORBD1, TORBJHS1, TORBJIS2.>
6795	19849	33134	2.13	9.0E-32	AV723978.1	EST_HUMAN	AV723978 HTB Homo sapiens cDNA clone HTBA007 5'
7598	20559	33919	0.93	9.0E-32	L31770.1	NT	Bos taurus vacuolar H <sup>+</sup> -ATPase subunit mRNA, complete cds
7848	20769		0.95	8.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
2060	15107	28126	3.05	8.0E-32	AI056770.1	EST_HUMAN	oz15609.x1 Soares_fetal_liver_spleen_1NF13_31 Homo sapiens cDNA clone IMAGE:1675384 3'
5559	18656	31601	0.89	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-e04 BN0048 Homo sapiens cDNA
4898	17913	30803	1.16	7.0E-32	P62591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P146)
12405	25176		7.68	7.0E-32	X17283.1	NT	Human chromosome 22 Immunoglobulin V(K) gene, part, with 5' breakpoint between orphion and neighbouring non-amplified region
2742	15736	28752	1.2	6.0E-32	AI478104.1	EST_HUMAN	hm34e10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2169994 3' similar to contains MER29.13 MER29 repetitive element ;
7691	20652		1.29	6.0E-32	BE088016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1035	14081	27032	17.73	5.0E-32	AF116927.1	NT	Homo sapiens PRO1181 mRNA, complete cds
931	13984		1.85	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7861	20605	34181	3.03	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7881	20803	34182	3.03	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8702	21970		1	4.0E-32	BE084410.1	EST_HUMAN	RC4-BT0311-141195-011408 BT0311 Homo sapiens cDNA
468	13529	28459	3.32	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1448	14481	27458	9.76	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
9749	22590	36147	19.97	3.0E-32	AV756934.1	EST_HUMAN	AV756934 BM Homo sapiens cDNA clone BMFBFBH12 5'
9749	22590	36148	19.97	3.0E-32	AV756934.1	EST_HUMAN	AV756934 BM Homo sapiens cDNA clone BMFBFBH12 5'
11270	24222	37747	2.81	3.0E-32	AA777621.1	EST_HUMAN	295a07.g1 Soares_fetal_liver_spleen_1NF13_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR18 THR repetitive element ;
11550	24491		1.46	3.0E-32	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862066 5'
12430	25197		5.4	3.0E-32	BE270088.1	EST_HUMAN	601458283F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12786	18336	31283	3.46	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11;17)(p13;p11.2)) translocated to, 4 (MILL14) mRNA



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12766	18336	31284	3.46	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritonax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
12937	25517		4.33	3.0E-32	BE276086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4918	17895	30827	0.97	2.0E-32	BE29613.1	EST_HUMAN	60117393F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
6381	19449	32860	0.87	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6524	19552	32959	6.66	2.0E-32	Z38133.1	NT	H sapiens mRNA for myosin
6524	19552	32960	6.86	2.0E-32	Z38133.1	NT	H sapiens mRNA for myosin
8621	21589	35006	2.19	2.0E-32	AA114294.1	EST_HUMAN	z166c08.1 Stratagene HeLa cell c3 937219 Homo sapiens cDNA clone IMAGE:563150 5'
8621	21589	35007	2.19	2.0E-32	AA114294.1	EST_HUMAN	z166c08.1 Stratagene HeLa cell c3 937219 Homo sapiens cDNA clone IMAGE:563150 5'
13049	25589	31683	4.17	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13049	25589	31684	4.17	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3110	16167		1.07	1.0E-32	BE743296.1	EST_HUMAN	60157320F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7265	19951	33289	6.73	1.0E-32	11439726	NT	Homo sapiens chromosome 11 open reading frame B (C11ORF8), mRNA
8943	21809	35334	6.78	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR_33 THR repetitive element;
3493	19540		5.7	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.s1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6590	19920		3.43	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8140	22106	35532	1.82	9.0E-33	BF347229.1	EST_HUMAN	602021194F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4156870 5'
11150	24110		4.03	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
63	13182	26068	2.4	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
63	13182	26069	2.4	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2169	15195	26206	2.43	7.0E-33	AI590115.1	EST_HUMAN	tor12b09.x1 NCI_CGAP_Lu2 Homo sapiens cDNA clone IMAGE:2178609 3' similar to contains OFR.1.1 OFR repetitive element;
2657	15554		7.82	7.0E-33	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE06 5'
2841	14737	27719	1.82	7.0E-33	AV730015.1	EST_HUMAN	AV730015 HTF Homo sapiens cDNA clone HTFANF08 5'
3256	16310		16.32	7.0E-33	AW971307.1	EST_HUMAN	EST336357 MAGC resequences, MAGI Homo sapiens cDNA
9296	22254		1.07	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
11178	24134	37654	2.89	7.0E-33	BF347229.1	EST_HUMAN	602021194F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4156870 5'
11578	24615	38071	2.85	7.0E-33	AW971588.1	EST_HUMAN	EST336357 MAGC resequences, MAGI Homo sapiens cDNA
12009	25182	31879	3.85	7.0E-33	AA601416.1	EST_HUMAN	hw07c05.s1 NCI_CGAP_Pln1 Homo sapiens cDNA clone IMAGE:1100981 3' similar to contains L1.1 L1 repetitive element;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3749	16791		0.69	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21O085
6165	19260	32464	1.09	8.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107.H06
6185	19260	32495	1.09	8.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107.H06
8925	21891	38319	7.62	8.0E-33	J04038.1	NT	Human glyceroldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
9050	22016	35440	3.18	6.0E-33		NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) [LOC33277]. mRNA
10371	23294	36769	1.73	8.0E-33	8755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10371	23294	36770	1.73	8.0E-33	8755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1792	14821		1.63	5.0E-33	BF373515.1	EST_HUMAN	OV1-F10169-100/700-271-402 F10169 Homo sapiens cDNA
1898	14823		1.27	5.0E-33	11141884	EST_HUMAN	Homo sapiens actin carrier family 5 (actinin transporter), member 7 (SLC5A7), mRNA
1914	14838	27633	1.31	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1914	14838	27634	1.31	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2280	15293		1.49	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21O085
4087	17121	30015	1.28	5.0E-33	AB014699.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
6823	19877	33166	51.92	5.0E-33	AA169080.1	EST_HUMAN	Z44506 st. Stragene HNT neuron (H937233) Homo sapiens cDNA clone IMAGE:532627 3' similar to contains Alu repetitive element;
10610	23532	37027	0.85	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10610	23532	37028	0.85	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
1130	14173		0.87	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21O007
2135	15152	28167	1.53	4.0E-33	4759987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2428	15435		2.92	4.0E-33	AA625621.1	EST_HUMAN	ab51b11.1 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:944317 5' similar to contains Alu repetitive element; contains MER28 b2 MER28 repetitive element;
2652	15554	28574	2.35	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21O010
4509	17634	30418	1.95	4.0E-33	AW293349.1	EST_HUMAN	UHF-B12-4H-C-03-UJI.x1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5477	18578	31487	21.95	4.0E-33	AA059053.1	EST_HUMAN	Z171a08.1 Stragene colon (H937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:K12671.m1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6532	18595	32857	2.14	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6532	18595	32858	2.14	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1091	14135		6.18	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3 MER29 repetitive element;
1092	14135		4.81	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI CGAP Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3 MER29 repetitive element;
2456	16894		0.91	3.0E-33	AY847851.1	EST_HUMAN	AY847851 GLC Homo sapiens cDNA clone GLC0609 3'
10905	23727	37228	1.02	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.e1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
18	13138		0.63	2.0E-33	AI160188.1	EST_HUMAN	q6b7g03.x1 Soares_fetal_heart_NHH119W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
105	13138		2.93	2.0E-33	AI160188.1	EST_HUMAN	q6b7g03.x1 Soares_fetal_heart_NHH119W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
4449	17475		4.22	2.0E-33	BE158039.1	EST_HUMAN	MR04-HT0405-16300-202-08 HT0405 Homo sapiens cDNA clone IMAGE:1675973 3' similar to
5021	18036	30620	0.82	2.0E-33	AA62883.1	EST_HUMAN	ab51g11.11 Stratagene lung carcinoma 537218 Homo sapiens cDNA clone IMAGE:944388 5' similar to
5129	18138	31015	2.58	2.0E-33	11421332	NT	q6b7g03.x1 Soares_fetal_liver_spleen_1NFLS.S1 Homo sapiens cDNA clone IMAGE:1880181 3'
5129	18138	31016	2.58	2.0E-33	11421332	NT	q6b7g03.x1 Soares_fetal_liver_spleen_1NFLS.S1 Homo sapiens cDNA clone IMAGE:1880181 3'
6563	18623	32888	1	2.0E-33	AI277482.1	EST_HUMAN	q6b7g03.x1 Soares_fetal_liver_spleen_1NFLS.S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to
8458	22420		2.29	2.0E-33	AI052268.1	EST_HUMAN	gbiM29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10879	23859	37411	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10879	23859	37412	0.9	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
9	13129		2.05	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5669	18764	31834	0.7	1.0E-33	AF106420.1	NT	Homo sapiens F-box protein FBL4 (FBL4) mRNA, complete cds
7637	20597	33981	1.18	1.0E-33	M13975.1	NT	Homo sapiens protein kinase C beta-1 type (PRKC81) mRNA, complete cds
10381	26010		0.73	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11377	24324	37853	1.72	1.0E-33	AF744220.1	EST_HUMAN	AV744220 CB Homo sapiens cDNA clone CBOAA11 5'
11680	24587	38157	1.79	1.0E-33	AW698818.1	EST_HUMAN	QV3-BN0047-230200-102-b3 BN0047 Homo sapiens cDNA
11973	26227	39448	2.59	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12685	25552		1.98	1.0E-33	AI827191.1	EST_HUMAN	wa88600.x1 NCI CGAP_Rd11 Homo sapiens cDNA clone IMAGE:248210 3'
12852	13129		3.4	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4844	17856		1.17	9.0E-34	BE155575.1	EST_HUMAN	PM4-HT0342-181199-001-D02 HT0352 Homo sapiens cDNA
13069	26003		3.44	9.0E-34	AI277185.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2181	15196	28216	0.93	8.0E-34	AI277185.1	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
8077	21014	34414	0.49	8.0E-34	BE069882.1	EST_HUMAN	MR4-BT0399-200100-001-H03 BT0399 Homo sapiens cDNA
1439	14472	27449	2.93	7.0E-34	U70845.1	EST_HUMAN	y115605.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
10359	14472	27449	0.6	7.0E-34	U70845.1	EST_HUMAN	y115605.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
12478	26227		1.69	7.0E-34	U12868.1	EST_HUMAN	y114010.r1 Soares placenta N22P Homo sapiens cDNA clone IMAGE:148722 5'
471	13543	26471	2.11	6.0E-34	U10691.1	NT	Human G2 protein mRNA, partial cds
471	13543	26472	2.11	6.0E-34	U10691.1	NT	Human G2 protein mRNA, partial cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12287	25103	31836	1.86	6.0E-34	U03688.1	NT	Mus musculus DAB219 hair-specific (hac1-1) gene
1897	14922		2.38	5.0E-34	7706500	NT	Human sapiens Npw38-binding protein Npw38 (LOC51729), mRNA
5101	18111	30983	4.58	5.0E-34	U30883.1	NT	Human sapiens factor SRP35-1 (SRP-35) mRNA, complete cds
9218	13517	35517	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11015	23880	37506	2.03	6.0E-34	AB037856.1	NT	Human sapiens mRNA for KAA1435 protein, partial cds
11583	24521		1.49	5.0E-34	AL163209.2	NT	Human sapiens chromosome 21 segment HS21C009
2014	15035	28046	1.71	4.0E-34	AL1804667.1	EST_HUMAN	RC4c03.11 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:2249194.3'
5223	18231	31108	0.84	4.0E-34	AW89252.1	EST_HUMAN	RC5-01078-260300-022-D02 O10076 Homo sapiens cDNA
9393	22355	37188	1.07	4.0E-34	BF208778.1	EST_HUMAN	601874860F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:410213.5'
6359	19428	32671	0.74	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11486	24429		3.18	3.0E-34	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3602080.5'
9303	22266	35598	1.93	2.0E-34	AI678101.1	EST_HUMAN	MEM29.2 MEM29 repetitive element:
9303	22266	35599	1.93	2.0E-34	AI678101.1	EST_HUMAN	wd35900LX1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170.3' similar to contains
11498	24439	37687	1.97	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
11498	24439	37688	1.57	2.0E-34	P51805	SWISSPROT	ADP ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1505	14538	27510	8.53	1.0E-34	P12236	SWISSPROT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3687	16730	29841	1.35	1.0E-34	AF003528.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4088	17132	30325	0.81	1.0E-34	AY003397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4088	17132	30026	0.81	1.0E-34	AY003397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4506	17531		6.11	1.0E-34	BE071414.1	EST_HUMAN	RC2-810506-240400-016-H08 B10506 Homo sapiens cDNA
6281	19334	32565	1.98	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3868969.5'
6281	19334	32566	1.98	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3868969.5'
9881	19334	36060	0.46	1.0E-34	P22266	SWISSPROT	OLEFACTORY RECEPTOR-LIKE PROTEIN F5
10355	22982	36450	14.47	1.0E-34	AL036635.1	EST_HUMAN	DKFZp584A1563.11 654 (synonym: hbr2) Homo sapiens cDNA clone DKFZp584A1563.5'
11516	24457	38007	1.71	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478.5'
11516	24457	38008	1.71	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478.5'
11530	24471	38022	3.22	1.0E-34		NT	Homo sapiens nucleobindin 2 (NJB2), mRNA
12654	25921		1.4	1.0E-34	AA807097.1	EST_HUMAN	cc31a11.1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1351316.3' similar to gb:X68203
12874	25507		4.01	1.0E-34	AL169210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FL14 PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C010

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	16702	28617	1.25	9.0E-35	AW963302.1	EST_HUMAN	h17b06.y1 NCL CGAP_GUI Homo sapiens cDNA clone IMAGE:268787 5'
227	13328		13.21	8.0E-35	6031190	NT	Homo sapiens prolactin (Prl) mRNA
1751	14780	27765	4.47	8.0E-35	BF58937.1	EST_HUMAN	nead3303.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
1751	14780	27769	4.47	8.0E-35	BF58937.1	EST_HUMAN	nead3303.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
4002	17919	30811	2.91	8.0E-35	BF183195.1	EST_HUMAN	075912 DIACYLGLYCEROL KINASE IOTA. ;
11049	24012	37537	1.84	8.0E-35	BE376480.1	EST_HUMAN	60180598F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4049324 5'
12402	25175		5.41	8.0E-35	BF66282.1	EST_HUMAN	60123949F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
6831	19689	32969	1.83	7.0E-35	11425417	NT	60218482F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300650 3'
1411	14444	27416	0.93	6.0E-35	AA757115.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1885	15006	28009	2.85	6.0E-35	8005975	NT	ah53103.st Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
4083	17117	30012	0.76	8.0E-35	AW297181.1	EST_HUMAN	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
8229	21188	34806	3.68	6.0E-35	6005921	NT	U1H.BWO-aid-4-05.0.U1st NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
9058	22024	35447	0.51	6.0E-35	X94232.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9058	22024	35448	0.51	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
10025	22952	39420	0.98	6.0E-35	AB002364.1	NT	H. sapiens mRNA for KIAA0359 gene, partial cds
10263	23188	36872	3.04	6.0E-35	AB037788.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
1722	14752	27737	61.8	5.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2765	15787	28805	0.9	5.0E-35	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3021	16079	29000	1.47	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4438	17464	30354	2.06	5.0E-35	AF022268.1	NT	Homo sapiens cdk2 kinase (CLK2), protein, ccd1, glucocorticoidase (GBA), and melanin genes, complete cds, melanin pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
4742	17762	30656	0.99	5.0E-35	BE249065.1	EST_HUMAN	TCBAPT03842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
8526	21493		4.74	5.0E-35	BE903922.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:1837448 3' similar to
8552	21520	34939	2.2	5.0E-35	A1208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
8552	21520	34940	2.2	5.0E-35	A1208765.1	EST_HUMAN	SW/Y249 HUMAN Q92559 HYPOTHETICAL PROTEIN KIAA0249. ;
11512	24453		2.39	5.0E-35	AA001788.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
1429	14463	27440	19.88	4.0E-35	BE257607.1	EST_HUMAN	SW/Y249 HUMAN Q92559 HYPOTHETICAL PROTEIN KIAA0249. ;
							2584F12.F1 Soares_fetal_liver_spleen_1NFLS_31 Homo sapiens cDNA clone IMAGE:428015 5'
							601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	14862	27859	7.91	4.0E-35	H91183.1	EST_HUMAN	y88a07.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTT3 repetitive element ;
4844	17861		0.83	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5145	18154		0.83	4.0E-35	BE408102.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401.5'
7416	20583		1.81	4.0E-35	BE350127.1	EST_HUMAN	h03g01.x1 NCI CGAP KIR13 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER29.b3 MER29 repetitive element ;
8863	21830	36253	8.37	4.0E-35	AL049599.1	EST_HUMAN	DKFZ49434.148.11 434 (synonym: hla3) Homo sapiens cDNA clone DKFZp49434.148 5'
1862	14616	27688	21.76	3.0E-35	BE268182.1	EST_HUMAN	601126260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2338	15349		3.36	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5413	18516	31383	27.9	3.0E-35	BF433100.1	EST_HUMAN	7n2fa09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TRQ9QZH7 Q9QZH7 F-BOX PROTEIN FBL2 ;
5413	18516	31384	27.9	3.0E-35	BF433100.1	EST_HUMAN	7n2fa09.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3565381 3' similar to TRQ9QZH7 Q9QZH7 F-BOX PROTEIN FBL2 ;
9844	22780		1.71	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-46, and partial cds, alternatively spliced
10535	22457	36954	0.83	3.0E-35	AW003063.1	EST_HUMAN	w03a05.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW-POL.1 HUMAN P10288 RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
108	15932	26146	0.83	2.0E-35	N86955.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1102	14232	27188	1.39	2.0E-35	T11000.1	EST_HUMAN	REPETITIVE ELEMENT
2227	15241	28260	5.04	2.0E-35	AB018413.1	NT	A971F Human heart Homo sapiens cDNA clone A971
2893	16989	28706	1	2.0E-35	AW689005.1	EST_HUMAN	H08a12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879166 3' similar to
3323	16374	29294	0.93	2.0E-35	6912459	NT	SW:1R12 HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3323	16374	29296	0.93	2.0E-35	6912459	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
3570	16815		1.06	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3930	16970	29883	1.42	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Fetal acute lymphoblastic leukemia Baylor-HQSO project=TCBA Homo sapiens cDNA clone TCBAP-4328
3930	16970	29884	1.42	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Fetal acute lymphoblastic leukemia Baylor-HQSO project=TCBA Homo sapiens cDNA clone TCBAP-4328
4697	17718		2.65	2.0E-35	H49239.1	EST_HUMAN	x1fa123.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5662	18758	31926	1.8	2.0E-35	BF332417.1	EST_HUMAN	Q10-BT0701-210400-189-604 BT0701 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7311	20282	33622	0.95	2.0E-35	BE832638.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
7311	20282	33623	0.95	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11148	24108	37834	11.23	2.0E-35	X68477.1	NT	H.sapiens PROS-27 mRNA
12158	16374	29284	2.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12158	16374	29285	2.39	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12340	25138	31851	1.47	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12340	25138	31852	1.47	2.0E-35	BE904978.1	EST_HUMAN	60149874F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:388869 5'
12854	25462		7.88	2.0E-35	AL163210.2	NT	60149874F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:388869 5'
12873	15832	26146	1.72	2.0E-35	N88985.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
48	13168	26073	5.28	1.0E-35	AA631949.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
48	13168	26074	5.28	1.0E-35	AA631949.1	EST_HUMAN	frf616 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
753	13814	28758	95.25	1.0E-35	AW389473.1	EST_HUMAN	frf616 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
753	13814	28757	95.26	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131059-005-d12 ST0162 Homo sapiens cDNA
910	13985		0.99	1.0E-35	T87947.1	EST_HUMAN	IL2-ST0162-131059-005-d12 ST0162 Homo sapiens cDNA
2549	15550	28571	3.02	1.0E-35	7705994	NT	y693a01.1f Source fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN
2778	15770	28790	1.85	1.0E-35	BE350127.1	EST_HUMAN	Homo sapiens hypophyseal protein (LOC51233), mRNA
2778	15770	28791	1.85	1.0E-35	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
3177	16232	29148	3.44	1.0E-35	AV650422.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
3177	16232	29149	3.44	1.0E-35	AV650422.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone GLCCE008 3'
4452	17478	30365	4.04	1.0E-35	7856905	NT	AV650422 GLC Homo sapiens cDNA clone GLCCE008 3'
4452	17478	30366	4.04	1.0E-35	7856905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
5688	18894	31853	1.54	1.0E-35	11528238	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
7189	18420	31221	0.98	1.0E-35	AW808665.1	EST_HUMAN	Mus musculus actin receptor interacting protein 1, subunit B (p50) (CHAF1B), mRNA
7189	18420	31222	0.98	1.0E-35	AW808665.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
7725	20691	34045	0.83	1.0E-35	AB033105.1	NT	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
7903	20846	34231	0.94	1.0E-35	11418002	NT	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
8900	25699	36312	3.17	1.0E-35	AU158956.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
8900	25699	36313	3.17	1.0E-35	AU158956.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
10942	23862	37377	0.63	1.0E-35	BF469594.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10942	23882	37376	0.83	1.0E-35	BF593594.1	EST_HUMAN	nao0606.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR-031341
12052	24025	38522	1.72	1.0E-35	AB028980.1	NT	O31341 BETA-GALACTOSIDASE 1
12052	24925	38523	1.72	1.0E-35	AB028980.1	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12057	24930		1.59	1.0E-36	AI525119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12188	25887		1.71	1.0E-35	11418274	NT	Promoter-7 D01.7 brimmar Homo sapiens cDNA 5'
12320	15550	28571	1.42	1.0E-35	77059944	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12404	25177		1.71	1.0E-35	11418110	EST_HUMAN	Homo sapiens hypodermal protein (LOC51233), mRNA
12747	25396		1.97	1.0E-36	BE792832.1	EST_HUMAN	Homo sapiens casin kinase 1, epsilon (CSNK1E), mRNA
4011	17050	29066	2.35	9.0E-36	AW821707.1	EST_HUMAN	601584833.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635985 5'
6123	19201	32425	0.75	8.0E-36	X78478.1	NT	RC9-3T0315-180200-013-412 ST0315 Homo sapiens cDNA
							B. bovis BBSc mRNA for scinderin
9585	22647	35098	0.61	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to endogenous retrovirus 9, 5' LTR
10516	23438		0.45	8.0E-36	7706259	NT	Homo sapiens CGJ-09 protein (LOC51605), mRNA
2942	16000	28923	1.05	7.0E-36	AW857578.1	EST_HUMAN	GM1-CT0315-001299-083-007 CT0315 Homo sapiens cDNA
3135	16102		4.05	7.0E-36	4557488	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7916	20659	34247	0.21	7.0E-36	U08872.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7916	20659	34245	0.21	7.0E-36	U08872.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
12558	25278	31778	2.01	7.0E-36	AF052051.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
2021	15042	28053	4.16	6.0E-36	77069222	NT	Homo sapiens glutathione transferase A4 gene, exon 1
24271	15434		5.3	6.0E-36	AB035346.1	NT	Homo sapiens niflurin 2 (NINJ2), mRNA
3653	16668	29811	1.88	6.0E-36	BF61501.1	EST_HUMAN	Homo sapiens TOL8 gene, exon 12
							U1-H.BW1-1env-s-12-0-J11 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5404	18507	31384	5.66	6.0E-36	AA35169.1	EST_HUMAN	h36306.x1 Soares_NSF_P8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126165 3' similar to
							gbMT11948 PANCREAT1 SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN).
							P52932 IMPORTIN ALPHA-2 SUBUNIT.
							Homo sapiens synphilin precursor, mRNA, complete cds
7316	20287	33620	3.48	6.0E-36	AW780143.1	EST_HUMAN	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
8999	21985	35390	2.51	6.0E-36	AF208161.1	NT	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
10585	23507		0.6	6.0E-36	CT16927.1	EST_HUMAN	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
							h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
11874	24756	36339	3.61	6.0E-36	AI380489.1	EST_HUMAN	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
12693	29804	31528	1.9	6.0E-36	BE737154.1	EST_HUMAN	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
138	13243	26173	12.86	5.0E-36	AJ271735.1	NT	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
2761	15753	29773	12.8	5.0E-36	BE388436.1	EST_HUMAN	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN
3626	16659	26581	1.32	5.0E-36	AL163209.2	NT	h36306.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3038627 3' similar to SW:IM2_HUMAN



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4827	17844	30743	1.21	5.0E-36	5729728	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4827	17844	30744	1.21	5.0E-36	5729728	NT	Homo sapiens API5-like 1 (API5L1), mRNA
8070	21007	34406	0.77	5.0E-36	11079227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12166	13243	28173	2.97	5.0E-36	ALJ271735.1	NT	Homo sapiens Xq pseudocentosomal region, segment 1/2
12455	25214	31832	3.03	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
1228	14266	27223	1.24	4.0E-36	BEQ10038.1	EST_HUMAN	PM3-3N0176-100400-401-g04 BN0176 Homo sapiens cDNA
1436	14469	27447	0.99	4.0E-36	P10265	SWISSPROT	RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE]; ENDONUCLEASE]
1652	14684	27658	1.63	4.0E-36	BE382574.1	EST_HUMAN	601385574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386.5'
2231	15245	1.64	4.0E-36	AW247772.1	EST_HUMAN	282002015prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020.5'	
3365	16415	26340	0.85	4.0E-36	BE386299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604169.5'
3365	16415	26341	0.85	4.0E-36	BE386299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604169.5'
4766	17804	30666	0.71	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5804	18695	32481	0.95	4.0E-36	RG4023.1	EST_HUMAN	31805.11 Soares placenta N2ZHP Homo sapiens cDNA clone IMAGE:139713.5'
6173	19248	34246	2.48	4.0E-36	M33320.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
7915	20859	34246	1.74	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exon 2-29
8901	21867	35290	1.2	4.0E-36	D81675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8901	21867	35291	1.2	4.0E-36	D81675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11332	24282	37806	1.8	4.0E-36	AA400370.1	EST_HUMAN	2068101.1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:743260.5'
12471	25220	1.86	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA	
12515	25768	8.26	4.0E-36	AV753622.1	EST_HUMAN	AV753623 TP Homo sapiens cDNA clone TPGABH01.5'	
697	13759	26891	3.9	3.0E-36	AF098910.1	NT	Homo sapiens neuroxin IIl-alpha gene, partial cds
1497	14630	27602	0.97	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1497	14630	27603	0.97	3.0E-36	AF110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
4630	17564	30442	8.81	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1 - pending), mRNA
3184	16239	29167	2.17	2.0E-36	BE256287.1	EST_HUMAN	607106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706.5'
4998	18011	30988	8.63	2.0E-36	AW690376.1	EST_HUMAN	QVQ-OT10030-240500-174-H04 OT10030 Homo sapiens cDNA :
5563	18660	31608	2.52	2.0E-36	AF207747.1	NT	Mus musculus p47-phox gene, complete cds
5948	19034	32227	3.89	2.0E-36	T08756.1	EST_HUMAN	ES106648 infant Brain, Bento Soares Homo sapiens cDNA clone HIBB128.5' end
6728	19784	33063	12.4	2.0E-36	T69628.1	EST_HUMAN	y44407.r1 Strathgery liver (#37224) Homo sapiens cDNA clone IMAGE:83508.5'
9743	22864	38138	0.82	2.0E-36	BF512794.1	EST_HUMAN	UHLBW1-annu-e-11-Q-U1 at NCL_CGAP_Sub07 Homo sapiens cDNA clone IMAGE:3071192.3'
9607	22728	38184	0.57	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9907	22728	36185	0.87	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isocapitase T-3) (USP13) mRNA
888	13941	26898	2.74	1.0E-36	BE409310.1	EST_HUMAN	601300836F NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3695480 5'
2155	15171	28169	1.08	1.0E-36	BE148523.1	EST_HUMAN	RC1-H10217-131169-021-n07 H10217 Homo sapiens cDNA
2155	15171	28169	1.08	1.0E-36	BE148523.1	EST_HUMAN	RC1-H10217-131169-021-n07 H10217 Homo sapiens cDNA
2212	15227	28248	1.35	1.0E-36	BF673761.1	EST_HUMAN	602135493F NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
3355	16406		1.34	1.0E-36	AF155962.1	NT	Homo sapiens human endogenous retrovirus W proC6-19 protease (pro) gene, partial cds
5818	18808	32092	0.82	1.0E-36	AL044448.1	EST_HUMAN	DKFZP434G022.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZP434G022 5'
8003	19088	32288	1.3	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6307	19378		3.80	1.0E-36	AI867714.1	EST_HUMAN	w637c12x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6528	19592	32852	1.34	1.0E-36	R26012.1	EST_HUMAN	y35610.1 Scores Infant brain TNIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN
6528	19592	32853	1.34	1.0E-36	R26012.1	EST_HUMAN	y35610.1 Scores Infant brain TNIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN
6838	19892	33187	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZP761A229.1 761 (synonym: hmyz2) Homo sapiens cDNA clone DKFZP761A229 5'
8293	21262	34671	2.77	1.0E-36	AA148034.1	EST_HUMAN	z551a12.1 Stratiote endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8293	21262	34672	2.77	1.0E-36	AA148034.1	EST_HUMAN	z551a12.1 Stratiote endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8398	21357	34764	1.15	1.0E-36	AA420467.1	EST_HUMAN	nc00408.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745870
8398	21357	34765	1.15	1.0E-36	AA420467.1	EST_HUMAN	nc00408.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745870
8520	21488	34802	0.48	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO101033 5'
8520	21488	34803	0.48	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO101033 5'
9384	22349	35781	2.72	1.0E-36	AF103668.1	EST_HUMAN	x62207.1 NCI_CGAP_Bn35 Homo sapiens cDNA clone IMAGE:2614357 3'
10473	23395	36892	3.65	1.0E-36	BF364189.1	EST_HUMAN	QV3-NN1023-010800-109-N01 NN1023 Homo sapiens cDNA
10691	23813	37107	0.86	1.0E-36	AW855988.1	EST_HUMAN	RC3-CT0279-040500-017-at10 CT0279 Homo sapiens cDNA
10691	23813	37108	0.86	1.0E-36	AW855988.1	EST_HUMAN	RC3-CT0279-040500-017-at10 CT0279 Homo sapiens cDNA
11294	24244	37771	2.84	1.0E-36	AW897636.1	EST_HUMAN	UHFH-BNC-ale-c03-04-J11.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078277 5'
11708	24674	38351	2.88	1.0E-36	AW504433.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12398	25136		5.61	1.0E-36	11418177	NT	Homo sapiens chromosome 21 segment HS21C013
12777	25414		4.97	1.0E-36	AL163213.2	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
13034	25579		4.02	1.0E-36	AF202723.1	NT	W80007.1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2604246 3'
7607	20568	33929	2.3	9.0E-37	AW009277.1	EST_HUMAN	w80007.1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2604246 3'
7607	20568	33930	2.3	9.0E-37	AW009277.1	EST_HUMAN	w80007.1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2604246 3'
3386	18416	28342	1.17	8.0E-37	4757978	NT	Homo sapiens chitinase (chitinase) 2 (CHN2) mRNA
5320	18426		1.6	8.0E-37	BE698077.1	EST_HUMAN	CNM-U70003-050900-503-009 U70003 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5927	19013	32206	3.79	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
5927	19013	32206	3.79	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
5977	19062	32263	6.06	8.0E-37	AW840940.1	EST_HUMAN	RC1-CN0008-210100-012-e09.1 CN0008 Homo sapiens cDNA
8216	21185	34595	6.98	8.0E-37	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IP22, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8. 9, 13 and 14 genes
1289	14324		2.33	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp434E0422 5'
1759	14788	27773	0.82	7.0E-37	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1759	14788	27774	0.92	7.0E-37	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5161	18170	31049	1.86	7.0E-37	AW988323.1	EST_HUMAN	EST380898 IMAGE: resseques, MAGJ Homo sapiens cDNA
11109	24069	37591	8.45	7.0E-37	AI817700.1	EST_HUMAN	WK25011.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTRS.12 PTRS repetitive element:
11241	24184	37712	1.83	7.0E-37	AI838702.1	EST_HUMAN	h07g03.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2105140 3' similar to contains L1.b3 L1 repetitive element:
8782	21749	35171	0.50	6.0E-37	AF169899.1	NT	Homo sapiens protocadherin alpha 10 alternative isoform (PCDH-alpha10) mRNA, complete cds
12803	25487		3.50	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
8212	19286	32518	4.33	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8212	19288	32519	4.33	6.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9109	22075	35501	0.88	6.0E-37	AV750211.1	EST_HUMAN	AV760211 NPC Homo sapiens cDNA clone NPC8GH09 5'
11285	24217		3.87	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
12333	25193		6.43	6.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exon 1, 2, and 3
2431	16438	28455	2.41	4.0E-37	AA702784.1	EST_HUMAN	280504.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4814	17831	30729	1.05	4.0E-37	MT0978.1	NT	Human endogenous retroviral DNA (4-1), complete retroiral segment
5288	18276		0.93	4.0E-37	N62051.1	EST_HUMAN	EST762g10 WATM10 Homo sapiens cDNA clone 52g10 similar to human STS G04101
6419	19486	32735	0.66	4.0E-37	AW794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9711	22664	36121	0.57	4.0E-37	AA843909.1	EST_HUMAN	alc08a02.s1 Soares sarathyroid tumor NHIPA Homo sapiens cDNA clone IMAGE:1405442 3'
2033	15052	28068	3.07	3.0E-37	AL048955.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp434L2418
2033	15052	28068	3.07	3.0E-37	AL048955.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp434L2418
2518	19522		1.74	3.0E-37	AW681150.1	EST_HUMAN	EST1373222 IMAGE: resseques, MAGF Homo sapiens cDNA
2876	16034		3.71	3.0E-37	AW981150.1	EST_HUMAN	EST1373222 IMAGE: resseques, MAGF Homo sapiens cDNA
5964	19049	32250	0.73	3.0E-37	AL138274.1	EST_HUMAN	DKFZp47G067_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp47G067 5'

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7804	20754	34130	0.75	3.0E-37	AI748952.1	EST_HUMAN	at3405.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373898 3' similar to TR-Q13357
381	13494	26426	3.06	2.0E-37	D89790.1	NT	Q13357 SIMILAR TO POGO ELEMENT ;
381	13494	26427	3.06	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1082	14126	27079	2.49	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1082	14126	27080	2.49	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'
1881	15002	28005	2.43	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3608	16048	29850	5.24	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXV1A (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polyepitide 1 (CYP27A1b) mRNA
5462	18564		0.74	2.0E-37	BF035327.1	EST_HUMAN	601458531FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
6698	19753	33030	0.55	2.0E-37	11960617	NT	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
6816	16870	33159	3.92	2.0E-37	AA346720.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
8326	21268	34713	0.51	2.0E-37	BE537764.1	EST_HUMAN	601067834FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8329	21298	34714	0.51	2.0E-37	BE537764.1	EST_HUMAN	601067834FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8372	21341	34752	3.33	2.0E-37	BF204032.1	EST_HUMAN	601869157FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111408 5'
11895	24766	36353	8.89	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12738	25607		1.51	2.0E-37	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
13074	25607		4.68	2.0E-37	11417972	NT	Homo sapiens chromosome 21 segment HS21C081
2099	15116	28138	5.41	1.0E-37	AL163281.2	NT	Homo sapiens ribonuclease II (RNS) mRNA, complete cds
3985	17025	29836	4.56	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease II (RNS) mRNA, complete cds
4191	17222	30111	1.08	1.0E-37	BE872365.1	EST_HUMAN	601448619FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5'
4978	17693	30882	2.21	1.0E-37	BE937119.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6119	19197		1.01	1.0E-37	7303360	NT	Mus musculus dogelin (Olog), mRNA
8557	21526	34943	0.77	1.0E-37	BE546032.1	EST_HUMAN	601072418FT NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
9037	22053	35476	3.45	1.0E-37	AA171406.1	EST_HUMAN	zp21002.1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610099 5' similar to contains L1 L2 L1 repetitive element ;
10971	23801	37405	0.44	1.0E-37	AF730743.1	EST_HUMAN	AV730743 HTF Homo sapiens cDNA clone HTF-AHG10 5'
11066	23019	37642	2.07	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HGT) processed pseudogene, complete cds
12648	28328		4.28	1.0E-37	BE77814.1	EST_HUMAN	CN3-FT0066-140700-243-307 FT0066 Homo sapiens cDNA
9572	15961	32150	1.87	8.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC38768), mRNA
1226	14264	27221	1.65	8.0E-38	11436955	NT	Homo sapiens Grp2-associated binder 2 (KIA0571), mRNA
2506	15509	28538	2.16	8.0E-38	BF346221.1	EST_HUMAN	602018401FT NCI_OGAP_Bln87 Homo sapiens cDNA clone IMAGE:4153992 5'
12698	14264	27221	1.44	8.0E-38	11436955	NT	Homo sapiens Grp2-associated binder 2 (KIA0571), mRNA
3065	18112	28027	1.86	6.0E-38	BF033033.1	EST_HUMAN	601455722FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5670	18765	31935	1.48	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5670	18765	31936	1.48	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7550	20513	33871	0.51	6.0E-38	8823130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7513	20573	33936	0.74	6.0E-38	AJ010868.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
7513	20573	33937	0.74	6.0E-38	AJ010869.1	NT	Homo sapiens mRNA for potassium channel Kv4.2
12189	25035	33937	3.19	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12077	25035	31765	18.01	6.0E-38	AB002069.1	NT	Homo sapiens DNA for Human P2X4, complete cds
13052	25733	31916	1.90	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
728	13789	26724	1.28	6.0E-38	AW971819.1	EST_HUMAN	EST383908 IMAGE resequences, MARG1 Homo sapiens cDNA
2460	15494	28487	1.24	6.0E-38	AJ237740.1	NT	Homo sapiens RIB1R gene (partial), exon 8
7228	20280	33584	1.8	6.0E-38	BE971610.1	EST_HUMAN	601450148FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE3854074 5'
118	13228	26154	3.65	4.0E-38	Z25466.1	NT	B laurus mitochondrial aspartate aminotransferase mRNA, complete CDS
118	13228	26155	3.65	4.0E-38	Z25466.1	NT	B laurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2110	15127	26155	3.88	3.0E-38	AF009530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3710	16753		1.24	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaf-liko) (HIRAP4), mRNA
3869	16808	29817	1.68	3.0E-38	PS3538	SWISSPROT	SSU72 PROTEIN
3869	16808	29818	1.68	3.0E-38	PS3538	SWISSPROT	SSU72 PROTEIN
6917	25571	33264	7.83	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7455	20421	33776	0.6	3.0E-38	AW302461.1	EST_HUMAN	AW04401.x1 NC1_CGAP_Bn63 Homo sapiens cDNA clone IMAGE2827009 3'
7832	20780	34167	0.57	3.0E-38	AA378327.1	EST_HUMAN	EST191188 Synovial sarcoma Homo sapiens cDNA 5' end
7844	20791	34167	0.57	3.0E-38	AA378327.1	EST_HUMAN	CM3-F10181-140700-241-407 F10181 Homo sapiens cDNA
8997	21693	35388	1.97	3.0E-38	BF373654.1	EST_HUMAN	Y68804.1 Scores melanocyte ZNFHM Homo sapiens cDNA clone IMAGE249775 5'
8997	21693	35389	1.97	3.0E-38	BF373654.1	EST_HUMAN	Y68804.1 Scores melanocyte ZNFHM Homo sapiens cDNA clone IMAGE249775 5'
10331	23255	31171	2.06	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12809	18333	31171	1.46	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
62	13172	26081	2.94	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1380	14414	27384	2.28	2.0E-38	5902087	NT	Homo sapiens SMY3 (suppressor of mit two 3, yeast) homolog 2 (SMY3H2), mRNA
1653	14685	27659	2.07	2.0E-38	AA437353.1	EST_HUMAN	ZW30401.1 Scores ovary tumor NHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
1853	14685	27660	2.07	2.0E-38	AA437353.1	EST_HUMAN	ZW30401.1 Scores ovary tumor NHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to
2418	15425	26448	1.11	2.0E-38	W76571.1	EST_HUMAN	SWJMA12_RABIT P45701 MANNOsyl-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
6271	18160	31040	0.79	2.0E-38	AA437181.1	EST_HUMAN	ZW66009.1 Scores_fetal_NH919W Homo sapiens cDNA clone IMAGE:345664 5' similar to
							ZW61400.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817687
							G817687 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	18897	32079	0.61	2.0E-38	Z28634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5807	18897	32080	0.61	2.0E-38	Z28634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7938	20927	34322	1.27	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8828	21795		5.59	2.0E-38	BE165980.1	EST_HUMAN	NR3-1170487-150200-1 (3-g01 HT0487 Homo sapiens cDNA
12242	25072		0.65	2.0E-38	FO8450.1	EST_HUMAN	HSC181031 normalized infant brain cDNA Homo sapiens cDNA clone c-1803
9316	22281	35711	1.21	2.0E-38	AF069755.1	NT	Homo sapiens cDNA clone IMAGE:745399 5' similar to TR:002710
9578	22538		1.04	2.0E-38	BE22258.1	EST_HUMAN	GAG POLYPROTEIN ;
10816	23736	37239	1.74	2.0E-38	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11818	24702	38284	4.82	2.0E-38	BE712780.1	EST_HUMAN	QV2-HT0699-080800-293-a05 HT0698 Homo sapiens cDNA
11955	24834	38429	3.68	2.0E-38	AF160501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11955	24834	38430	3.66	2.0E-38	AF160501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12240	25071		3.39	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCKX407 5'
12242	25072		2.13	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12538	25262		2.81	2.0E-38	M55530.1	NT	Human topoisomerase 2
12548	25271	31810	6.8	2.0E-38	M55541.1	EST_HUMAN	CHR220560 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
13055	25599		3	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1095	14139		2.38	1.0E-38	AA401570.1	EST_HUMAN	zu02002.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:745399 5' similar to contains element MER19 repetitive element ;
2015	15036	28547	1.92	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2035	15084	28071	1.17	1.0E-38	7681989	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2602	15006	28532	2.01	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CKNK) gene, exon 7
4182	17213	30101	0.96	1.0E-38	AB037683.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4352	17378	30259	10.48	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4352	17378	30260	10.48	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4627	17848	30536	0.63	1.0E-38	8922545	NT	Homo sapiens hypodermal protein FLJ10600 (FLJ10600), mRNA
5143	18152	31032	0.77	1.0E-38	AA077628.1	EST_HUMAN	7844H06 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7844H06
6143	19218	32448	6.58	1.0E-38	7303360	NT	Mus musculus obogelin (Obog), mRNA
6143	19218	32448	6.58	1.0E-38	7303360	NT	Mus musculus obogelin (Obog), mRNA
7854	20594	33957	3.03	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9508	22471	35915	0.93	1.0E-38	11422260	NT	Homo sapiens hypodermal protein FLJ10600 (FLJ10600), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9765	22706	36162	6.34	1.0E-39	BE350127.1	EST_HUMAN	h09q01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146259 3' similar to contains MER26.b3 MER29 repetitive element.
12401	25712		2.08	1.0E-39	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
96	13176	26087	5.73	8.0E-39	4502312	NT	Homo sapiens ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 16kD (A1P6C) mRNA
1356	14420	27368	0.94	8.0E-39	4758226	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1846	14872		1.54	8.0E-39	AL623404.1	EST_HUMAN	wh63f10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL PROTEIN.
2106	15122	28142	5.19	7.0E-39	AL163227.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
11160	24116	37845	1.8	6.0E-39	BF331826.1	EST_HUMAN	QV1-B110631-040900-357-402 B110631 Homo sapiens cDNA
12681	25545		3.12	6.0E-39	BE570394.1	EST_HUMAN	7634-03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284366 3' similar to WP-R151.6 CE00828
1008	14088	27010	1.43	5.0E-39	AF003528.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2568	19056	28976	8.13	5.0E-39	A1750154.1	EST_HUMAN	atd604.x1 Bardstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.11 LTR7 repetitive element ;
12680	25356		2.82	5.0E-39	11420289	NT	Homo sapiens hypothetical protein FLJ10893 (FLJ10803), mRNA
562	19622	28542	20.77	4.0E-39	AB015810.1	NT	Chlorocibius aerophilus mRNA for ribosomal protein S4X, complete cds
3587	19632	29550	0.92	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5628	19014	32207	0.65	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
5628	19014	32208	0.65	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
8411	21380	34788	1.14	4.0E-39	AA682949.1	EST_HUMAN	a692g04.s1 Striatagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element ;
9684	22637	30032	0.61	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9684	22637	30032	0.61	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12704	23393		3.29	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12516	25441		3.15	4.0E-39	BE839452.1	EST_HUMAN	QV6-FN0063-260900-278-c06 FN0063 Homo sapiens cDNA
49	13169	28076	14.8	3.0E-39	AA631949.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13169	28076	14.8	3.0E-39	AA631949.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
49	13169	28077	14.8	3.0E-39	AA631949.1	EST_HUMAN	hmfr16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12233	25065	38193	6.14	3.0E-39	A1084557.1	EST_HUMAN	ox63a10.s1 Scores_NHNPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
12233	25065	38194	6.14	3.0E-39	A1084557.1	EST_HUMAN	ox63a10.s1 Scores_NHNPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12822	26100		11.16	3.0E-39	H37693.1	EST_HUMAN	yf5f506.s1 Soares retina N2b-HR Homo sapiens cDNA clone IMAGE:190854 3'
898	13953		9.79	2.0E-39	BE409203.1	EST_HUMAN	607301807F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
913	13988		13.84	2.0E-39	AJ525119.1	EST_HUMAN	prom1n7.D01.1 b7v1mur Homo sapiens cDNA 5'
1033	14078		4.67	2.0E-39	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1532	14565		24.51	2.0E-39	AW372318.1	EST_HUMAN	PM0-B70340-21.285-003-302 B70340 Homo sapiens cDNA
1860	15011	28017	3.62	2.0E-39	AA720574.1	EST_HUMAN	hw21.g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
2636	15635	28659	2.3	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
4431	17458	30349	1.56	2.0E-39	BE370207.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
5568	18665	31624	4.2	2.0E-39	AA508890.1	EST_HUMAN	hg8603.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
7694	20555	33915	2.34	2.0E-39	AA080857.1	EST_HUMAN	zn06102.r1 Stralagene HNT neuron (R937233) Homo sapiens cDNA clone IMAGE:546851 5'
7776	20729	34101	0.61	2.0E-39	AL153202.2	NT	Homo sapiens chromosome 21 segment HS21C002
7776	20729	34102	0.61	2.0E-39	AL153202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8653	21621	35041	0.56	2.0E-39	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9851	22787		1.32	2.0E-39	AA084331.1	EST_HUMAN	am86c11.s1 Stralagene schizo brain ST1 Homo sapiens cDNA clone IMAGE:1630198 3'
9884	22911		0.53	2.0E-39	AB066690.1	EST_HUMAN	tu35c03.xt NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253052 3'
11781	24689	38271	2.56	2.0E-39	D96984.1	NT	Human mRNA for KIAA0205 gene, partial cds
1516	14548	27520	3.52	1.0E-39	AJ006345.1	NT	Homo sapiens KVL0T1 gene
1516	14548	27521	3.52	1.0E-39	AJ006345.1	NT	Homo sapiens KVL0T1 gene
1333	14568	27535	0.96	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4689	17710	30803	6.87	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE cDNAs, MAGB Homo sapiens cDNA
4689	17710	30804	6.87	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE cDNAs, MAGB Homo sapiens cDNA
4731	17761	30843	8.48	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5432	18634	31442	0.87	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5432	18634	31443	0.87	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5711	18805	31982	1.2	1.0E-39	T69376.1	EST_HUMAN	yx28a06.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains A1u repetitive element/contains LTR1 repetitive element;
5747	18841	32023	4.7	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
5747	18841	32024	4.7	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
7000	20126		1.68	1.0E-39	11438728	NT	Homo sapiens bubby like protein 3 (TULP3), mRNA
7589	20560	33911	2.1	1.0E-39	D78132.1	NT	Homo sapiens mRNA for res-related GTP-binding protein, complete cds
8910	21876	35302	0.96	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13827	26545	1.8	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1209	14275	27234	14.84	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1236	14276	27235	14.84	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1), mRNA
1443	14476	27453	0.99	9.0E-40	4507612	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
3789	16839	29746	0.85	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1), mRNA
3997	18375	29643	4.05	9.0E-40	A5033070.1	NT	Homo sapiens mRNA for KIAA 1244 protein, partial cds
4527	17401	30281	0.78	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopoldase T-3) (USP13), mRNA
3054	18111	29028	0.91	8.0E-40	AA078185.1	EST_HUMAN	HT15A04 Chromosome 7 HLA cDNA library Homo sapiens cDNA clone HT15A04
3945	16985		2.39	8.0E-40	BE396541.1	EST_HUMAN	901289558FT NIH_MGC, 8 Homo sapiens cDNA clone IMAGE:3819188 5'
7685	20924	34317	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7685	20924	34318	2.22	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11243	24196	37715	1.76	7.0E-40	AL163240.2	NT	Homo sapiens chromosome 21 segment HS21C048
2737	15751	28746	7.5	6.0E-40	AA361275.1	EST_HUMAN	ESTT0527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2737	15731	28747	7.5	6.0E-40	AA361275.1	EST_HUMAN	ESTT0527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6049	19130		2.05	6.0E-40	BE504765.1	EST_HUMAN	h240901.x1 NCI_CGAP, CG8 Homo sapiens cDNA clone IMAGE:3210480 3'
8270	18343		1.32	6.0E-40	7681959	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7121	20055	33359	3.38	6.0E-40	11439763	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7121	20055	33360	3.38	6.0E-40	11439763	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10336	23280	36738	9.47	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC/GF04 3'
10336	23280	36739	9.47	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLC/GF04 3'
2812	16611	28635	1.12	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1894	14819	27915	3.21	4.0E-40	AI680005.1	EST_HUMAN	H81b01.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O75505 O73505 POL PROTEIN-1;
4415	15134		2.22	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4415	17442	30333	8.57	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8218	21187	34597	0.44	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8324	21293	34707	4.81	4.0E-40	AA742800.1	EST_HUMAN	h34e10.1 NCI_CGAP_B14 Homo sapiens cDNA clone IMAGE:122212
8410	22376	33612	5.53	4.0E-40	BE009418.1	EST_HUMAN	PIMC-BN0167-070500-002-H12 BN0167 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9410	22375	35873	5.53	4.0E-40	BC009416.1	EST_HUMAN	P10-BN017-07060-002-h12 BN0167 Homo sapiens cDNA
11071	24033	37557	1.66	4.0E-40	AW841955.1	EST_HUMAN	RC1-CN0017-12020-012-e04 CN0017 Homo sapiens cDNA
4158	17169	30077	1.02	3.0E-40	AI025949.1	EST_HUMAN	WT1207.x1 NCL_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2380549 3'
6007	19695	33540	0.66	3.0E-40	4506736	NT	Homo sapiens fibronectin protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6766	19650	33135	7.89	3.0E-40	11417342	NT	Homo sapiens sema domain, seven transmembrane domain repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8724	21892	35118	3.94	3.0E-40	5454167	NT	Homo sapiens HIV associated factor (XAP4) mRNA
6320	22265	35715	1.23	3.0E-40	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
6559	22528	35977	1.34	3.0E-40	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11597	24535	35092	9.3	3.0E-40	6005813	NT	Homo sapiens canine thymidine protein kinase (NDR), mRNA
325	13416		4.59	2.0E-40	AI223036.1	EST_HUMAN	cg52008.x1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
705	13854		26.29	2.0E-40	AW303868.1	EST_HUMAN	xr24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW-RS9_MOUSE
1642	14665		1.77	2.0E-40	AV731501.1	EST_HUMAN	P97461 4C5 RIBOSOMAL PROTEIN S5.1
1961	14974	27073	1.94	2.0E-40	4508188	NT	Homo sapiens proteasome (prosome, multicatalytic subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1951	14974	27074	1.94	2.0E-40	4508188	NT	Homo sapiens proteasome (prosome, multicatalytic subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2065	15102	28119	1.01	2.0E-40	AI095582.1	EST_HUMAN	w60411.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR.Q91828 Q91829
2179	15194	28215	1.84	2.0E-40	5453592	NT	ZINC FINGER PROTEIN.1
2700	15606		1.79	2.0E-40	BE275932.1	EST_HUMAN	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
3143	16200	29111	4.44	2.0E-40	5453592	NT	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
4837	17953	30845	1.7	2.0E-40	AL163280.2	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4937	17953	30846	1.7	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5237	18245	31117	1.12	2.0E-40	4505880	NT	Homo sapiens chromosome 21 segment HS21C080
884	13939		1.63	1.0E-40	AA225985.1	EST_HUMAN	Homo sapiens plasminogen (PLG) mRNA
2630	15628	26653	1.47	1.0E-40	BF036981.1	EST_HUMAN	nc09a08.x1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:3869303 5'
2696	19692		1.54	1.0E-40	BE018948.1	EST_HUMAN	b679410.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR.Q82168 Q82169
2747	15740	28756	1.38	1.0E-40	BF541030.1	EST_HUMAN	SYNTAXIN 17.1
2747	15740	28757	1.39	1.0E-40	BF541030.1	EST_HUMAN	802088904F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
3303	19362		1.59	1.0E-40	4507142	NT	802088904F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
4540	17681	30549	4.18	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
							Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6394	19482	32695	0.73	1.0E-40	W92708.1	EST_HUMAN	278711.11 Scorses, fetal_liver, spleen, INFLS_51 Homo sapiens cDNA clone IMAGE:418317.3
6394	19482	32696	0.73	1.0E-40	W92708.1	EST_HUMAN	278711.11 Scorses, fetal_liver, spleen, INFLS_51 Homo sapiens cDNA clone IMAGE:418317.3
7293	20285	33659	1.92	1.0E-40	AA573201.1	EST_HUMAN	142604.61 NCI CGAP_A41 Homo sapiens cDNA clone IMAGE:995167.3
7293	20285	33660	1.92	1.0E-40	AA573201.1	EST_HUMAN	142604.61 NCI CGAP_A41 Homo sapiens cDNA clone IMAGE:995167.3
7443	20409	33761	0.84	1.0E-40	P28808	SWISSPROT	POL POLYPEPTIDE [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
11282	24214	37738	2.42	1.0E-40	AU149345.1	EST_HUMAN	AU149345.1 Homo sapiens cDNA clone NT2R44002122.3
12659	25847	37738	14.2	1.0E-40	BF334112.1	EST_HUMAN	MR2-GT0222-211059-002-e10 GT0222 Homo sapiens cDNA
12813	25922		1.64	1.0E-40	Z00015.1	NT	H. sapiens (Vik) gene (w/ repetitive L-family member (cos 2D)
8254	21223	34633	1.59	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C03
826	15852	26840	1.81	7.0E-41	AI934394.1	EST_HUMAN	wp04H04.x1 NCI CGAP_Xig11 Homo sapiens cDNA clone IMAGE:2463895.3
826	15852	26841	1.81	7.0E-41	AI934394.1	EST_HUMAN	wp04H04.x1 NCI CGAP_Xig11 Homo sapiens cDNA clone IMAGE:2463895.3
837	18442	31193	0.86	7.0E-41	11545770	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
8124	19202	32428	2.97	7.0E-41	11419208	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
8488	19553	32803	1.08	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7186	18417	31218	0.88	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11793	24691	39272	2.6	7.0E-41	4758446	NT	Homo sapiens guanine nucleotide binding protein 10 (GNQ10) mRNA
13072	25844		10.83	7.0E-41	11417972	NT	Homo sapiens pectadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
280	13376	26304	0.65	6.0E-41	AB037163.1	NT	Homo sapiens DSCRB5 mRNA, complete cds
2120	15137	28167	1.67	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
8304	21278	34694	1.59	6.0E-41	BF513783.1	EST_HUMAN	U1H-BW7-amp-b-03-O-U1.st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421.3
1519	14849	27938	1.75	5.0E-41	TG2528.1	EST_HUMAN	yc03910.a1 Stradiene lung (#637210) Homo sapiens cDNA clone IMAGE:76628.3
4134	17166		1.03	5.0E-41	4885638	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6898	19755		2.06	5.0E-41	BE087042.1	EST_HUMAN	PM4-BT0347-281168-002-F11 BT0347 Homo sapiens cDNA
391	13466		1.73	4.0E-41	BE119318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1100	14144	27094	1.18	4.0E-41	AU118244.1	EST_HUMAN	AU118244 HEMBA1 Homo sapiens cDNA clone HEMBA1005683.5
1408	14441	27411	9.16	4.0E-41	AI027117.1	EST_HUMAN	ov45606.s1 Scorses, parathyroid, tumor, NbhPA Homo sapiens cDNA clone IMAGE:1648794.3 similar to TRC00597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1408	14441	27412	9.16	4.0E-41	AI027117.1	EST_HUMAN	ov45606.s1 Scorses, parathyroid, tumor, NbhPA Homo sapiens cDNA clone IMAGE:1648794.3 similar to TRC00597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1420	14453	27427	2.75	4.0E-41	AB006881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1641	14873	27646	6.9	4.0E-41	AI500408.1	EST_HUMAN	imbdgda.x1 NCL_OGAP_Bin25 Homo sapiens cDNA clone IMAGE:2165598 3' similar to contains OIR.b1 OIR repetitive element.
2859	15958	28876	3.55	4.0E-41	AI229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2859	15958	28877	3.55	4.0E-41	AI229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4169	17169	30085	2.25	4.0E-41	X92885.1	NT	H.sapiens Unas1 1bp sensitive site (HSS-3) enhancer element
6658	18715		1.31	4.0E-41	AV759295.1	EST_HUMAN	AV759295 Homo sapiens cDNA clone BMBH006 5'
10052	22979	36446	8.41	4.0E-41	BF304683.1	EST_HUMAN	00188095F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4122119 5'
11981	24858		11.55	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CUAAC007 5'
947	14000	26952	2.51	3.0E-41	AB030176.1	NT	Homo sapiens PAO-H19 mRNA for peptidylarginine diaminase type II, complete cds
4352	17389	30271	2.6	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5148	18157		1.15	3.0E-41	AB033774.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5559	18588	31625	9.45	3.0E-41	X87688.1	NT	H.sapiens mRNA for putative p64 Cl CP protein
6518	19581	32839	1.61	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7473	20439	33787	0.62	3.0E-41	AA335168.1	EST_HUMAN	EST04683 Jurkat T-cells VI Homo sapiens cDNA 5' and
8072	21009	34407	0.52	3.0E-41	R54795.1	EST_HUMAN	Y75008.1 Soares breast 2NDPBT Homo sapiens cDNA clone IMAGE:154975 5'
12116	24056	35587	3.45	3.0E-41	AV594941.1	EST_HUMAN	OYO-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12116	24986	35588	3.45	3.0E-41	AV594941.1	EST_HUMAN	OYO-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12116	25040		1.49	3.0E-41	AA609788.1	EST_HUMAN	af7710.31 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1031947 3'
1841	14595	27570	15.21	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1975	14595	27568	2.15	2.0E-41	AA331640.1	EST_HUMAN	EST135818 Embryo, 8 week I Homo sapiens cDNA 5' end
2228	15242	28207	1.37	2.0E-41	D66982.1	NT	Human mRNA for KIAA0207 gene, complete cds
2278	15299	28314	4.43	2.0E-41	X89531.1	NT	G.gallus DNA for ZNF80 gene homolog
2839	14595	27570	7.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3851	16891	29785	0.9	2.0E-41	5932106	NT	Homo sapiens tot of sevenless (Drosophila) homolog 1 (SOST) mRNA
4652	17673	30550	1.13	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4652	17673	30551	1.13	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
5617	18713	31871	0.61	2.0E-41	AA594575.1	EST_HUMAN	nc1202.61 NCL_OGAP_Ph161 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:552851_rna1
6782	19837	33121	0.85	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7935	20877	34297	6.35	2.0E-41	AF038404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8148	21055	34484	0.8	2.0E-41	11422047	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8403	21372	34780	1.83	2.0E-41	M96944.1	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog) like (ORC5L), mRNA
8403	21372	34781	1.63	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8433	21402	34815	1.47	2.0E-41	AA328295.1	EST_HUMAN	EST31723 Embrya, 12 week Homo sapiens cDNA 5' end
8326	22291	35721	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9722	22713	38167	0.72	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9722	22713	38168	0.72	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11815	24700	38281	2.21	2.0E-41	AA372637.1	EST_HUMAN	EST184856 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3219	16274	29167	1.33	1.0E-41	BE889735.1	EST_HUMAN	901445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848803 5'
3219	16274	29168	1.33	1.0E-41	BE889735.1	EST_HUMAN	901445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848803 5'
4589	17619	30512	7.8	1.0E-41	6878468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
7026	18368	31278	0.49	1.0E-41	H80070.1	EST_HUMAN	3x1803.s1 Soares melanocytes 2N6HM Homo sapiens cDNA clone IMAGE:262061 3'
9773	22714	38169	1.73	1.0E-41	AI217698.1	EST_HUMAN	q75610.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11494	24437	37686	1.55	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-190200-040-F09 CT0213 Homo sapiens cDNA
12332	25132	37686	2.72	1.0E-41	11626291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8965	21632	35639	1.06	9.0E-42	BE178191.1	EST_HUMAN	RC0-H70813-210300-032-d01 HT0813 Homo sapiens cDNA
8526	22492	35940	3.08	9.0E-42	11690161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
8526	22492	35940	3.08	9.0E-42	11690161	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
463	13836	28462	6.85	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2118	15195	28155	1.18	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5197	18206	31080	1.05	8.0E-42	6879031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nadd1), mRNA
12376	25650		28	8.0E-42	AA493896.1	EST_HUMAN	hnt0702.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G494304 G494304
12394	25726		1.55	8.0E-42	AV088062.1	EST_HUMAN	367BP EXPRESSED SEQUENCE TAG mRNA
932	13986		1.49	7.0E-42	AL163285.2	NT	367004.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2502174 3' similar to contains OFR.L2
8814	21791		0.6	7.0E-42	R10963.1	EST_HUMAN	OFR repetitive element
9599	22603	36052	1.87	7.0E-42	A1204398.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
11508	24450	38000	3.47	7.0E-42	AA569592.1	EST_HUMAN	y85041.f1 Soares fetal liver spleen TNF.L3 Homo sapiens cDNA clone IMAGE:1287174 5'
11508	24450	38001	3.47	7.0E-42	AA569592.1	EST_HUMAN	y85041.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1873	14698	27855	3.35	6.0E-42	AF012872.1	NT	m23007.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:314652
1873	14698	27855	3.35	6.0E-42	AF012872.1	NT	m23007.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:314652
2297	15009		5.49	8.0E-42	AV238856.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 200 (p4K200) mRNA, complete cds
							Homo sapiens phosphatidylinositol 4-kinase 200 (p4K200) mRNA, complete cds
							362008.x1 NCL_CGAP_HNT10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.11 L1
							repetitive element

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5039	18052		1.48	6.0E-42	AI284770.1	EST_HUMAN	qu24h09.x1 NCL_GGAP_B12 Homo sapiens cDNA clone IMAGE:1665781 similar to contains Alu repetitive element
5043	18040	31580	1.8	6.0E-42	AB028690.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5943	18840	31580	1.37	6.0E-42	AB028690.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
6905	18840		5.89	6.0E-42	AJ271735.1	NT	Homo sapiens X4 pseudautosomal region, segment 1/2
138	13241		1.7	5.0E-42	BE217813.1	EST_HUMAN	h31611.x1 NCL_GGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176052 3'
438	13512	29443	4.65	5.0E-42	5730038	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
487	13560		1.37	5.0E-42	5730038	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
488	13561		1.07	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6844	19897	33191	1.07	5.0E-42	11433063	NT	Homo sapiens myobulatin related protein 3 (MTMR3), mRNA
6844	19897	33192	1.07	5.0E-42	11433063	NT	Homo sapiens myobulatin related protein 3 (MTMR3), mRNA
6871	20194	35522	2.81	5.0E-42	11417657	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7409	20376	33277	1.6	5.0E-42	AF071569.1	NT	Homo sapiens neelin (RELN) mRNA
8110	21047	34447	0.51	5.0E-42	4826977	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
9131	22097	35524	2.98	5.0E-42	AB037715.1	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10970	23890	37403	0.48	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10970	23890	37404	0.48	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
12087	24959	39555	3.28	5.0E-42	X98411.1	NT	H. sapiens mRNA for myosin-IE
12087	24959	39555	3.28	5.0E-42	X98411.1	NT	H. sapiens mRNA for myosin-IE
754	13813	28758	23.04	4.0E-42	AF050566.1	NT	Homo sapiens MHC class 1 region
754	13815	28759	23.04	4.0E-42	AF050566.1	NT	Homo sapiens MHC class 1 region
1067	14112	27062	2.03	4.0E-42	AF160011.1	NT	Homo sapiens fibronectin III (FN3) mRNA, complete cds
4223	17252	30139	1.24	4.0E-42	X69417.1	NT	H. sapiens PROS-27 mRNA
4255	17284	30168	1.12	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
4277	17206	30186	4.28	4.0E-42	4508498	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4613	17834	30525	10.99	4.0E-42	4508498	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5280	18295	31165	1	4.0E-42	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5290	18295	31165	1	4.0E-42	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10850	23700	37269	0.54	4.0E-42	AW371201.1	EST_HUMAN	CMO-BT0282-171 289-127-B03 BT0282 Homo sapiens cDNA
11010	23575	37469	1.88	4.0E-42	AW618930.1	EST_HUMAN	RC1-S10278-040400-018-H11 ST0278 Homo sapiens cDNA
11010	23876	37500	1.88	4.0E-42	AW618930.1	EST_HUMAN	RC1-S10278-040400-018-H11 ST0278 Homo sapiens cDNA
11741	24926	38205	2.89	4.0E-42	BF035327.1	EST_HUMAN	60145851F1 NIK_MGC_66 Homo sapiens cDNA clone IMAGE:3662066 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1479	14512	27498	4.08	2.0E-42	BF376834.1	EST_HUMAN	RCO-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2402	15409	28433	0.93	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKGC Homo sapiens cDNA clone GKCCBB08.5
2422	15429	28433	3.65	2.0E-42	AW698344.1	EST_HUMAN	RC3-NN0070-270400-041 LH0 NN0070 Homo sapiens cDNA
2432	15439	28436	3.27	2.0E-42	AW250589.1	EST_HUMAN	2819283.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283.3
5850	18840	32124	11.89	2.0E-42	AW655388.1	EST_HUMAN	EST367493 IMAGE sequences, MAGC Homo sapiens cDNA
5850	18840	32125	11.89	2.0E-42	AW655388.1	EST_HUMAN	EST367493 IMAGE sequences, MAGC Homo sapiens cDNA
6938	18894	32971	0.73	2.0E-42	AB29146.1	NT	Human hepatocyte growth factor (HGF) mRNA, complete cds
6918	18888	33283	0.77	2.0E-42	AD52586.1	EST_HUMAN	ow683d05.1 Soares_fetal_liver_spleen_1NF15_S1 Homo sapiens cDNA clone IMAGE:1653417.3
10201	23126	36612	1.17	2.0E-42	BE538918.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE3447620.5
10415	23337	36822	0.61	2.0E-42	P61649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
10415	23337	36823	0.61	2.0E-42	P61649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
10974	23884	37408	0.82	2.0E-42	AW634834.1	EST_HUMAN	RCO-L T0001-160200-032-d11 LT0001 Homo sapiens cDNA
12045	24919	38515	1.48	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
735	13785	26734	2.47	1.0E-42	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
1043	14080	27042	0.78	1.0E-42	AW268009.1	EST_HUMAN	UJ-H-B11-afn-e-04-O-U1at NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2721871.3
1103	14147	27087	1.27	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1103	14147	27088	1.27	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1247	15862	27248	12.89	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
1247	15862	27249	12.89	1.0E-42	AF087166.1	NT	encoding mitochondrial protein, complete cds
1711	14741	27725	2.08	1.0E-42	14423216	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
2046	15065	28085	1.05	1.0E-42	AF110266.1	NT	encoding mitochondrial protein, complete cds
2551	15553	28573	1.88	1.0E-42	5174458	NT	Homo sapiens PDIPE1 gene, exon 17
2975	16033	28956	10.93	1.0E-42	4505524	NT	Homo sapiens PDIPE1 gene, exon 17
3721	16784	28675	2.43	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3948	16888	29003	1.02	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4274	17303	30183	1.86	1.0E-42	AL163260.2	NT	Homo sapiens chromosome 21 segment HS21C060
4824	17645	30533	0.77	1.0E-42	AW13617.1	EST_HUMAN	RC3-ST0197-461089-012-603 ST0197 Homo sapiens cDNA
4776	17768	30688	2.44	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4776	17768	30689	2.44	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4813	17830	30728	5.31	1.0E-42	4506788	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
4897	18012	30859	0.78	1.0E-42	Z46120.1	EST_HUMAN	HSC0F071 normalized Infant brain cDNA Homo sapiens cDNA clone c-0707

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10446	23368	38959	4.15	9.0E-43	4757869	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
663	13719	28541	14	8.0E-43	AV756824.1	EST_HUMAN	AV756824 CB Homo sapiens cDNA clone CBLAKH08 5'
653	13719	28542	14	8.0E-43	AV756824.1	EST_HUMAN	AV756824 CB Homo sapiens cDNA clone CBLAKH08 5'
701	13763	28595	4.8	8.0E-43	8923278	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20287) mRNA
701	13763	28596	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20287) mRNA
701	13763	28597	4.8	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20287) mRNA
5783	18875	32057	0.78	8.0E-43	H13652.1	EST_HUMAN	Y08a11.11 Sources placenta N2bHP Homo sapiens cDNA clone IMAGE:148172 5'
3955	16698	28613	7.28	7.0E-43	AW246442.1	EST_HUMAN	2822251.Sprma NIH_MGC 7 Homo sapiens cDNA clone IMAGE:282251 5'
9121	22087		3.41	7.0E-43	AI1936748.1	EST_HUMAN	W989601.x1 NCJ CGAP Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
1347	14382		14.15	6.0E-43	AA461890.1	EST_HUMAN	OT15475 UNNAMED HERV-H PROTEIN contains LTR7.b1 LTR7 repetitive element ;
2598	15598		2.91	5.0E-43	AV708201.1	EST_HUMAN	ribosomal protein L30 (HUMAN);
6444	19509	32759	2.16	6.0E-43	8655973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
7093	20027	33331	1.91	6.0E-43	AW468387.1	EST_HUMAN	h30b04.x1 Sources NIH_MPU S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 MER1 repetitive element ;
10210	23135	39622	2.31	6.0E-43	AA195154.1	EST_HUMAN	G230641 DB1, COMPLETE CDS, xcoletins element P7R7 repetitive element ;
11437	24380		2.08	6.0E-43	AL119158.1	EST_HUMAN	DKFZP761L1712 J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761L1712 5'
144	13247		1.8	6.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
503	13576	28406	3.96	5.0E-43	AA392780.1	EST_HUMAN	EST195033 testis 1 Homo sapiens cDNA 5' end
2859	15919	28840	1.63	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANCO8 5'
6438	20021	33323	1.15	5.0E-43	AI613506.1	EST_HUMAN	W22607.x1 NCJ CGAP Bm62 Homo sapiens cDNA clone IMAGE:2260452 3'
7087	20021	33323	0.65	5.0E-43	AI613506.1	EST_HUMAN	W22607.x1 NCJ CGAP Bm62 Homo sapiens cDNA clone IMAGE:2260452 3'
8528	21496	34670	0.7	5.0E-43	AA442271.1	EST_HUMAN	z6f4603.x1 Sources testis NIH Homo sapiens cDNA clone IMAGE:757420 5'
8528	21496	34671	0.7	5.0E-43	AA442271.1	EST_HUMAN	z6f4603.x1 Sources testis NIH Homo sapiens cDNA clone IMAGE:757420 5'
9231	22167	34911	0.59	6.0E-43	H74277.1	EST_HUMAN	Y449312.1 Sources fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:229510 5'
9719	22747	36168	4.22	5.0E-43	AA465288.1	EST_HUMAN	aa33308.x1 NCJ CGAP GOB1 Homo sapiens cDNA clone IMAGE:815055 5'
10763	23884	37180	2.36	5.0E-43	AI733244.1	EST_HUMAN	065210.x5 NCJ CGAP Ldb Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P00591 P00591
10802	23729	37225	1.45	5.0E-43	AL049110.1	EST_HUMAN	PV14 GENE ;
11115	24075	37598	4.88	5.0E-43	AW693007.1	EST_HUMAN	DKFZP434D0119 J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434D0119
11795	23941	37463	3.46	5.0E-43	X15804.1	NT	MR2-SN0007290400-004-002 SN0007 Homo sapiens cDNA Human mRNA for alpha-actinin



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
974	18816	26979	3.95	4.0E-43	AF003928.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9331	18437	31189	1.18	4.0E-43	AI056338.1	EST_HUMAN	047703.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:1669013 3'
8505	19569	32821	0.76	4.0E-43	5956005	NT	Homo sapiens glycyl-tRNA synthetase (GARS), mRNA
7337	20308		1.94	4.0E-43	11418793	NT	Homo sapiens proteoglycan beta 6 (PCDH6), mRNA
8518	21486	34900	5.73	4.0E-43	AI244341.1	EST_HUMAN	q77602.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.03
8518	21486	34901	5.73	4.0E-43	AI244341.1	EST_HUMAN	q77602.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.03
10878	23600	37095	1.39	4.0E-43	6005897	NT	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
12306	25115		6.35	4.0E-43	R20950.1	EST_HUMAN	YD0605.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element;
1218	14256		3.85	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1704	14734	27716	1.63	3.0E-43	X97899.1	NT	H sapiens gene encoding La autoantigen
3586	19631	29549	1.32	3.0E-43	S69002.1	NT	AML1-EV1-1=AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4319	17348	30232	1.02	3.0E-43	AA548154.1	EST_HUMAN	nk55d08.x1 NCI CGAP_P77 Homo sapiens cDNA clone IMAGE:1017410
5003	18017	30904	0.98	3.0E-43	AB037885.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
5424	18527	31405	0.51	3.0E-43	IM68269.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 6
5424	18527	31406	0.51	3.0E-43	M59259.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 8
5698	19030	32777	0.9	3.0E-43	D34613.1	NT	Human TBXA31 gene for thromboxane synthase, promoter region and exon 1
8402	19557	32807	1.86	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
8462	19557	32808	1.86	3.0E-43	7305360	NT	Mus musculus obogelin (Obog), mRNA
8890	19942	33238	4.38	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8503	21471		8.69	3.0E-43	AA458824.1	EST_HUMAN	ea88f11.x1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:938413 3' similar to contains THR12 THR repetitive element;
9172	22138	35584	1.82	3.0E-43	7081721	NT	Homo sapiens hypobulbar protein (HSA011816), mRNA
10223	23148	36637	0.6	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbonyltransferase (H. sapiens) [LOC383848], mRNA
185	13285		8.29	2.0E-43	AI180784.1	EST_HUMAN	q661c09.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element;
6620	18878	32855	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;

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6620	10678	32956	0.95	2.0E-43	BE222778.1	EST_HUMAN	h135a08.x1 NCL CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
7491	20496	33814	1.07	2.0E-43	AW207380.1	EST_HUMAN	MER40 repetitive element 1
8651	21619		9.34	2.0E-43	UA3701.1	NT	U1H-B1-afn-09-Q-U1.s1 NCL CGAP_Sup3 Homo sapiens cDNA clone IMAGE:2721712 3'
11632	24473		2.08	2.0E-43	TG3007.1	EST_HUMAN	Human ribosomal protein L28a mRNA, complete cds
1657	14689	27694	4.13	1.0E-43	AF154838.1	NT	F8105 Fetal brain Stragelene Homo sapiens cDNA clone FB105 3' end similar to LINE-1
1657	14689	27695	4.13	1.0E-43	AF154838.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1717	14747	27733	2.13	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2734	15726	28742	5.67	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210084
5484	18584	31498	0.77	1.0E-43	4885544	NT	602022313F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157660 5'
6764	19818	33068	8.3	1.0E-43	4507168	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6764	19818	33069	6.3	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
7159	18391	31235	1.67	1.0E-43	R49751.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4) mRNA
8284	21233	34844	0.97	1.0E-43	AF175265.1	NT	Y64067.1 Scars Infant brain T1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
8401	21370		3.16	1.0E-43	AF175265.1	NT	SPBD38, MOUSE P28658 BRAIN PROTEIN DN38:
9189	22155	35584	30.83	1.0E-43	AF168490.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
10954	23576	37073	0.62	1.0E-43	AW963576.1	EST_HUMAN	Homo sapiens 6q22.1 region and MTG8 (CBFA211) gene, partial cds
11311	24281	37187	5.9	1.0E-43	AW963229.1	EST_HUMAN	EST375749 MAGE resequences, MAGEB Homo sapiens cDNA
11893	24559	38236	3.35	1.0E-43	AI984681.1	EST_HUMAN	w87101.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2484705 3'
12244	25074		2.8	1.0E-43	AL137864.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12542	25255	31808	2.24	1.0E-43	AI975416.1	EST_HUMAN	DKFZp781D1015.1 J1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781D1015 5'
12745	25394	31757	2.8	9.0E-44	11418322	NT	w89804.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2318775 3'
891	13946	26504	7.09	8.0E-44	AI222685.1	EST_HUMAN	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
891	13946	26505	7.09	8.0E-44	AI222685.1	EST_HUMAN	q123g01.x1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
891	13946	26506	7.09	8.0E-44	AI222685.1	EST_HUMAN	q123g01.x1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
891	13946	26507	7.09	8.0E-44	X04354.1	NT	H sapiens DNA for Cdc6 GMP-PDE gene
10702	23624	37120	0.47	9.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10702	23624	37120	0.47	9.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11495	24442	37993	3.83	8.0E-44	Y10495.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11895	24872	38469	2.24	8.0E-44	29139.1	NT	Homo sapiens myosin mRNA, partial cds
12495	25237	31801	2.95	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12536	25577	31698	1.53	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHF82122), mRNA
12970	25765	31516	2.69	8.0E-44	11418069	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13029	25977	31608	1.58	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHF82122), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
660	13728		0.87	7.0E-44	R09035.1	EST_HUMAN	ye89d01.11 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:124920 5'
2243	15297	28283	0.95	7.0E-44	5031898	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2877	16036	28957	2.88	7.0E-44	AF048728.1	NT	Homo sapiens minisatellite ms32 repeat region
2977	16036	28958	2.89	7.0E-44	AF048728.1	NT	Homo sapiens minisatellite ms32 repeat region
3876	18915	28924	2.35	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4270	17289	30177	1.07	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4270	17289	30178	1.07	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5168	18177	31055	1.04	7.0E-44	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8526	21494	34908	5.87	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y78AA1 Homo sapiens cDNA clone Y78AA1000498 3'
8223	19297	32631	0.65	6.0E-44	Z20046.1	EST_HUMAN	HSAAAD0YU P, Human foetal Brain Whole tissue Homo sapiens cDNA
12070	24943	38558	1.83	6.0E-44	AW954050.1	EST_HUMAN	EST366120 IMAGE resequences, MAGC Homo sapiens cDNA
303	13397		3.19	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
332	13421		2.89	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
8220	21199	34598	3.85	5.0E-44	AI598523.1	EST_HUMAN	tr-00002.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9730	22707		2.65	5.0E-44	AI124571.1	EST_HUMAN	OFR OFR repetitive element
9429	19473	28982	3.2	4.0E-44	AI163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5050	18062		1.02	4.0E-44	AI433225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7711	20688	34035	0.66	4.0E-44	BE893178.1	EST_HUMAN	BT102.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8614	21582	34698	0.64	4.0E-44	L21948.1	NT	BT1080501F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
9230	22198		0.49	4.0E-44	BE176918.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11669	24608	39095	8.23	4.0E-44	U93878.1	NT	RC3-HT0385-01040-023-038 HT0385 Homo sapiens cDNA
1801	14829		0.95	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
2537	19539	28562	0.95	3.0E-44	BE68026.1	EST_HUMAN	Homo sapiens karyophilin alpha 6 (importin alpha 7) (KPNA6) mRNA
3114	16171	22081	6.12	3.0E-44	AA169851.1	EST_HUMAN	BT1491520FT NIH_MGC_69 Homo sapiens cDNA clone IMAGE:38363839 5'
3005	16948	28859	1.71	3.0E-44	AA337234.1	EST_HUMAN	z018805.11 Stridagene fetal retina 537202 Homo sapiens cDNA clone IMAGE:609777 5'
8074	21011	34410	0.55	3.0E-44	BE894820.1	EST_HUMAN	EST42298 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
6977	22830	36284	0.68	3.0E-44	AF005273.1	NT	60151054FF1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1051	14097	27047	1.04	2.0E-44	4826685	NT	Sus scrofa domestica submaxillary apocynin mRNA, complete cds
1051	14097	27048	1.04	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1212	14250		2.62	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1212	14250		2.62	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMAP21), mRNA
1315	14350	27318	5.49	2.0E-44	AF133398.1	NT	Homo sapiens transmembrane trafficking protein (TMAP21), mRNA
1315	14350		5.49	2.0E-44	AF133398.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds

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Table 4

### Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1370	14404	27374	1.05	2.0E-44	BE465325.1	EST HUMAN	hm1T4g05.xt NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW OXYB_HUMAN
2161	15177	28198	2.67	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN .
2818	16516		2.01	2.0E-44	S801833.NT	NT	Homo sapiens foetus-type bone marrow zinc finger protein 4 mRNA, complete cds
3484	16530	28455	1.16	2.0E-44	D87675.1	EST	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (GLAPS4), mRNA
4600	17621	30514	1.8	2.0E-44	AW864376.1	EST HUMAN	Homo sapiens vesicle transport-related protein (KIAA05917), mRNA
6214	19288	33521	1.59	2.0E-44	11448901.NT	EST	PMA-SN0016-120500-009-a04 SN0016 Homo sapiens cDNA
							Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7037	18369	31286	1.73	2.0E-44	AF036908.1	NT	Homo sapiens general transcription factor 21 (GTF2D) mRNA, alternatively spliced product, complete cds
7845	20065	33970	3.8	2.0E-44	11418226.NT	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7845	20065	33971	3.8	2.0E-44	11419226.NT	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8771	21738	35158	0.72	2.0E-44	7708370.NT	NT	Homo sapiens vesicle transport-related protein (KIAA05917), mRNA
8771	21738	35159	0.72	2.0E-44	7708370.NT	NT	Homo sapiens vesicle transport-related protein (KIAA05917), mRNA
8966	21892	35357	1.83	2.0E-44	BE388058.1	EST HUMAN	B01-288914P1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:3613568 5'
							TCSBP1-E2765 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project/TCSA Homo sapiens cDNA clone TCSBP1-2766
12152	25010		1.44	2.0E-44	BE244902.1	EST HUMAN	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12698	25869		1.32	2.0E-44	4826983.NT	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
13047	26397		1.58	2.0E-44	11628283.NT	NT	Homo sapiens Micalten/NIK-related kinase (MNK), mRNA
547	13174	26084	7.76	1.0E-44	7957334.NT	NT	Homo sapiens Missshaper/NIK-related kinase (MNK), mRNA
54	13174	26085	7.76	1.0E-44	7957334.NT	NT	Homo sapiens Missshaper/NIK-related kinase (MNK), mRNA
562	13650	26564	1.85	1.0E-44	AW853132.1	EST HUMAN	RC1-CIT0249-030300-028-H12 CIT0249 Homo sapiens cDNA
1202	14241		1.85	1.0E-44	AV1694003.1	EST HUMAN	RC1-BN0039-110300-012-B01 BN0039 Homo sapiens cDNA
1677	14910		7.03	1.0E-44	AL169303.2	NT	Homo sapiens chromosome 21 segment HS21 C103
							zw53402.1 Soares, total, fetus, NB2HFB, Bw Homo sapiens cDNA clone IMAGE:773703 5' similar to contains THR 13 THR repetitive element;
2233	15247	28270	4.49	1.0E-44	AA43454.1	EST HUMAN	zw53402.1 Soares, total, fetus, NB2HFB, Bw Homo sapiens cDNA clone IMAGE:773703 5' similar to contains THR 13 THR repetitive element;
2233	15247	28271	4.49	1.0E-44	AA43454.1	EST HUMAN	contains THR 13 THR repetitive element;
2290	15889	28327	0.95	1.0E-44	AA439066.1	EST HUMAN	2889711.1 Soares, testis, testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
							Homo sapiens transcription factor IQHM enhancer 3, JM11 protein, JM4 protein, JM6 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds; and L-type calcium channel alpha 2
2770	15702	28768	2.5	1.0E-44	AF198779.1	NT	aad1c08.e1 Soares, NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
3798	18780		3.01	1.0E-44	AA458066.1	EST HUMAN	Homo sapiens alpha satellite DNA, MT monomer type
6156	18165	31043	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, MT monomer type
6156	18165	31044	0.64	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, MT monomer type

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8603	21576	34991	1.17	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequenced, MAGJ Homo sapiens cDNA
8608	21578	34992	1.17	1.0E-44	AW967073.1	EST_HUMAN	EST379147 MAGE resequenced, MAGJ Homo sapiens cDNA
8680	21859	35385	1.29	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS210309
9381	22348	35778	0.99	1.0E-44	A037183.1	EST_HUMAN	ga89.07.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2009628 3'
11354	24304		12.74	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBT503 5'
11658	24740	35325	3.23	1.0E-44	10092664	NT	Homo sapiens Sushi domain (SOR repeat) containing (BK65A6.2), mRNA
11917	24798	35388	2.7	1.0E-44	AW849567.1	EST_HUMAN	RG1-CT0195-150569-011-C08 CT0198 Homo sapiens cDNA
11917	24798	35388	2.7	1.0E-44	AW849567.1	EST_HUMAN	RG1-CT0195-150569-011-C08 CT0198 Homo sapiens cDNA
4609	17690	30522	1.16	8.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4609	17690	30522	1.16	8.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6806	19890	33147	1.52	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0965 protein, partial cds
2528	16532	28563	1.57	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5119	16129	31005	8.65	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8444	21473	34627	0.85	8.0E-45	AA377985.1	EST_HUMAN	EST00853 Synovial sarcoma Homo sapiens cDNA 5' end
2669	16027		0.96	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
1556	14588		1	8.0E-45	AG75425.1	EST_HUMAN	w696c05.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.t1 L1 repetitive element;
4003	17042		3.46	8.0E-45	AW157570.1	EST_HUMAN	aw8307.x1 Schneider field brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to
12836	28548		1.83	6.0E-45	11418213	NT	SW-R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
893	13948		1.56	5.0E-45	AL163203.2	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
2018	16036	28050	4.86	5.0E-45	BF333627.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210303
						EST_HUMAN	CHM-CN0044-180200-515-01 CN0044 Homo sapiens cDNA
						EST_HUMAN	ga8467.x1 NCI CGAP_CLI1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
3223	16278	29203	1.49	5.0E-45	AI523768.1	EST_HUMAN	P00084 PAIRED BOX PROTEIN PAX-1 ;
						EST_HUMAN	272803.at Soares_testis_JNHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element
5590	16696	31654	8.41	5.0E-45	AA3397781.1	EST_HUMAN	TAR1 repetitive element ;
6135	19212	32439	1.46	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6135	19212	32440	1.48	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6163	19258	32491	0.84	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6163	19258	32492	0.84	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
8133	19384	32625	1.07	5.0E-45	11489288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8513	19394	32626	1.07	5.0E-45	11489288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8619	21587	35003	0.66	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9398	22351	35792	1.29	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12003	24880	38476	2.3	5.0E-45	8923698	NT	Homo sapiens golin-like protein (GLP), mRNA
1146	14188	27139	10.78	4.0E-45	X93828.1	NT	H. sapiens ART14 gene
2289	18311	28331	1.91	4.0E-45	BE285622.1	EST_HUMAN	80119440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
4836	17598	30446	0.72	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
9308	22273					EST_HUMAN	nc26907.s1 NCL_OGAP_P11 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element;
12167	26904	31416	1.4	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
4115	16393	32878	0.99	3.0E-45	171480.1	EST_HUMAN	343507.r1 Scarsa fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6394	19433	32878	1.13	3.0E-45	8756851	NT	Mus musculus dynein, axon, heavy chain 11 (Dhact1), mRNA
6394	19433	32877	1.13	3.0E-45	8753951	NT	Mus musculus dynein, axon, heavy chain 11 (Dhact1), mRNA
8704	21761		1.63	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8143	22109	35535	3.82	3.0E-45	4768461	NT	Homo sapiens golgi autoantigen, polgin subfamily a, 2 (GOLGA2) mRNA
10670	23592	37087	10.98	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12654	25898		4.13	3.0E-45	X89211.1	NT	Homo sapiens DNA for endogenous retroviral like element
2511	18514		1.96	2.0E-45	AL163216.2	NT	Homo sapiens chromosome 21 segment HS21C018
3045	18102	29016	1.8	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6871	19728	33004	6.17	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7898	20812	34189	1.25	2.0E-45	BE762184.1	EST_HUMAN	80148778F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870838 5'
8768	21725	35148	1.08	2.0E-45	AV1634634.1	EST_HUMAN	RCQ-LT0001-150200-032-411 LT0001 Homo sapiens cDNA
11154	28704	37639	25.96	2.0E-45	BE3834350.1	EST_HUMAN	MF0-HT0023-109800-201-a02 HT0523 Homo sapiens cDNA
11611	24462	38002	3.5	2.0E-45	AA48970.1	EST_HUMAN	aa8712.r1 Streptococcus felis 937202 Homo sapiens cDNA clone IMAGE:835319 5' similar to
11832	24715	38289	1.87	2.0E-45	AW270260.1	EST_HUMAN	TR-G1144559 G1744689 R-SLY1.1
11832	24715	38300	1.67	2.0E-45	AW270260.1	EST_HUMAN	xp72a03.x1 NCL_OGAP_Oy40 Homo sapiens cDNA clone IMAGE:2746868 3'
12999	25655		3.46	2.0E-45	11418157	NT	xp72a03.x1 NCL_OGAP_Oy40 Homo sapiens cDNA clone IMAGE:2746868 3'
124	13462		1.84	2.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
409	13462		2.09	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
473	13545	28474	1.93	1.0E-45	4506412	NT	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
1178	14218	27175	1.94	1.0E-45	7657260	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3120	16177	25088	7.12	1.0E-45	U32169.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGRIN), mRNA
3303	16560	29477	0.84	1.0E-45	8858558	NT	Human pro-alpha2 chain of collagen type XI (COL11A2) gene, complete cds
4503	17526	30413	4.06	1.0E-45	BE386633.1	EST_HUMAN	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
			0.84	1.0E-45	BE386633.1	EST_HUMAN	601289110F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3816903 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4757	17777		1.01	1.0E-45	H57443.1	EST_HUMAN	y05802.1 Soares fetal liver spleen TNF $\alpha$ Homo sapiens cDNA clone IMAGE:204393 5'
8365	21334	34746	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8365	21334	34746	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8365	21334	34746	0.57	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8954	21920	35346	0.85	1.0E-45	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9476	22440	35580	4.82	1.0E-45	BE887843.1	EST_HUMAN	601811228F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9680	22633	36287	1.03	1.0E-45	AB002207.1	NT	Human mRNA for KIAA0289 gene, partial cds
12369	25165	31856	9.31	1.0E-45	11418098	NT	Homo sapiens protein kinase C, alpha binding protein (PRK-CABP), mRNA
12551	25274		9.31	1.0E-45	11528291	NT	Homo sapiens hypophthalmin protein FLJ20454 (FLJ20454), mRNA
12556	25277		6.48	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RAN-GAP1), mRNA
12962	25532	31715	3.98	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
8570	21638	34959	1.68	9.0E-46	5910293	NT	Mus musculus keratin complex 2, gene 5g (Krt2-5g), mRNA
8831	21947		7.02	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10845	23765	37264	9.09	9.0E-46	AW246994.1	EST_HUMAN	2822449.Sprimo NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2448	15453	28474	11.23	8.0E-46	AI433281.1	EST_HUMAN	132108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132169 3' similar to gb:J00314_jna2
2448	15453	28475	11.23	8.0E-46	AI433281.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8369	21358		6.79	8.0E-46	BE107244.1	EST_HUMAN	132108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132169 3' similar to gb:J00314_jna2
2248	15262	28239	1.17	7.0E-46	U46007.1	NT	TUBULIN BETA-1 CHAIN (HUMAN);
4811	17632		3.58	7.0E-46	BE386166.1	EST_HUMAN	RC5-HT10605-280200-012-C12 HT05008 Homo sapiens cDNA
4845	17662		1.14	7.0E-46	BE064386.1	EST_HUMAN	Rattus norvegicus espin mRNA, complete cds
6160	19235	32496	3.92	7.0E-46	8922708	NT	601277729F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
6842	19700	32976	1.95	7.0E-46	BF105945.1	EST_HUMAN	RC4-BT0310-110300-016-F10 BT0310 Homo sapiens cDNA
2765	15757	28778	5.63	6.0E-46	AI884381.1	EST_HUMAN	Homo sapiens hypophthalmin protein FLJ10847 (FLJ10847), mRNA
2765	15757	28779	5.63	6.0E-46	AI884381.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042739 5'
6252	16025	32556	10.15	8.0E-46	AI835448.1	EST_HUMAN	wm3108.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER18.12
7426	20363	33743	0.76	6.0E-46	AW513244.1	EST_HUMAN	MER18 repetitive element;
7609	20570	33933	0.51	6.0E-46	BF509740.1	EST_HUMAN	U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER18.12
225	13305		6.47	5.0E-46	AL163210.2	NT	U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER18.12
3639	16866	29508	1.01	5.0E-46	BE577194.1	EST_HUMAN	U44 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER18.12

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## Single Exon Probes Expressed in Bone Marrow

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3539	16886	29500	1.01	5.0E-46	BE677194.1	EST_HUMAN	768107.x1 Lupskl_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6899	19951	33248	1.84	5.0E-46	BF590442.1	EST_HUMAN	nae38007.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR-O75202
7128	20104	33415	3.97	5.0E-46	BF347229.1	EST_HUMAN	OT5202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
7302	20273	33609	0.67	5.0E-46	AW682283.1	EST_HUMAN	602021164F1 NCI CGAP_Bmr? Homo sapiens cDNA clone IMAGE:4156670 5'
7614	20574	33938	0.59	5.0E-46	BE549744.1	EST_HUMAN	QV4-ST0212-120100-076-109 ST0212 Homo sapiens cDNA
642	13708		2.88	4.0E-46	AA601143.1	EST_HUMAN	na54e09.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:3230481 3'
							na54e09.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104320 3' similar to gb-X63741_nae1
							FIBULIN-1, ISOFORM A, PRECURSOR (HUMAN);
1715	14746	27729	7.61	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3006836 3' similar to gb-X14009_nae1
							LYSOZYME C PRECURSOR (HUMAN) contains element MER37 repetitive element ;
1716	14746	27730	7.91	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3006836 3' similar to gb-X14009_nae1
2749	15742	28759	3.26	4.0E-46	M16048.1	NT	LYSOZYME C PRECURSOR (HUMAN) contains element MER37 repetitive element ;
4447	17473	30361	0.95	4.0E-46	AB014822.1	NT	Human endogenous retrovirus RTVL-H2
4447	17473	30362	0.95	4.0E-46	AB014822.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5194	19203	31076	0.78	4.0E-46	BE044260.1	EST_HUMAN	Homo sapiens mRNA for KIAA0622 protein, partial cds
5194	19203	31077	0.78	4.0E-46	BE044260.1	EST_HUMAN	h042a07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5511	18611	31542	2.11	4.0E-46	M36852.1	NT	h042a07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5511	18611	31543	2.11	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12792	25422	31737	2.91	4.0E-46	AB02059.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
4421	17448	30336	1.21	3.0E-46	4506378	NT	Homo sapiens DNA for Human P2XM, complete cds
4809	17826	30722	2.84	3.0E-46	Z73960.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4809	17828	30723	2.84	3.0E-46	Z73960.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
9102	22068	35494	10	3.0E-46	AI831462.1	EST_HUMAN	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Lambda; VLambda
9358	22323	35750	0.59	3.0E-46	U08950.1	NT	THR repetitive element ;
9358	22323	35751	0.59	3.0E-46	U08950.1	NT	Human AD amyloid mRNA, complete cds
11898	24779	38365	2.01	3.0E-46	D31765.1	NT	Human AD amyloid mRNA, complete cds
							Human mRNA for KIAA0081 gene, partial cds
							nae0609.s1 NCI CGAP_Go3 Homo sapiens cDNA clone IMAGE:860408 3' similar to contains THR.b2 THR
839	13985	26850	10.84	2.0E-46	AA468848.1	EST_HUMAN	repetitive element ;



Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1584	14597		2.13	2.0E-46	AA678246.1	EST_HUMAN	227211.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431609 3'
1647	14676	27652	4.43	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
6010	18024	30410	1.06	2.0E-46	AA399288.1	EST_HUMAN	256602.1 Soares_fetal_NHT Homo sapiens cDNA clone IMAGE:3849297 5'
7726	20582	34046	7.69	2.0E-46	8910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA
8404	21373		1.18	2.0E-46	BE889151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
11576	24514		1.82	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145032), mRNA
12857	25741	31619	3.22	2.0E-46	AW27214.1	EST_HUMAN	xt78103.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2769789 3'
1237	14273	27233	6.69	1.0E-46	4502864	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2286	15302	28328	3.26	1.0E-46	AW878518.1	EST_HUMAN	EST390625 MAGe resequences, MAGe Homo sapiens cDNA
2408	15416	28440	2.9	1.0E-46	H87330.1	EST_HUMAN	EST48065 WATM1 Homo sapiens cDNA clone 48b095
3262	18318	28238	1.32	1.0E-46	AA631912.1	EST_HUMAN	nt78b02.x1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132385 similar to gb:X76717 H.sapiens
4908	17925		2.93	1.0E-46	AB023197.1	NT	MT-11 mRNA (HUMAN).
5784	18876	32058	7.08	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6089	25653	32352	5.57	1.0E-46	8923762	NT	7692601.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6099	25653	32383	5.57	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6766	19820	33102	0.65	1.0E-46	BF199247.1	EST_HUMAN	744607.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3657852 3' similar to contains element
11211	18876	32058	3.61	1.0E-46	BF194707.1	EST_HUMAN	MER22 repetitive element ;
12322	25124	31845	1.52	1.0E-46	BE531102.1	EST_HUMAN	7692601.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12322	25124	31848	1.52	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215398 5'
13066	25600		4.54	1.0E-46	AV718377.1	EST_HUMAN	602072284F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4215398 5'
767	13826		3.24	9.0E-47	AJ271735.1	NT	AV718377 DCB Homo sapiens cDNA clone DCBAIE03 5'
4686	17993	30873	3.91	9.0E-47	AW770928.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 112
6513	19577	32832	1.98	9.0E-47	11425439	NT	h93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009634 3' similar to TR:O75703
12816	25643	31432	2.25	9.0E-47	11417868	NT	HYPOPHETICAL 12.4 KD PROTEIN ;
1825	14852	27846	47.72	8.0E-47	Y18536.1	NT	Homo sapiens zinc finger protein ZNF266 (ZNF266), mRNA
1825	14852	27847	47.72	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA
2728	15722	28739	1.77	8.0E-47	5453955	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3036	16094	29012	2.12	8.0E-47	AJ220043.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
							Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3640	16683	29598	0.78	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
3640	16683	29599	0.78	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GSK family kinase MINK-2, complete cds
5284	18282	31131	0.65	8.0E-47	7682421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
2555	15557	28575	2.2	5.0E-47	AL163246.2	NT	Homo sapiens chromosome 21, segment HS21C046
6040	22008	35427	0.49	6.0E-47	U77054.1	EST_HUMAN	HS217054 Human Homo sapiens cDNA clone NT
6831	22575	39025	6.5	6.0E-47	AI695189.1	EST_HUMAN	ts98102.x1 NCI CGAP Kd11 Homo sapiens cDNA clone IMAGE:228669 3'
10070	22697	39465	0.86	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
10070	22697	39466	0.88	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6729	19765	33064	6.58	5.0E-47	11423972	NT	Homo sapiens CDG37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11147	24107		4.6	5.0E-47	M78590.1	EST_HUMAN	EST100738 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HBC087
1400	14433	27403	4.48	4.0E-47	4557656	NT	Homo sapiens ETA binding protein p300 (EP300) mRNA
7008	20132	33447	0.98	4.0E-47	BE938956.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8825	21792	35214	2.45	4.0E-47	BE516483.1	EST_HUMAN	601280466F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3822437 5'
8825	21792	35215	2.45	4.0E-47	BE516483.1	EST_HUMAN	601280466F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3822437 5'
8895	21931	35356	0.81	4.0E-47	AW893777.1	EST_HUMAN	RC3-BN0034-220300-075-025 BN0034 Homo sapiens cDNA
11954	24833		5.51	4.0E-47	AW515509.1	EST_HUMAN	xx69607.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
546	13617	29598	1.73	3.0E-47	BE07684.1	EST_HUMAN	Q64282 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]:
546	13617	29599	1.73	3.0E-47	BE07684.1	EST_HUMAN	601497659F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3869721 5'
819	13877	28826	6.7	3.0E-47	N57483.1	EST_HUMAN	601497659F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3869721 5'
844	13967	28948	7.86	3.0E-47	AL163284.2	NT	W54604.s1 Soares, multiple sclerosis, 2NBMSP Homo sapiens cDNA clone IMAGE:277327 3'
3315	10368	29288	0.7	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21, segment HS21C084
3900	17030		6.21	3.0E-47	U83181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4969	17417	30301	0.98	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SDF) mRNA, partial cds
6128	19206	32429	4.78	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6128	19206	32430	4.78	3.0E-47	AW408800.1	EST_HUMAN	UJ-HF-BM0-adv-d-07-Q-J1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6716	19772		1.72	3.0E-47	AJ222413.1	EST_HUMAN	UJ-HF-BM0-adv-d-07-Q-J1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7608	20569	33932	0.59	3.0E-47	AI819755.1	EST_HUMAN	q04097.x1 Soares, NFL, T, C8G, S1 Homo sapiens cDNA clone IMAGE:1843716 3'
9185	22151	35570	0.59	3.0E-47	AW63798.1	EST_HUMAN	w11h08.x1 NCI CGAP Kd12 Homo sapiens cDNA clone IMAGE:2402559 3'
9185	22151	35580	0.59	3.0E-47	AW63798.1	EST_HUMAN	w11h08.x1 NCI CGAP Kd12 Homo sapiens cDNA clone IMAGE:2402559 3'
9185	22151	35580	0.59	3.0E-47	AW63798.1	EST_HUMAN	EST1375669 MAGE resequences, MAGEH Homo sapiens cDNA
969	14021	29673	2.24	2.0E-47	AL163209.2	NT	EST1375669 MAGE resequences, MAGEH Homo sapiens cDNA
969	14021	29674	2.24	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
969	14021	29674	2.24	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

Table 4  
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1570	14603		1.08	2.0E-47	AI969278.1	EST_HUMAN	wg5b502.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2479851 3'
1597	14620	27604	2.2	2.0E-47	7662109	EST	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1687	14716	27698	3.87	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.g1 NC1 CGAP_C03 Homo sapiens cDNA clone IMAGE:337607 3'
4374	17402	30282	1.82	2.0E-47	4504586	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4411	17459	30327	1.48	2.0E-47	AA595922.1	EST_HUMAN	nt23g07.g1 NC1 CGAP_P11 Homo sapiens cDNA clone IMAGE:314852
4411	17459	30328	1.48	2.0E-47	AA595922.1	EST_HUMAN	nt23g07.g1 NC1 CGAP_P11 Homo sapiens cDNA clone IMAGE:314852
4534	17557	30445	1.68	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4850	17897	30760	1.22	2.0E-47	AV985168.1	EST_HUMAN	EST1377239 IMAGE resequences, MAGI Homo sapiens cDNA
5187	18198		0.7	2.0E-47	A041128.1	EST_HUMAN	o61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5880	18989	32160	1.22	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6088	19188	32380	1.29	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6088	19188	32381	1.29	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7864	25692		1.43	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8297	21288	34677	1.76	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9297	21269	34678	1.76	2.0E-47	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9068	22034	35437	1.75	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9845	22781	36235	0.76	2.0E-47	11528138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11800	23955	37478	2.31	2.0E-47	M76126.1	NT	Human tyrosine kinase receptor (cd) mRNA, complete cds
12358	25886	31415	2.12	2.0E-47	R42423.1	EST_HUMAN	y92a06.x1 Soares_infant brain 1N19 Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFR repetitive element;
1404	14437	27466	6.91	1.0E-47	A1333420.1	EST_HUMAN	qp55h03.x1 Soares_fetal lung_NEHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3835	18875	29776	1.18	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3835	18875	29777	1.18	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
6112	18122	30697	2.55	1.0E-47	AW813908.1	EST_HUMAN	RC3-ST0187-130400-017-102 ST0197 Homo sapiens cDNA
7244	18879	33276	6.6	1.0E-47	AI880688.1	EST_HUMAN	at19a06.x1 Barelhead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
9220	22168		0.77	1.0E-47	AW064648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10721	23643	37136	2.41	1.0E-47	L30115.1	NT	h18a41.1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26328
1816	14648	27623	3.85	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3568	18614	28558	0.7	9.0E-48	BF355947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5763	18855	32036	0.84	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calicium channel alpha1E subunit (CAONAT1E) gene, exons 7-49, and partial cds, alternatively spliced
5763	18855	32036	0.84	9.0E-48	BE888196.1	EST_HUMAN	CM2.MTO100-310700-260-105 MTO100 Homo sapiens cDNA
						EST_HUMAN	60161714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
						EST_HUMAN	60161714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6220	19294	32528	0.6	9.0E-48	AI833168.1	EST_HUMAN	at5h09.x1 Barsstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377899 3' similar to TR-O60844
6351	19420	32681	0.73	9.0E-48	AU123240.1	EST_HUMAN	O60844 HOMOLOG OF RAT ZMOOGEN GRANULE MEMBRANE PROTEIN. ;
11452	24395	37640	2.49	9.0E-48	BE393813.1	EST_HUMAN	AUT23240 NT2RMT Homo sapiens cDNA clone NT2RMT000978 5'
1255	14291		1.5	8.0E-48	4501900.NT	EST_HUMAN	601310479F1 NIH_JMG_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1256	14291		1.54	8.0E-48	4501900.NT	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3152	16209	29123	3.31	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3152	16209	29124	3.31	8.0E-48	AW768477.1	EST_HUMAN	h1671b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb-X64707
491	13684		1.84	7.0E-48	AB033036.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
492	13564		22.61	7.0E-48	AB033035.1	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
1496	14529	27501	1.04	7.0E-48	6912719.NT	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1643	14675	27648	4.5	7.0E-48	6730039.NT	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA
6707	19763	33042	24.74	7.0E-48	11416831.NT	EST_HUMAN	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3812	16657	29575	1.2	6.0E-48	AI761111.1	EST_HUMAN	w169R03.x1 NCL CGAP_Ki672 Homo sapiens cDNA clone IMAGE:2398573 3'
6176	19251	32484	1.12	6.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE7/5, complete cds
6953	20177	33502	0.69	6.0E-48	11420965.NT	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7702	25687	34022	0.56	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
7702	25687	34023	0.56	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
9479	22443	36885	1.94	6.0E-48	AF026816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9896	22852	36311	1.78	6.0E-48	11427428.NT	NT	Homo sapiens hypothetical protein FLJ11009 (FLJ11009), mRNA
10047	22974	36441	3.3	6.0E-48	AA180080.1	EST_HUMAN	z645006.s1 Strategene hNT neuron (z637233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element.
3320	18313	28292	1.58	6.0E-48	4628691.NT	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A), mRNA
8921	21897	35314	1.11	5.0E-48	BE084410.1	EST_HUMAN	RC4-B103T11-141199-071-108 BT0311 Homo sapiens cDNA
11305	24256	37782	2.83	6.0E-48	AI620420.1	EST_HUMAN	tu47a02.x1 NCL CGAP_Px28 Homo sapiens cDNA clone IMAGE:2254754 3'
1385	14419	27398	1.33	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKG Homo sapiens cDNA clone GIKORE12 5'
1993	15014	28020	18.21	3.0E-48	4885170.NT	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6), mRNA
1993	15014	28021	18.21	3.0E-48	4885170.NT	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6), mRNA
3429	16477	29396	0.93	3.0E-48	AF172453.1	NT	Homo sapiens opiod growth factor receptor mRNA, complete cds
3647	16690	26806	0.75	3.0E-48	AW664531.1	EST_HUMAN	h1145712.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872256 3' similar to SW:DCRB_HUMAN
4275	17304		0.9	3.0E-48	AA008541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
							z04g03.11 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5697	18081	32278	2.41	3.0E-48	BE084571.1	EST_HUMAN	MR2-BT0657-060400-201-s10 BT0657 Homo sapiens cDNA
7215	20237	33571	1.06	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-F-147D
8734	21702		4.11	3.0E-48	AA69930.1	EST_HUMAN	PTF3 repetitive element;
11221	24174	37700	6.89	3.0E-48	BF514170.1	EST_HUMAN	UHR-BW1-anti-10Q-U1st1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
5	13126	26025	2.4	2.0E-48	AA46507.1	EST_HUMAN	Z680c3.1 Scores ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:810052 5'
47	13167	26072	1.23	2.0E-48	AA631940.1	EST_HUMAN	frn167 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-23
1223	14261		0.65	2.0E-48	H24278.1	EST_HUMAN	ym5610.r1 Scores infant brain IN1B Homo sapiens cDNA clone IMAGE:82182 5' similar to SP-M8B_MOUSE P35803 MEMBRANE GLYCOPROTEIN;
4562	17585	30477	0.82	2.0E-48	BE246055.1	EST_HUMAN	TCBAP-1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-T C8A Homo sapiens cDNA clone TCBAP3842
5912	18998	32188	0.63	2.0E-48	AA613171.1	EST_HUMAN	ncf18g01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
5912	18998	32189	0.63	2.0E-48	AA613171.1	EST_HUMAN	ncf18g01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
7762	20715	34086	3.9	2.0E-48	AB040634.1	NT	Homo sapiens mRNA for KIAA11601 protein, partial cds
7762	20715	34087	3.9	2.0E-48	AB040634.1	NT	Homo sapiens mRNA for KIAA11601 protein, partial cds
7777	20730	34103	3.52	2.0E-48	11498238	NT	Homo sapiens v-rel avian reticulocytodifferentiation viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8698	21699	35089	1.37	2.0E-48	AV743451	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBGCGG10 5'
12318	13126	26025	3.8	2.0E-48	AA46507.1	EST_HUMAN	Z680c3.1 Scores ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:810052 5'
58	13177	26039	3.37	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
874	13930	26888	1.61	1.0E-48	452168	NT	Homo sapiens amyloid beta (A4) precursor protein (protein nepril-in, Alzheimer disease) (APP), mRNA
1077	14122	27073	1.8	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
1077	14122	27074	1.8	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
1299	14335	27288	5.09	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1933	14957	27854	14.5	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3590	16547	29473	0.93	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C049
6420	19487	32736	1.17	1.0E-48	A1898077.1	EST_HUMAN	td7601.x1 NCI CGAP_C616 Homo sapiens cDNA clone IMAGE:2075804 3' similar to TR-O14588 O14588 SIMILARITY TO U73941;
6420	19487	32737	1.17	1.0E-48	A1898077.1	EST_HUMAN	td7601.x1 NCI CGAP_C616 Homo sapiens cDNA clone IMAGE:2075804 3' similar to TR-O14588 O14588 SIMILARITY TO U73941;
6848	19708		1.03	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6748	19802	33082	0.7	1.0E-48	AB028694.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6748	19802	33083	0.7	1.0E-48	AB028694.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7471	20437	33764	3.15	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9183	22149	35578	0.49	1.0E-48	4758665	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9183	22149	35577	0.49	1.0E-48	4758665	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9589	22530	35980	1.19	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9523	22587	36017	7.13	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9824	22808	36280	0.69	1.0E-48	BE188410.1	EST_HUMAN	QV3-HT0613-060400-147-401 HT0513 Homo sapiens cDNA
9841	22868	36330	4.48	1.0E-48	BF304883.1	EST_HUMAN	601880306F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10736	23658	37151	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10738	23658	37152	3.85	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
12260	25630		1.63	1.0E-48	W26785.1	EST_HUMAN	1566 Human retina cDNA, randomly primed sublibrary Homo sapiens cDNA
6171	19248	32478	3	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6171	19248	32479	3	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
7017	20143	33450	0.57	8.0E-49	AA842035.1	EST_HUMAN	ns181633.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184021 5'
8635	21605	35029	3.32	8.0E-49	U23850.1	NT	Human insulin 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10348	23272	36748	2.1	8.0E-49	AB009881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
11204	24158	37688	2.32	8.0E-49	AI623722.1	EST_HUMAN	ts33d12.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element/contains element PTR5 repetitive element.
140	13468	26398	2.24	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mRNA
140	13468	26399	2.24	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mRNA
393	13468	26398	1.53	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mRNA
393	13468	26399	1.53	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mRNA
394	13468	26398	2.06	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mRNA
394	13468	26399	2.06	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPass, 4 (PSMC4) mRNA
1225	14263	27220	2.85	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21084
5535	18632	31571	1.57	7.0E-49	AI807191.1	EST_HUMAN	w25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358663 3' similar to TR:O54923
5545	18642	31582	1.33	7.0E-49	AL120637.1	EST_HUMAN	DKFZp762C033.s1 762 (synonym: hnc2) Homo sapiens cDNA clone DKFZp762C033 3'
5903	18632	31571	0.84	7.0E-49	AI807191.1	EST_HUMAN	w25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358663 3' similar to TR:O54923
188	13299	26227	86.86	6.0E-49	AW791740.1	EST_HUMAN	h65f05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17206.40S
4142	17173	30062	1.14	6.0E-49	AL182091.1	EST_HUMAN	O54923 RSEC15. ;
6582	18642	32906	0.85	6.0E-49	AJ140742.1	EST_HUMAN	h65f05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE); DKFZp761A193.s1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A193 3' AJ140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'

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11609	24547	38107	2	6.0E-49	AW452218.1	EST_HUMAN	UHH-B13-alc-a-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11972	24850	38446	4.09	6.0E-49	AA369556.1	EST_HUMAN	EST177625 Pancreas tumor III Homo sapiens cDNA 5' end
11972	24850	38447	4.09	6.0E-49	AA369556.1	EST_HUMAN	EST177625 Pancreas tumor III Homo sapiens cDNA 5' end
12645	25723	1.7	6.0E-49	AA707567.1	EST_HUMAN	EST_HUMAN	Z2808.s1 Soares fetal liver spleen INFIL.S1 Homo sapiens cDNA clone IMAGE:451694 3'
713	13715	28708	8.21	6.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
713	13715	28709	8.21	6.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1809	14837	27828	3.44	5.0E-49	AA172121.1	EST_HUMAN	z026c07.r1 Spinalgene neuroepithelium (HS37231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233228 G233228 RYLV-H PROTEIN ; contains LTR7.3 LTR7 LTR7 repetitive element ;
2760	15752	28772	9.75	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cde
3286	16340	28259	6.07	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC63392), mRNA
626	13697	26514	25.9	4.0E-49	AW189533.1	EST_HUMAN	X08501.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2676563 3' similar to WP:B0350.2B
7457	20423	33778	1.06	4.0E-49	Z26934.2	NT	CE00703 ;
7457	20423	33779	1.06	4.0E-49	Z26934.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7487	20452	33811	0.88	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
7487	20452	33812	0.88	4.0E-49	11525737	NT	(GALNAc-T8) (GALNT8), mRNA
8109	21046	34446	0.71	4.0E-49	7692209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
8216	22182	35514	0.53	4.0E-49	11425374	NT	(GALNAc-T8) (GALNT8), mRNA
9218	22182	35515	0.53	4.0E-49	11425374	NT	Homo sapiens cDNA clone IMAGE:362977 5'
12506	25939		8.71	4.0E-49	AA210798.1	EST_HUMAN	z0605.r1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:362977 5'
12594	25937		3.19	4.0E-49	AF240783.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
552	13632	28549	1.27	3.0E-49	X68568.1	NT	H. sapiens mRNA for acyl-CoA carboxylase
2956	15653		1.83	3.0E-49	AA019131.1	EST_HUMAN	H. sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
5019	18033	30910	2.11	3.0E-49	U46959.1	NT	repetitive element ;
7650	20510	33978	10.32	3.0E-49	H30478.1	EST_HUMAN	Human type IV collagen (COL4A4) gene, exon 40
11633	24570	38134	1.54	3.0E-49	AA337551.1	EST_HUMAN	EST128e12 WAT TMT Homo sapiens cDNA clone 25e12
662	13728		3.89	2.0E-49	BE169980.1	EST_HUMAN	EST142572 Endometrial tumor Homo sapiens cDNA 5' end
3239	16291	29213	1.6	2.0E-49	N28446.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
							Y233066.r1 Soares melanocyte 2N0HM Homo sapiens cDNA clone IMAGE:262571 5'

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3583	16628	29547	0.78	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6900	19862	33249	1.14	2.0E-49	AV717038.1	EST_HUMAN	AV717038 DCB Homo sapiens cDNA clone DCBALB01 5'
8436	21405		1.62	2.0E-49	M86033.1	EST_HUMAN	EST026558 Fetal brain, Striatum (cat#63206) Homo sapiens cDNA clone HFBCV50
12603	25821		2.67	2.0E-49	AF163964.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
900	13955		9.35	1.0E-49	BF035327.1	EST_HUMAN	6014389331F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:362086 5'
1557	14589	27560	1.27	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1818	14845	27837	3.33	1.0E-49	BE255216.1	EST_HUMAN	601115709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3356273 5'
5433	18835	31444	5.72	1.0E-49	BF131007.1	EST_HUMAN	601820353F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052032 5'
6198	19270	32505	0.87	1.0E-49	H18291.1	EST_HUMAN	YH48N04.r1 Soares adult brain N26H8B5Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP-GBG1_HUMAN Q06447 GUANINE NUCLEO TIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6202	19276	32510	1	1.0E-49	AJW96460.1	EST_HUMAN	EST378713 IMAGE resequences, MAGH Homo sapiens cDNA
7427	20384	33744	0.58	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCYD11 5'
7427	20394	33745	0.58	1.0E-49	AV703000.1	EST_HUMAN	AV703000 ADB Homo sapiens cDNA clone ADBCYD11 5'
7433	20400	33753	3.3	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7433	20400	33754	3.3	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7520	20485	33846	2.2	1.0E-49	N25884.1	EST_HUMAN	W78G12.s1 Soares, placenta, 80g/week. 2NBP89c9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65973 KINESIN HEAVY CHAIN (HUMAN);
7520	20485	33847	2.2	1.0E-49	N25884.1	EST_HUMAN	W78G12.s1 Soares, placenta, 80g/week. 2NBP89c9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65973 KINESIN HEAVY CHAIN (HUMAN);
8414	21383	34790	0.59	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8414	21383	34791	0.69	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9023	21989		0.78	1.0E-49	8594184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
9344	23009	33734	1.14	1.0E-49	BE40540.1	EST_HUMAN	60130892F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10485	23407	38903	1.22	1.0E-49	AL043129.2	EST_HUMAN	DKFZ9434D2423.J1 43k (synonym: hies3) Homo sapiens cDNA clone DKFZ9434D2423 5'
11399	24344	37877	1.59	1.0E-49	AB020335.1	NT	Homo sapiens Pancreas-specific TSA305 mRNA, complete cds
11640	24577	38143	3.12	1.0E-49	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12147	26007		1.7	1.0E-49	BE159343.1	EST_HUMAN	MRO-HT0407-010200-006-02.H10407 Homo sapiens cDNA
12502	25241		2.78	1.0E-49	11418322	NT	Homo sapiens cathecin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6844	25697		1.06	9.0E-50	BE259758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3651888 5'
171	13273	26108	3.9	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS210002
720	13782	26716	2.14	8.0E-50	X65097.2	NT	Homo sapiens mRNA for VIP receptor 2
720	13782	26717	2.14	8.0E-50	X65097.2	NT	Homo sapiens mRNA for VIP receptor 2
1778	14807	27793	4	8.0E-50	4501880	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2710	15704	28720	2.18	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA



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621	13688	26604	0.88	7.0E-50	BE088591.1	EST_HUMAN	QV0-BT0703-280400-211-03 BT0703 Homo sapiens cDNA
6552	20176	33500	1.21	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6852	20178	33501	1.21	7.0E-50	BF091922.1	EST_HUMAN	RC6-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7628	20460	33652	0.82	7.0E-50	AA627822.1	EST_HUMAN	nc559a12.x1 NCL CGAP_C99 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X68397.6GS
11108	24068	37560	28.05	7.0E-50	AI872137.1	EST_HUMAN	hm55911.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2499908 3'
8556	21524		6.89	6.0E-50	BE044076.1	EST_HUMAN	nc38904.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
11166	24124	37652	7.98	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
11166	24124	37653	7.98	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1808	14836	27826	1.18	5.0E-50	BF332938.1	EST_HUMAN	GMO-BT0792-300500-398-505 BT0792 Homo sapiens cDNA
1808	14838	27827	1.18	5.0E-50	BF332938.1	EST_HUMAN	GMO-BT0792-300500-398-505 BT0792 Homo sapiens cDNA
8448	22412		5.85	5.0E-50	AA557883.1	EST_HUMAN	nc45810.x1 NCL CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element:
918	13972		1.45	4.0E-50	AA601143.1	EST_HUMAN	nc54609.x1 NCL CGAP_S81 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X63741_ma1
6497	19581	32813	0.54	4.0E-50	11440983	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7445	20411	33763	0.93	4.0E-50	BE087536.1	EST_HUMAN	Homo sapiens cysteinyl-IRNA synthetase (CARS), mRNA
1958	14978	28649	2.89	3.0E-50	M18048.1	NT	Human endogenous retrovirus RTV(L-H2
2925	15528	28649	1.11	3.0E-50	BE259186.1	EST_HUMAN	601108777F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3950309 5'
3310	16363	29283	0.88	3.0E-50	AA746142.1	EST_HUMAN	nc03006.x1 NCL CGAP_K03 Homo sapiens cDNA clone IMAGE:1322627 3'
6834	19887	33190	0.6	3.0E-50	11416317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6834	19887	33181	0.6	3.0E-50	11416317	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
6929	20163	33472	1.56	3.0E-50	11421514	NT	Homo sapiens similar to serine domain, immunoglobulin domain (Ig), short basic domain, secreted, (hemaphrodit) 3A (H. sapiens) (LOC63232), mRNA
7606	20849	34234	4.3	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7606	20849	34235	4.3	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
8929	21895	35323	0.91	3.0E-50	BE01589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10177	23102	36582	1.1	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1595 protein, partial cds
10168	23111	36595	0.96	3.0E-50	11418514	NT	Homo sapiens k-complex 10 (e murine top homolog) (TCP10), mRNA
10885	23005	37309	0.74	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0269 gene, partial cds
11438	24381	37920	1.99	3.0E-50	11436955	NT	Homo sapiens Grib2-associated binder 2 (KIA0671), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11792	23047	37468	8.4	3.0E-50	AJ245621.1	NT	Homo sapiens CTL-2 gene
778	13837		6.8	2.0E-50	AF055066.1	NT	Homo sapiens MHC class 1 region
1081	14126	27078	6.73	2.0E-50	4557792	NT	Homo sapiens midline 1 (Ox12/BBB syndrome) (MID1) mRNA
1437	14470	27448	0.95	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
3300	16353	29272	0.83	2.0E-50	AF11168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4269	17318	30197	0.75	2.0E-50	D86424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
7051	20073	33380	0.51	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001609 5'
8659	21627	35047	1.09	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8659	21627	35048	1.09	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8769	21766	35189	6.78	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8769	21766	35190	6.78	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10244	23169	36557	1.43	2.0E-50	8910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
10244	23169	36558	1.43	2.0E-50	8910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
11971	24849		1.52	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
482	13535	26401	2.26	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2273	15381		8.27	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
7970	20909		0.85	1.0E-50	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10553	23475	36970	0.87	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6095	19174	32390	1.01	9.0E-51	AW511225.1	EST_HUMAN	H444602 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:095636
6350	18419	32600	0.71	9.0E-51	AJ744857.1	EST_HUMAN	095636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II;
6020	21986	35407	0.65	9.0E-51	AI791154.1	EST_HUMAN	p67h03.e1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9679	22032	33088	1.21	9.0E-51	AAU43738.1	EST_HUMAN	ab22g04.x5 Stragene lung (4937210) Homo sapiens cDNA clone IMAGE:841693 3' similar to
9658	22704	36245	0.52	9.0E-51	AI791154.1	EST_HUMAN	SW:PSN_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
9658	22794	36246	0.52	9.0E-51	AI791154.1	EST_HUMAN	SW:PSN_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
11804	23359	37463	1.51	9.0E-51	H69078.1	EST_HUMAN	YW24p09.1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:486352 5'
11804	23359	37464	1.51	9.0E-51	H69078.1	EST_HUMAN	YW24p09.1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
4599	17620	30513	6.51	8.0E-51	AA610942.1	EST_HUMAN	h98E009 at NCL_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb-X12671_nen1
7914	20357	34246	2.04	8.0E-51	11436587	NT	Heterogeneous NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
9819	22068		0.88	9.0E-51	AU138590.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73/NIN-CC-38), mRNA
							AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3295	16348	29268	1.68	7.0E-51	AW889218.1	EST_HUMAN	QV4-NT0028-200-400-180-405 NT0028 Homo sapiens cDNA xp34a03.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR-0829-40 Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
3374	16424	29349	0.72	7.0E-51	AW274720.1	EST_HUMAN	DKFZ4434B2228_r1.434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2228 5'
4198	17227	30116	1.4	7.0E-51	AL079828.1	EST_HUMAN	DKFZ4434B2228_r1.434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2228 5'
4198	17227	30117	1.4	7.0E-51	AL079828.1	EST_HUMAN	DKFZ4434B2228_r1.434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2228 5'
4378	17406	30286	1.64	7.0E-51	AW286603.1	EST_HUMAN	UHR-BWO-alp-b-05-Q11st NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:2729817 3'
11893	24870	39465	2.13	7.0E-51	AF161449.1	NT	Homo sapiens HSP C331 mRNA, partial cds
1530	14563	27534	0.91	6.0E-51	6678763	NT	Homo sapiens putative DNA binding protein (M99), mRNA
1896	15017	28024	5.54	6.0E-51	7657266	NT	Homo sapiens KIAA0829 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
3487	16533	29458	17.23	6.0E-51	7657266	NT	Homo sapiens KIAA0829 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0829), mRNA
4338	17365	30247	0.69	6.0E-51	8910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4338	17365	30248	0.69	6.0E-51	8910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6105	19184	32403	2.8	6.0E-51	X01788.1	NT	Human hemoglobin related (Hpr) gene exon 3
6116	19184	32417	6.29	6.0E-51	AF070063.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6116	19184	32418	8.29	6.0E-51	AF070063.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6925	20149	33469	1.13	6.0E-51	4506726	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7076	20988	33408	1.03	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56960), mRNA
7157	18389	31233	2.29	6.0E-51	11428665	NT	Homo sapiens cerebral cell adhesion molecule (FJ11042), mRNA
9492	22456	35895	0.62	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9492	22456	35896	0.62	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
10042	22669	39456	2.04	6.0E-51	7651535	NT	Homo sapiens B9 protein (B9), mRNA
10120	23048	36525	1.14	6.0E-51	U60093.1	NT	Human ankyrin (ANK1) gene, exon 2
11593	24523	39078	1.65	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor HS21C003
792	13851	29795	9.57	6.0E-51	AL183203.2	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
804	13862	28812	1.6	6.0E-51	4507500	NT	Novel human gene mapping to chromosome X
693	16666	26998	1.23	6.0E-51	AL193204.1	NT	Homo sapiens 26S proteasome-associated part homolog (POH1) mRNA
1612	14644	27620	1.02	6.0E-51	5031980	NT	Homo sapiens mRNA for nucleoporin 155
2559	15600	28619	7.72	5.0E-51	AJ007558.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3665	17005	29919	1.85	5.0E-51	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3665	17005	29920	1.85	5.0E-51	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
11610	24548	38108	4.07	5.0E-51	9503136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
135	13240	26171	1.53	3.0E-51	AI697348.1	EST_HUMAN	tr1603.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1180	14221	27177	3.31	3.0E-51	AI697346.1	EST_HUMAN	tr1603.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1940	14864	27661	1.09	3.0E-51	AA211268.1	EST_HUMAN	2657001.s1 Striatum INT neuron (6837233) Homo sapiens cDNA clone IMAGE:649008 3'
4354	17381	30263	2.23	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
7831	20779	34157	1.2	3.0E-51	RI16914.1	EST_HUMAN	y647c08.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
9197	22167		4.32	3.0E-51	M29003.1	NT	Human hRNIP C2 protein mRNA
9423	26008		0.46	3.0E-51	AW593777.1	EST_HUMAN	le04d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
12610	25435		1.36	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
369	13452	26390	1.19	2.0E-51	4607768	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angiogen syndrome) (UBEGA) mRNA
699	13752	26678	0.69	2.0E-51	BE391063.1	EST_HUMAN	601285694.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
699	13752	26678	0.68	2.0E-51	BE391063.1	EST_HUMAN	601285694.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1997	14727	27710	4.99	2.0E-51	AA233352.1	EST_HUMAN	z00d05.r1 Striatum NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:664890 5' similar to TRG233228 G233228 RTV-LH PROTEIN; contains LTR7.8, LTR7 repetitive element;
3745	16787	29699	2.46	2.0E-51	AI462415.1	EST_HUMAN	tr27g03.x1 NCI_CGAP_Ki67 Homo sapiens cDNA clone IMAGE:2131732 3'
4521	17646	30433	0.69	2.0E-51	AW137826.1	EST_HUMAN	UI-H811-adj-4-02-U1.s1 NCI_CGAP_Su53 Homo sapiens cDNA clone IMAGE:1325603 3' similar to SW:NM1_MOUSE P36436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5513	18613	31545	0.57	2.0E-51	AI752851.1	EST_HUMAN	63409.x5 NCI_CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NM1_MOUSE P36436 GLUTAMATE [NM2A] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
5513	18613	31546	0.57	2.0E-51	AI752851.1	EST_HUMAN	601470446.F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
6131	19208	32433	4.17	2.0E-51	BE782015.1	EST_HUMAN	Homo sapiens diacylglycerol kinase lutea (DGK) gene, exon 23
7531	20494		0.68	2.0E-51	AF219227.1	NT	Homo sapiens cell recognition molecule Casar2 (KIAA0866) mRNA
7690	20948	34012	0.91	2.0E-51	7682349	NT	Homo sapiens cell recognition molecule Casar2 (KIAA0866) mRNA
9046	22012	35434	1.54	2.0E-51	BE901894.1	EST_HUMAN	601678787.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3859613 5'
9046	22012	35435	1.54	2.0E-51	BE901894.1	EST_HUMAN	601678787.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3859613 5'
9399	22554	35785	0.97	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1) mRNA
9870	22623	36276	1.35	2.0E-51	AI917078.1	EST_HUMAN	tr74d07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;
9962	22989	36350	6.78	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9877	22904	39388	0.53	2.0E-51	AB007928.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10789	23720	37223	1.54	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone KBGAF05 5'
10838	23758	37258	1.14	2.0E-51	AA378559.1	EST_HUMAN	EST191296 Synovial sarcoma Homo sapiens cDNA 5' end
11655	18613	31545	7.03	2.0E-51	AJ732851.1	EST_HUMAN	cb34009.x5 NCI CGAP K165 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NM1_MOUSE
11655	18613	31546	7.03	2.0E-51	AJ732851.1	EST_HUMAN	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
12122	24981	38592	2.3	2.0E-51	AA011868.1	EST_HUMAN	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR;
12803	25430	31740	2	2.0E-51	11419159	NT	P03401.1f Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429872 5'
114	13226	26149	8.48	1.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24)) homolog; translocated to, 4 (MLL14), mRNA
1491	14524	30352	33.7	1.0E-51	AV742248.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
4437	17463	30353	0.99	1.0E-51	4759071	NT	AV742248 CB Homo sapiens cDNA clone CBFBGCG12 5'
4437	17463	30353	0.99	1.0E-51	4759071	NT	Homo sapiens small inducible cyclin subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5463	18686	31478	3.84	1.0E-51	T18882.1	EST_HUMAN	Homo sapiens small inducible cyclin subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
7611	20854	34242	0.68	1.0E-51	AI672632.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b12058
8235	21204	34609	0.79	1.0E-51	BF434359.1	EST_HUMAN	7696502.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3944091 3' similar to TR:P87892 P87892
12073	26012		1.67	1.0E-51	AV760590.1	EST_HUMAN	PROTEASE;
12569	25293		5.29	9.0E-52	AA77621.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSGB02 5'
153	13256	26184	9.3	8.0E-52	AA720574.1	EST_HUMAN	ZB95A07.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
1495	14528	27500	1.77	8.0E-52	X94900.1	NT	contains THR13 THR repetitive element;
1662	14694	27659	2.98	8.0E-52	11965028	NT	THR repetitive element;
1662	14694	27659	2.98	8.0E-52	11965028	NT	H. sapiens mRNA for laminin-5, alpha2b chain
1682	14694	27670	2.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ135556 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
4018	14694	27669	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ135556 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
4018	14694	27670	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ135556 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
7760	20713	34082	0.69	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 58KD (TGFB1), mRNA
7760	20713	34083	0.69	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 58KD (TGFB1), mRNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9367	22332	35762	1.55	7.0E-52	W56471.1	EST_HUMAN	z556a08.r1 Soares, parathyroid tumor, NHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element;
1191	14231		0.65	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271289-049-407 BT0537 Homo sapiens cDNA
1703	14733	27715	3.37	6.0E-52	AF109807.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
9819	19906	32059	1.08	6.0E-52	AI208784.1	EST_HUMAN	qq44p04.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11543	24484	39037	1.63	6.0E-52	BE048172.1	EST_HUMAN	z46h04.y1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE:2281671 5' similar to SW_PGBM_MOUSE C05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE
4468	17495	30383	1.16	5.0E-52	Z78998.1	NT	PROTEOLYCLAN CORE PROTEIN PRECURSOR;
9747	22688	38144	0.47	5.0E-52	11437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1070	14702	27677	1.25	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1803	14831	27818	1.15	4.0E-52	4758943	NT	Homo sapiens nucleoprotein 153kD (NUP155) mRNA
4769	17789	30692	1	4.0E-52	AI76814.1	EST_HUMAN	w89b02.x1 NCL CGAP K1412 Homo sapiens cDNA clone IMAGE:2400459 3'
5358	18464	31334	1.41	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5359	18464	31335	1.41	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7643	20885	34276	0.66	4.0E-52	11525731	NT	Homo sapiens RAD51-interacting protein (PIR51), mRNA
8373	21342	34763	2.33	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915936 5'
8879	21848	35288	6.18	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12428	25164		3.05	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12806	25488		4.73	4.0E-52	AB020559.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4116	17152		11.15	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
594	13634	26550	1.97	2.0E-52	M10376.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
584	19334	28551	1.97	2.0E-52	M10676.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2030	15049	28064	1.43	2.0E-52	AB033076.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds
2507	15510	28537	1.95	2.0E-52	BE207575.1	EST_HUMAN	bb9b007.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb-X16463 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE)
2146	15739		10.45	2.0E-52	BF677882.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5013	18027	30912	3.28	2.0E-52	AI37188.1	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5049	18061	30936	0.98	2.0E-52	AI141802.1	EST_HUMAN	qa56e05.s1 Soares, NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1660784 3'
5049	18061	30940	0.98	2.0E-52	AI141802.1	EST_HUMAN	qa56e05.s1 Soares, NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1660784 3'
5786	18880	32062	3.71	2.0E-52	AW648041.1	EST_HUMAN	IL3-CT0214-231258-053-E12 CT0214 Homo sapiens cDNA
6503	19587	32819	1.7	2.0E-52	11141688	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
6872	19928	33221	1.04	2.0E-52	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7120	20106	33416	0.73	2.0E-52	AF792146.1	EST_HUMAN	cc45d12.y5 NCI CGAP B2 Homo sapiens cDNA clone IMAGE:1608311 5'
8121	21058	34465	0.62	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8121	21058	34468	0.52	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9000	21068		11.89	2.0E-52	AF14780.1	NT	Musca domestica beta-tubulin mRNA, complete cds
9288	22254	35684	0.87	2.0E-52	AA778795.1	EST_HUMAN	2456305.x1 Soares fetal liver spleen INFLS.S1 Homo sapiens cDNA clone IMAGE:453272 3'
9834	22683		1.05	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15SD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10474	23366	36893	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and maliner transposase fusion gene (SETMAR) mRNA
10474	23366	36894	6.19	2.0E-52	5730038	NT	Homo sapiens SET domain and maliner transposase fusion gene (SETMAR) mRNA
11538	24470	38029	3.09	2.0E-52	AB31462.1	EST_HUMAN	wf49c04.x1 NCI CGAP Lur19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element
11538	24479	38030	3.09	2.0E-52	AB31462.1	EST_HUMAN	wf49c04.x1 NCI CGAP Lur19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element
11551	24492	38048	2.73	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DOB Homo sapiens cDNA clone DCBAIE03 5'
11680	24648		12.63	2.0E-52	W70260.1	EST_HUMAN	z649g12r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11839	24818		2.73	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2) mRNA
12231	25982	31300	18.5	2.0E-52	AW126297.1	EST_HUMAN	xt72607.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element contains element LTR2 repetitive element
12633	26319		7.5	2.0E-52	AB08685.1	EST_HUMAN	wf67005.x1 Soares NFL_T_OBC.S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TRQ18559 Q16959 CARBOXYLTERASE
534	13605	26524	1.45	1.0E-52	AA634445.1	EST_HUMAN	zu79h12.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743879 3'
1373	14407	27377	9.6	1.0E-52	4504026	NT	Homo sapiens glutamate-aminotransferase (glutamine synthase) (GLUL) mRNA
2542	15544		2.17	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3072	16129	29041	1.99	1.0E-52	S61070.1	NT	poliovirus transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
5406	18509	31366	4.22	1.0E-52	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6533	19586	32859	2.4	1.0E-52	U38564.1	NT	Human PMS2 related (HPMSR2) gene, complete cds
7684	20623	33957	2.36	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8150	21087	34486	0.55	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (bt2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8808	21776		1.13	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8943	22806	35955	0.7	1.0E-52	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10941	23861		1.21	1.0E-52	AL020370.1	EST_HUMAN	db0805.y1 Morton Fetal Oocyte Homo sapiens cDNA clone IMAGE:2483145 5'
10951	23871		1.14	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11117	24077	37601	1.84	1.0E-52	U48298.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (PTPCAAX1) mRNA, complete cds
13114	29633	31608	1.3	1.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3805	18846	29752	0.0	9.0E-53	4506084	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4418	17445	30336	0.91	8.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12477	29226		2.55	7.0E-53	BF238465.1	EST_HUMAN	60180477.F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5'
12881	29589		6.21	7.0E-53	AI421782.1	EST_HUMAN	644707.X1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.11 THR repetitive element;
5216	18224	31098	0.89	6.0E-53	BE295719.1	EST_HUMAN	G01175776.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3530946 5'
4126	17159	30047	3	5.0E-53	4758543	NT	Homo sapiens heteronucleic nuclear ribonucleoprotein C (C1IC2) (HNRPC) mRNA
12110	24980	39550	1.54	5.0E-53	BE729270.1	EST_HUMAN	60156162.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831175 5'
12522	23283		1.67	5.0E-53	AW615563.1	EST_HUMAN	RC3-STO1697-15T089-Q11-g10 STO197 Homo sapiens cDNA
51	13171	26079	2.37	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21O085
51	13171	26080	2.37	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21O085
4858	17876	30764	1.11	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
9771	22712		0.62	4.0E-53	AI613037.1	EST_HUMAN	Y06804.X1 NCI_CGAP_UR3 Homo sapiens cDNA clone IMAGE:2276327 3'
10114	23040		0.71	4.0E-53	F13080.1	EST_HUMAN	HSC3D041 normalized infant brain cDNA Homo sapiens cDNA clone c-34d4
11548	24489	39044	2.63	4.0E-53	BF128701.1	EST_HUMAN	601810969.F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
11548	24489	38045	2.63	4.0E-53	BF128701.1	EST_HUMAN	601810969.F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2659	15666	28685	2.64	3.0E-53	AB026988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3744	16786	29568	1.01	3.0E-53	AW050836.1	EST_HUMAN	w22207.x1 Soares Diagnostics, colon NHCD Homo sapiens cDNA clone IMAGE:2558798 3'
6499	18569	31511	0.62	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5707	18802	31979	1.09	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6318	18389	32829	0.85	3.0E-53	BE160025.1	EST_HUMAN	Q17-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7305	20276	33613	0.68	3.0E-53	Y10386.3	NT	H. sapiens graf gene
7305	20276	33614	0.68	3.0E-53	Y10386.3	NT	H. sapiens graf gene
8647	21615	35037	12.56	3.0E-53	S72943.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9211	22177	35607	0.65	3.0E-53	S72943.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
9412	22377		9.53	3.0E-53	5901953	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
458	13531		2.53	2.0E-53	AA366556.1	EST_HUMAN	Homo sapiens FGFRI oncogene partner (FOP), mRNA
2335	15346	26367	6.08	2.0E-53	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
2543	15545		11.44	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ translocating, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2736	15730	28744	1.17	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2736	15730	28745	1.17	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3232	16287	29208	1.46	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3258	16313	28234	0.8	2.0E-53	AF033822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4088	17122	30016	2.78	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
4520	17545	30432	1.23	2.0E-53	4506692	NT	Homo sapiens SKA955 homologue (SKAP-HOM) mRNA
5193	18202	31074	0.96	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5193	18202	31075	0.96	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5500	18600	31512	3.33	2.0E-53	BF334740.1	EST_HUMAN	PM1-C70368-170800-001-403 C70368 Homo sapiens cDNA
5500	18600	31513	3.33	2.0E-53	BF334740.1	EST_HUMAN	PM1-C70368-170800-001-403 C70368 Homo sapiens cDNA
8203	21173	34583	1.13	2.0E-53	AW975598.1	EST_HUMAN	EST7387707 MAGE sequences, MAGN Homo sapiens cDNA
8340	21309		0.61	2.0E-53	AA095952.1	EST_HUMAN	15429 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9763	22704		16.48	2.0E-53	AW245976.1	EST_HUMAN	2822685 Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822685 5'
1440	14473	27430	2	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3421	16469	29388	1.29	1.0E-53	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5001	18016	30902	1.32	1.0E-53	BE296388.1	EST_HUMAN	G01178725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631919 5'
6850	19903	33198	1.73	1.0E-53	BF364201.1	EST_HUMAN	CM4-N1029-150800-543-602 NN1029 Homo sapiens cDNA
7459	20425	33781	0.84	1.0E-53	BE012071.1	EST_HUMAN	RCS-BN1058-270400-031-001 BN1058 Homo sapiens cDNA
8267	21236	34647	0.58	1.0E-53	AA249072.1	EST_HUMAN	19571 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9444	22408	35845	13.12	1.0E-53	X76538.1	NT	H.sapiens mRNA for hMRNPcore protein A1
12105	24976	38574	3.08	1.0E-53	X98411.1	NT	H.sapiens mRNA for myosin-IE
12105	24976	38575	3.08	1.0E-53	X98411.1	NT	H.sapiens mRNA for myosin-IE
5375	25636	31353	5.13	8.0E-54	4506786	NT	H.sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
206	13309	28238	1.73	8.0E-54	BE386786.1	EST_HUMAN	G0127263F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1652	14878	27874	2.4	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6045	19127	32353	23.25	8.0E-54	6005700	NT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 8 (ABCAB), mRNA
11882	24841	38434	1.67	8.0E-54	AW592568.1	EST_HUMAN	H44605.k1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2934752 3'
11882	24841	38435	1.67	8.0E-54	AW592568.1	EST_HUMAN	H44605.k1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2934752 3'
384	13497	28429	1.85	7.0E-54	AA812537.1	EST_HUMAN	at79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1977049 3' similar to contains MER30.13 MER30 repetitive element;
1847	14873	27699	1.51	7.0E-54	Y16945.1	NT	Homo sapiens mRNA for monocytic chemotactic protein-2

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2215	15228	28252	4.54	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_6to9weeks_2NHHP6to9W Homo sapiens cDNA clone IMAGE:267395 3' similar to contains LTR7 L3 LTR7 repetitive element ;
10487	23409	36906	1.91	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) [LOC63182], mRNA contains ORF.11 ORF repetitive element ;
11623	24561		3.26	7.0E-54	AI160180.1	EST_HUMAN	q567g03.x1 Soares_fetal_heart_NbHP19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element ;
25	13145	25045	2.05	6.0E-54	AB003918.1	NT	Homo sapiens DNA for MCB, exon 4, 5 and partial cds
395	13498	26430	0.67	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
385	13498	26431	0.67	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3298	16349	29269	0.99	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3546	16592	29517	0.99	6.0E-54	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21047
4030	17068	29969	1.48	6.0E-54	4502872	NT	Homo sapiens chloride channel 5 (CLCN5) mRNA
4480	17514	30402	0.78	6.0E-54	AV754746	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4519	17836	30734	0.94	6.0E-54	AV724655.1	EST_HUMAN	AV724655 HTB Homo sapiens cDNA clone HTBACE02 5'
4890	17897	30796	1.85	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4909	17926		1.23	6.0E-54	Y06946.1	NT	H. sapiens shc pseudogene, p86 isoform
5035	17926		1.27	6.0E-54	Y06946.1	NT	H. sapiens shc pseudogene, p86 isoform
11771	23926	37446	1.6	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
11771	23926	37447	1.6	6.0E-54	11433623	NT	Homo sapiens KIAA0071 protein (KIAA0071), mRNA
2160	15176	28197	3.75	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
184	13284		319.6	4.0E-54	AF110103.1	NT	Tupala bangleri beta-actin mRNA, partial cds
957	14010	29963	29.88	4.0E-54	AA306764.1	EST_HUMAN	EST117698 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1822	14848	27842	2.91	4.0E-54	D38821.1	NT	Human mRNA for KIAA0077 gene, partial cds
1822	14848	27843	2.91	4.0E-54	D38821.1	NT	Human mRNA for KIAA0077 gene, partial cds
3217	16272		1.03	4.0E-54	AI935096.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
7524	20468		0.68	4.0E-54	BE544889.1	EST_HUMAN	O02711 PRO-POL-DUTPAZE POLYPROTEIN ;
63	13209	26133	13.65	3.0E-54	AA373487.1	EST_HUMAN	601075004.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461017 5'
2632	16631		1.1	3.0E-54	AI908757.1	EST_HUMAN	EST1165371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6007	18060	32290	1.52	3.0E-54	4502434	NT	IL-BT189-190369-007 BT189 Homo sapiens cDNA Homo sapiens BAX non-receptor tyrosine kinase (BAX) mRNA
7619	20579	33942	1.49	3.0E-54	AA844081.1	EST_HUMAN	ab92c08.x1 Soares_pretibial_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7619	20579	33943	1.49	3.0E-54	AA844081.1	EST_HUMAN	ab92c08.x1 Soares_pretibial_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
8081	21018	34418	0.51	3.0E-54	AI726922.1	EST_HUMAN	wg4b111.x1 Soares_NSIF_PB_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367933 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11363	24312		4.82	3.0E-54	11434808	NT	Homo sapiens goli autoantigen, golin subfamily a, 5 (GOLGA5), mRNA
11423	24367	37602	3.55	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NC1 CGAP_Bm57 Homo sapiens cDNA clone IMAGE:4193121 5'
11686	24681	38239	2.11	3.0E-54	AA393362.1	EST_HUMAN	27071217 Soares, Isatis, NIH Homo sapiens cDNA clone IMAGE:72727 5' similar to TR-G191315
12334	25134	31850	4.08	3.0E-54	AW954558.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;
12380	26942		1.67	3.0E-54	AW748965.1	EST_HUMAN	EST366629 IMAGE resequencing, MAGG Homo sapiens cDNA
543	13709	29929	0.22	2.0E-54	5031900	NT	RC1-B70313-137189-011-B08 BT0313 Homo sapiens cDNA
1387	14401	27371	1.48	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
							Homo sapiens nuclear antigen Sp100 (SP100) mRNA
1550	14583	27554	1.32	2.0E-54	AA655008.1	EST_HUMAN	m78a09.x1 NC1 CGAP_P03 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2546	15547	28570	1.04	2.0E-54	AW163175.1	EST_HUMAN	eu92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW-CUL1_HUMAN Q13616 CULLIN HOMOLOG 1;
2608	15607	28631	1.45	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21Q010
2905	15984	28887	1.4	2.0E-54	AW057524.1	EST_HUMAN	w90b12.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552827 3' similar to TR:Q2084 Q2084 PHOSPHOLIPASE C NEIGHBORING;
3159	16005		5.43	2.0E-54	AA532925.1	EST_HUMAN	tr45g09.x1 NC1 CGAP_P03 Homo sapiens cDNA clone IMAGE:995488 similar to gb-X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4232	17261		1.73	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4470	17466		1.18	2.0E-54	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4914	17631	30822	0.89	2.0E-54	7706446	NT	Homo sapiens peptidylarginine deaminase type III (LOC57102), mRNA
5278	18284	31147	1.07	2.0E-54	4506952	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5551	18648	31591	1.8	2.0E-54	4759069	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5684	18779	31952	1.25	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NC1 CGAP_Bm57 Homo sapiens cDNA clone IMAGE:2291348 5'
5956	18946	32131	3.9	2.0E-54	11428857	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5991	19046	32245	10.03	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1191 protein, partial cds
5991	19046	32245	10.03	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1191 protein, partial cds
6514	18868	33157	0.77	2.0E-54	AF008915.1	NT	Homo sapiens EVI5 homologue mRNA, complete cds
6983	20206	35555	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6983	20206	35555	0.73	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
							Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
7330	20301	33645	7.68	2.0E-54	11428544	NT	Homo sapiens mRNA for brain natriuretic receptor, complete cds
9987	22914	36370	4.03	2.0E-54	AB01026.1	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10059	23292	30768	1.61	2.0E-54	11429127	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10480	23402	36859	0.88	2.0E-54	11416762	NT	

Table 4.

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10480	29402	38900	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
12034	24910		4.31	2.0E-54	7657454	NT	Homo sapiens pascadillo (zbrf1sh) homolog 1, containing BRCT domain (PES1), mRNA
4492	17517		1.6	1.0E-54	BF315418.1	EST_HUMAN	601589230P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
9081	22047	35470	0.51	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC53182), mRNA
10815	29337	37035	0.51	1.0E-54	AA412409.1	EST_HUMAN	zu10609.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:731484 5'
10815	29337	37036	0.61	1.0E-54	AA412409.1	EST_HUMAN	zu10609.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:731484 5'
12998	25554		4.2	1.0E-54	ALU077341.1	EST_HUMAN	ALU077341 Suparno cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-clutamyl transpeptidase mRNA, 5 end
10724	23848	37139	0.95	9.0E-56	BE081469.1	EST_HUMAN	QV2-B10635-165400-143-112 BT0635 Homo sapiens cDNA
1318	14353		0.98	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1321	14356		2.63	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11528	24469		1.73	8.0E-55	AW408714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:268967 5'
12980	25167		1.3	8.0E-55	BE327189.1	EST_HUMAN	hw08406.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182315 3' similar to TR-Q821J8
1083	14127	27081	1.52	7.0E-55	R06948.1	EST_HUMAN	Q921J8 43 KDA SECRETORY PROTEIN ; SP-C661_BOVIN P10897 CYTOCHROME ; x078c02.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2803522 3' similar to TR-Q80365
9156	22122		1.54	7.0E-55	AW103839.1	EST_HUMAN	O60365 FOS39564_1_1 ;
9538	22499	35947	1.22	7.0E-55	AA899581.1	EST_HUMAN	al23a11.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1407280 3'
9570	22532	35952	2.15	7.0E-55	AA198909.1	EST_HUMAN	ALU198909 PLACET Homo sapiens cDNA clone PLACE1011576 5'
11544	24485	35038	8.31	7.0E-55	AI661096.1	EST_HUMAN	tc28f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11544	24485	35039	8.31	7.0E-55	AI661096.1	EST_HUMAN	tc28f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12158	25004		1.8	7.0E-55	H48714.1	EST_HUMAN	y478d03.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:201893 5'
12986	28876		1.78	7.0E-55	H23398.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52444 5'
11843	24726	38313	1.85	6.0E-56	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1785	14814	27798	1.3	5.0E-55	AA704971.1	EST_HUMAN	z95b09.x1 Soares fetal liver, spleen, 1N1LS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
1785	14814	27798	1.3	5.0E-55	AA704971.1	EST_HUMAN	z95b09.x1 Soares fetal liver, spleen, 1N1LS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
6890	19747	35023	1.95	5.0E-55	4502240	NT	Homo sapiens arylsulfinatase E (chondrocyte-specific) (ARSE), mRNA
6890	19747	35024	1.95	5.0E-55	4502240	NT	Homo sapiens arylsulfinatase E (chondrocyte-specific) (ARSE), mRNA
7237	20258	33592	0.69	5.0E-55	7382477	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP8), transcript variant 5, mRNA
7513	20478	33839	0.68	5.0E-55	11434422	NT	Homo sapiens specific-type POZ protein (SPO1), mRNA
8327	21288	34711	0.74	5.0E-55	11528467	NT	Homo sapiens BCL2-associated atypical protein (BAG1), mRNA
9399	22384	35798	2.67	5.0E-55	4506502	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA), mRNA

Table 4

### Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Database Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9874	22627		1.9	6.0E-65	BE004386.1	EST_HUMAN	RC4-BT0310-110300-016-10 BT0310 Homo sapiens cDNA
10397	23319	36801	1.31	6.0E-56	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10397	23319	36802	1.31	6.0E-56	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10582	23504	36987	1.2	8.0E-55	5443765	NT	Homo sapiens nel (chicken)-like 2 (NEL2), mRNA
12419	25189		3.4	6.0E-55	14171972	NT	Homo sapiens nel (chicken)-like 2 (NEL2), mRNA
57	15831	26088	1.49	4.0E-56	AW067594.1	EST_HUMAN	EST17370084 IMAGE rescuallike, MAOE Homo sapiens cDNA
673	13737	26694	31.1	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM17A1) mRNA
1517	14549		1.97	4.0E-55	BF081411.1	EST_HUMAN	7852x10.v1 Soares, NSF, F8, SW, OT, PA, P_S1 Homo sapiens cDNA clone IMAGE:3350043 3' similar to contains 1,13,11, repetitive element;
2040	15059	28076	1.04	4.0E-55	4509180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2040	15059	28076	1.04	4.0E-55	4509180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2097	15114	28134	8.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2097	15114	28135	8.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2319	15530	28354	2.05	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
11	8887	21655	11	4.0E-56	AL163210.2	NT	Homo sapiens chromosome 21 segment HSTC010
11993	24503		2.89	4.0E-55	W28193.1	EST_HUMAN	43c5 Human retina cDNA randomly primed subclibrary Homo sapiens cDNA
12335	25135		3.64	4.0E-55	BF039441.1	EST_HUMAN	1803575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6751	18095	33086	0.78	3.0E-55	AA077156.1	EST_HUMAN	7809A09 Chromosome 17 Fetal Brain cDNA Library Homo sapiens cDNA clone 7809A09
12271	25093		1.91	3.0E-55	BF78519.1	EST_HUMAN	PM1-1710603-090300-001-008 Homo sapiens cDNA
13007	25560		1.9	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HSTC0084
3377	13461	26391	2.24	2.0E-55	X57147.1	NT	Human endogenous retrovirus pH8.1 (ERV9)
953	13623		1.89	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
650	13719	26638	3.26	2.0E-55	4507296	NT	Homo sapiens synlabin-binding protein 1 (STXBP1) mRNA, and translated products
							Homo sapiens ubiquitin ligase E3A (Homo papilloma Virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
2970	16028	26951	1.02	2.0E-55	4607798	NT	GM1-HT0878-150800-357-403 HT0878 Homo sapiens cDNA
4808	17825	30721	2.19	2.0E-55	BE718986.1	EST_HUMAN	ULHF-BN0-ata-5-06-9-JUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
7747	25989	34067	0.89	2.0E-55	AW607688.1	EST_HUMAN	h786h08.x1 NCI CGAP_K4111 Homo sapiens cDNA clone IMAGE:3134463 3'
9420	22385	35823	0.81	2.0E-56	BF224462.1	EST_HUMAN	h786h08.x1 NCI CGAP_K4111 Homo sapiens cDNA clone IMAGE:3134463 3'
9420	22385	35824	0.81	2.0E-55	BF224462.1	EST_HUMAN	h786h08.x1 NCI CGAP_K4111 Homo sapiens cDNA clone IMAGE:3134463 3'
							em8h08.x1 Stratiagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884185 3' similar to contains THR b2, THR repetitive element;
9516	22478		6.16	2.0E-55	A002836.1	EST_HUMAN	QV0-BN0147-280400-273-g06 BN0147 Homo sapiens cDNA
9596	22568		0.78	2.0E-55	BE007869.1	EST_HUMAN	U0310h08.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:214078 3'
10607	23529	37024	0.43	2.0E-56	AL439401.1	EST_HUMAN	U0310h08.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:214078 3'
11265	24245	37775	1.64	2.0E-56	AL111934.1	EST_HUMAN	AL111934.4 HEMBA11 Homo sapiens cDNA clone HEMBA1005583 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12113	24983	38554	1.51	2.0E-55	BE86059.1	EST_HUMAN	601307716F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:309076 5'
66	13212	28136	2.4	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
191	13292	28218	93.01	1.0E-55	U09823.1	NT	Oryzolepis cuniculus New Zealand white elongation factor 1 alpha (Rubeifaz2) mRNA, complete cds
576	13645	28558	0.75	1.0E-55	A028718.1	EST_HUMAN	068503.X1 Soares Testis_NHT Homo sapiens cDNA clone IMAGE:164460 3'
1152	14194	27146	4.22	1.0E-55	A020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1967	14988	27990	1.65	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1967	14988	27991	1.65	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2333	15344		3.96	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2345	15624	28376	1.31	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y1 (TTY1) mRNA, partial cds
2524	15627	28548	52.04	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2561	15682	28580	4.62	1.0E-55	A007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2567	15682	28581	4.62	1.0E-55	A007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2619	15617	28641	4.78	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
2801	15793	28811	0.98	1.0E-55	AB033045.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3420	16468	29398	0.98	1.0E-55	W28169.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4015	17054	29955	4.23	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4323	17362	30238	1.08	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4762	17762		1.21	1.0E-55	N77261.1	EST_HUMAN	Y444g03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:245620 5'
4865	17862	30756	1.79	1.0E-55	AB037163.1	NT	Homo sapiens DSCR3b mRNA, complete cds
4865	17862	30770	1.79	1.0E-55	AB037163.1	NT	Homo sapiens DSCR3b mRNA, complete cds
5177	18186	31093	1.3	1.0E-55	8823125	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
5576	18671	31634	0.56	1.0E-55	AF119958.1	NT	Homo sapiens PRG1851 mRNA, complete cds
6402	19470	32718	7	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
8402	19470	32719	7	1.0E-55	11433046	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7282	20015		0.68	1.0E-55	AF199420.1	NT	Homo sapiens F-box protein FBL4 (FBL4), mRNA, complete cds
8321	21290	34704	1.25	1.0E-55	11432854	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8321	21290	34705	1.25	1.0E-55	11432854	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8410	21379	34785	0.49	1.0E-55	11421649	NT	Homo sapiens SKAP65 homolog (SKAP-HOM), mRNA
8418	21387	34796	1.27	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
8418	21387	34797	1.27	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11776	23931	37452	1.65	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11785	23950	37471	1.68	1.0E-55	T10046.1	EST_HUMAN	seq1575 b4HB3MA C6b-HAP-F1 Homo sapiens cDNA clone b4HB3MA-C6b-HAP-F161 5' similar to similar to Chinese Hamster DHFR-compliment protein mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11902	24783	38371	1.74	1.0E-55	10587821	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
7690	20551	33912	1.89	9.0E-56	BE379074.1	EST_HUMAN	60123702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:369552 5'
2743	18737	28753	6.5	7.0E-56	H19934.1	EST_HUMAN	Y02903.1 Soares adult brain Homo sapiens cDNA clone IMAGE:173044 5' similar to contains TAR repetitive element:
7802	20845	34228	2.13	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231039-013-407 CT0252 Homo sapiens cDNA
7602	20846	34230	2.13	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231039-013-407 CT0252 Homo sapiens cDNA
1701	14731	27713	1.99	5.0E-56	AW697712.1	EST_HUMAN	U3-BN0583-170200-011-107 BN0583 Homo sapiens cDNA
9516	22478	35923	0.61	5.0E-56	AW015507.1	EST_HUMAN	U1-H-B10p-eau-e-05-Q1-81 NCI CGAP Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10754	23676	28730	1.7	5.0E-56	W28189.1	EST_HUMAN	49c3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12507	25950	31309	5.41	5.0E-56	H55095.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
30	13150	26049	12.5	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	13150	26050	12.5	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2719	15713	28730	4.9	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2719	15713	28731	4.9	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2823	13508	26516	3.69	4.0E-66	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2843	15620	28644	1.18	4.0E-56	AB32483.1	EST_HUMAN	w009f08.x1 NCI CGAP G08 Homo sapiens cDNA clone IMAGE:2306181 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE:
2843	15620	28644	1.18	4.0E-56	AB32483.1	EST_HUMAN	w009f08.x1 NCI CGAP G08 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE:
2843	15620	28645	1.16	4.0E-56	AB32483.1	EST_HUMAN	w009f08.x1 NCI CGAP G08 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW:DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE:
6387	19455	32700	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19455	32701	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10572	23792	37293	3.94	4.0E-56	AF043346.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11268	24220	37743	7.82	4.0E-56	AF498065.1	EST_HUMAN	tn65g12.x1 NCI CGAP_Bln25 Homo sapiens cDNA clone IMAGE:2163048 3'
11268	24220	37744	7.82	4.0E-56	AF498065.1	EST_HUMAN	tn65g12.x1 NCI CGAP_Bln25 Homo sapiens cDNA clone IMAGE:2163048 3'
1345	14390	27349	1.74	3.0E-66	8924029	NT	Homo sapiens hypothetical protein PR01304 (PR01304), mRNA
1778	14808	27794	0.99	3.0E-56	8912749	NT	Homo sapiens 5'-3' xonbinuclease 2 (XRN2), mRNA
3142	18189	29109	1.83	3.0E-56	AA325826.1	EST_HUMAN	EST28859 Cerebellum II Homo sapiens cDNA 5' end
3142	18189	29110	1.83	3.0E-56	AA325826.1	EST_HUMAN	EST28859 Cerebellum II Homo sapiens cDNA 5' end
3947	18887	18887	1.73	3.0E-56	AF050606.1	NT	Homo sapiens MHC class I region
3938	16978	29893	1.1	3.0E-56	BE393512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4454	17480	30386	4.84	3.0E-66	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C068
4003	17624	30517	2.34	3.0E-56	5602085	NT	Homo sapiens superfamily viral-like activity 2 (S. cerevisiae homolog)-like (SKI/2L), mRNA
4841	17858		1.81	3.0E-56	BE863572.1	EST_HUMAN	601438154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5767	18659	32038	1.64	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, ovine and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5767	18659	32039	1.64	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, ovine and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7068	20380	33369	5.05	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2) mRNA
9168	22734	33560	5	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5) mRNA
10172	23097	36577	1.12	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10846	23766	37265	1.63	3.0E-56	11434936	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
11643	24560	35147	4.57	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11643	24560	35148	4.57	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11683	24860	39465	7.16	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
11683	24860	39466	7.16	3.0E-56	U46900.1	NT	Homo sapiens NACP/alpha-synuclein gene, exon 5
12378	25160	31812	2.86	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12378	25160	31813	2.86	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
525	13566		1.92	2.0E-56	AA198818.1	EST_HUMAN	zz52a08.x1 Stratagene neuroepithelium (R637231) Homo sapiens cDNA clone IMAGE:545206 3'
734	15848	26732	2.02	2.0E-56	BE064396.1	EST_HUMAN	RC4-BT0310-110300-015-R10 BT0310 Homo sapiens cDNA
734	15849	26733	2.02	2.0E-56	BE064396.1	EST_HUMAN	RC4-BT0310-110300-015-R10 BT0310 Homo sapiens cDNA
2392	15400	28425	1.22	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (GGPR-A) mRNA, complete cds
2392	15400	28426	1.22	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (GGPR-A) mRNA, complete cds
3001	16059	28978	1.62	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3327	16378		1.71	2.0E-56	AB009891.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3544	16560	29515	1.16	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADS Homo sapiens cDNA clone ABDCFG10 5'
7297	20269	33604	1.24	2.0E-56	5730038	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
981	14032		1.28	1.0E-56	AF160930.1	NT	Musca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3698	16731	29842	2.08	1.0E-56	AW59833.1	EST_HUMAN	hg23ct1.x1 NC1 CGAP G06 Homo sapiens cDNA clone IMAGE:2946452 3'
3698	16731	29843	2.08	1.0E-56	AW59833.1	EST_HUMAN	hg23ct1.x1 NC1 CGAP G06 Homo sapiens cDNA clone IMAGE:2946452 3'
5071	16081	30962	1.22	1.0E-56	AI005162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
6895	20121	33435	0.66	1.0E-56	AV508520.1	EST_HUMAN	MR3-S70203-160100-204-002 ST0203 Homo sapiens cDNA
10316	23239		0.61	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4268	23330	36815	1.82	1.0E-56	AW845967.1	EST_HUMAN	RC2-CT0169-220999-001-E02 CT0163 Homo sapiens cDNA
10406	13691		2.17	9.0E-57	AW80885.1	EST_HUMAN	QV2-OT0033-070300-152-H03 OT0033 Homo sapiens cDNA
11554	24494	38050	1.51	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11554	24494	38051	1.51	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11850	24733	38520	2.23	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
14	13134	28032	1.11	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371). mRNA
287	13391	28318	3.14	8.0E-57	AW810405.1	EST_HUMAN	XQ54D10.41 NCI CGAP Bm33 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
885	13940	26988	0.74	8.0E-57	AW284599.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
1833	14360	27858	2.18	8.0E-57	AA459109.1	EST_HUMAN	z551b72.f1 Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:767151 5'
4848	17982	30952	1.11	8.0E-57	4557830	NT	Homo sapiens glutamate receptor, ionotropic, AMPA 4 (GRIA4) mRNA
5073	18083	30965	1.32	8.0E-57	BE266018.1	EST_HUMAN	6008444407.F1 NIH_VGC_17 Homo sapiens cDNA clone IMAGE:2560864 6'
5312	25949	31435	1.69	8.0E-57	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2). mRNA
5539	19601	32863	0.54	8.0E-57	AB020705.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
6608	19686	32941	12.05	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6908	19686	32942	12.05	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7882	20640	34003	0.71	8.0E-57	7692263	NT	Homo sapiens KIAA0716 gene product (KIAA0716). mRNA
8024	20681	34357	2.69	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8024	20681	34358	2.69	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
10848	23768	37287	0.44	8.0E-57	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5). mRNA
11807	13134	28032	2.8	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371). mRNA
12088	24960	39557	1.67	8.0E-57	11431260	NT	Homo sapiens Ras suppressor protein 1 (RSU1). mRNA
12733	25386	31751	3.29	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1). mRNA
12749	25386	31751	3.39	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1). mRNA
3263	16317	29237	1.09	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7). mRNA
3263	16317	29238	1.09	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7). mRNA
3284	16338	29238	0.65	7.0E-57	8005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8). mRNA
3891	16931	28840	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphotyrosine 4-kinase 230 (p4k230) mRNA, complete cds
3891	16931	28841	2.63	7.0E-57	AF012872.1	NT	Homo sapiens phosphotyrosine 4-kinase 230 (p4k230) mRNA, complete cds
4816	17833	30731	1.03	7.0E-57	U11059.2	NT	Homo sapiens large conductance calcium- and voltage-dependent potassium channel alpha subunit (MaxK) mRNA, complete cds
13075	25984		3.96	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3766	18808	29718	2.12	4.0E-57	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
805	13863	28813	0.93	3.0E-57	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1334	14368		59.49	3.0E-57	AA230279.1	EST_HUMAN	nc1307.51 NCI CGAP P4 Homo sapiens cDNA clone IMAGE:1008037 similar to SW-PS10_HUMAN
2400	15407	28431	0.95	3.0E-57	AA348335.1	EST_HUMAN	EST64770 Hippocampus II Homo sapiens cDNA 5' end

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2714	15708	28724	1.19	3.0E-57	BE676622.1	EST_HUMAN	733b10.x1 NC1_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20293;
2714	15708	28725	1.19	3.0E-57	BE676622.1	EST_HUMAN	733b10.x1 NC1_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20293;
3711	18764		28.47	3.0E-57	AW653964.1	EST_HUMAN	CE20293;
6145	19220	32450	1.37	3.0E-57	11225603	NT	RC3-COT0234-110300-027-410 CT0254 Homo sapiens cDNA
6246	19319	32549	3.49	3.0E-57	BE706537.1	EST_HUMAN	6015580967.1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3644302 5'
8484	21452	34870	2.61	3.0E-57	W28130.1	EST_HUMAN	426 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8510	21478	34891	1.9	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
8510	21478	34892	1.9	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
8524	21592	35011	0.69	3.0E-57	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
8772	21739	35160	0.69	3.0E-57	J05282.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
9210	22178	35608	4.95	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9505	22609	36060	0.7	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
9505	22609	36061	0.7	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11658 (FLJ11658), mRNA
11254	24207	37726	2.98	3.0E-57	AW248374.1	EST_HUMAN	2820473 Sptmne NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12384	25951	31314	7.53	3.0E-57	W23871.1	EST_HUMAN	25-45d11.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
1500	14533	27504	1.05	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1500	14533	27505	1.05	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3452	16498		2.19	2.0E-57	AL163204.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3562	16608	29529	0.65	2.0E-57	R07702.1	EST_HUMAN	yes9h01.r1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:125609 5'
3562	16608	29530	0.65	2.0E-57	R07702.1	EST_HUMAN	yes9h01.r1 Soares_fetal_liver_spleen_1NfLS Homo sapiens cDNA clone IMAGE:125609 5'
3551	16901	29907	0.88	2.0E-57	BE073264.1	EST_HUMAN	MRO-BT0561-060300-103-503 BT0561 Homo sapiens cDNA
4538	17961	30448	6.69	2.0E-57	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C083
5139	18148	31027	1.74	2.0E-57	AL163205.2	NT	Homo sapiens chromosome 21 segment HS21C006
5751	18846		1.67	2.0E-57	AA016131.1	EST_HUMAN	z031.c05.r1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1:13 L1 repetitive element;
6150	19225		32.23	2.0E-57	BF115268.1	EST_HUMAN	16R204.x1 NC1_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.11
6293	19355	32591	0.7	2.0E-57	11431281	NT	16R222 repetitive element;
8878	21944	33368	1.02	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Oxy-Cys), member 22 (SCYA22), mRNA
10205	23130	36617	1.63	2.0E-57	AF057722.1	NT	Homo sapiens cell-line KGT transcriptional regulatory protein p54 mRNA, complete cds
11601	24539	36987	1.88	2.0E-57	11424084	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11601	24539	36988	1.88	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11601	24539	36989	1.88	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11642	24579	38145	1.74	2.0E-57	AJ245503.1	NT	Homo sapiens perlecan mRNA for PEX5 related protein
11642	24579	38146	1.74	2.0E-57	AJ245503.1	NT	Homo sapiens perlecan mRNA for PEX5 related protein
2240	16264	28278	1.49	1.0E-57	AW503208.1	EST_HUMAN	UHF-BNO-alk-g-07-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
9041	22007		4.47	1.0E-57	BE043031.1	EST_HUMAN	h332603.x1 NCL CGAP_Luz24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246
12537	25261		3.65	1.0E-57	AW470791.1	EST_HUMAN	h333006.x1 NCL CGAP_Kir12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
5760	18853	32033	1.01	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12705	25424	31738	2.37	8.0E-58	BE395061.1	EST_HUMAN	601309495F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
591	13658		2.43	8.0E-58	BE868715.1	EST_HUMAN	601445048F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
655	13721	26644	2.84	8.0E-58	AI798376.1	EST_HUMAN	U34507.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
655	13721	26645	2.84	8.0E-58	AI798376.1	EST_HUMAN	U34507.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1874	14899	27897	1.98	8.0E-58	11434821	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1874	14899	27898	1.98	8.0E-58	11434821	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2987	16045		2.65	8.0E-58	7706132	NT	Homo sapiens DHHCT protein (LOC61304), mRNA
7449	20415	33769	0.95	7.0E-58	BE561071.1	EST_HUMAN	601348704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
11203	24157		4.99	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
11275	24227	37753	2.79	7.0E-58	AW504109.1	EST_HUMAN	UHF-BNO-alk-g-10-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078987 5'
11275	24227	37754	2.79	7.0E-58	AW504109.1	EST_HUMAN	UHF-BNO-alk-g-10-Q-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078987 5'
2395	15393	28419	4.05	6.0E-58	AI30689.1	EST_HUMAN	AU130689 NT2R23 Homo sapiens cDNA clone NT2R3001263 5'
2912	15970	28893	1.62	6.0E-58	BE242150.1	EST_HUMAN	TCAAPE1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylar-HQSC project=TCAA Homo sapiens cDNA clone TCAAP-1219
2912	15970	28894	1.62	6.0E-58	BE242150.1	EST_HUMAN	TCAAPE1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylar-HQSC project=TCAA Homo sapiens cDNA clone TCAAP-1219
6294	16386	32605	1.18	6.0E-58	AF105911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10672	23694	37091	1.02	6.0E-58	11434748	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12629	25316		1.41	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
300	13394	26321	4.35	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
711	13773	28707	7.63	5.0E-58	BE763984.1	EST_HUMAN	RCA-NT0057-160600-018-005 NT0057 Homo sapiens cDNA
1199	14239	27195	3.77	5.0E-58	AW797948.1	EST_HUMAN	GM8-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1199	14239	27196	3.77	5.0E-58	AW797948.1	EST_HUMAN	GM8-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1200	14238	27195	3.1	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-a07 UM0043 Homo sapiens cDNA
1200	14239	27196	3.1	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-a07 UM0043 Homo sapiens cDNA
3334	16355	29305	3.85	5.0E-58	AA988183.1	EST_HUMAN	089607.at NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1603508.3
4287	17346	30185	0.95	5.0E-58	AG59745.1	EST_HUMAN	089607.at NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2238468.3 similar to SW-PRO2_ACACA
5710	18804		2.2	5.0E-58	11486282	NT	P19984 PROFILIN II;
8302	19373	32612	5.97	5.0E-58	H23072.1	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAG1), mRNA
6534	19557	32660	0.94	5.0E-58	AL160285.2	NT	Ym511007.7 Scores infant brain N1B Homo sapiens cDNA clone IMAGE:52071.5
6915	19873	32951	1.16	5.0E-58	11421330	NT	Homo sapiens epical protein, Xenopus laevis-like (APXL), mRNA
6945	20169	33482	0.7	5.0E-58	AF051334.1	NT	Homo sapiens ribin (NBS) mRNA, complete cds
6945	20169	33483	0.7	5.0E-58	AF051334.1	NT	Homo sapiens ribin (NBS) mRNA, complete cds
7313	20284	33625	0.8	5.0E-58	4885400	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCOS) mRNA
8302	21271	34693	7.52	5.0E-58	8922693	NT	Homo sapiens hypoblast protein FLJ10826 (FLJ10826), mRNA
8936	21664	35098	0.76	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9955	22648	36103	1.34	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6P) mRNA
9955	22648	36104	1.34	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNASE6P) mRNA
10216	23141	36629	1.01	5.0E-58	11430547	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA
10482	23404	36901	1.86	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10766	23687	37183	0.51	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10766	23687	37184	0.51	5.0E-58	AB014511.1	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12352	25878		2.17	5.0E-58	11822383	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
12781	25904		1.48	5.0E-58	11428423	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
13015	25665		2.08	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
373	13459	26388	1.85	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
797	13856	26803	1.42	4.0E-58	4504634	NT	Homo sapiens interferin 10 receptor, beta (IL-10RB), mRNA
1484	14487	27471	1.14	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA
2639	15638	28661	2.02	4.0E-58	U36251.1	NT	Human beta-prime-adeptin (BAN22) gene, exon 3
3336	16387	28308	1.11	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3753	16795	29708	1.02	4.0E-58	6031690	NT	Human EGF-like repeats and discoidin-like domains 3 (EDL3), mRNA
8120	21057	34454	0.69	4.0E-58	BE463857.1	EST_HUMAN	hy18602.XT NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:3197842.3
11671	24607	38184	7.52	4.0E-58	11424059	NT	Homo sapiens E1B-65kDa-associated protein 5 (E1B-AP5), mRNA
335	13424		0.84	3.0E-58	R17879.1	EST_HUMAN	y510a2.1 Scores infant brain N1B Homo sapiens cDNA clone IMAGE:31693.5

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1390	14424	27393	2.32	3.0E-58	4768981	NT	Homo sapiens peptide YY (PYY) mRNA
3193	19248	29165	2.57	3.0E-58	BF59848.1	EST_HUMAN	602185786FT NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4306943 5'
3193	19248	29166	2.57	3.0E-58	BF59848.1	EST_HUMAN	602185786FT NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4306943 5'
6300	19458	32703	0.61	3.0E-58	BE089509.1	EST_HUMAN	CV0-810702-170400-194-03 B10702 Homo sapiens cDNA
6597	19947	32916	0.79	3.0E-58	F07056.1	EST_HUMAN	RSC11 G861 normalized infant brain cDNA Homo sapiens cDNA clone c-11p08
6767	19851	33136	3.92	3.0E-58	AV712677.1	EST_HUMAN	AV712677 DCA Homo sapiens cDNA clone DCAAZG04 5'
6930	13902	26944	8.85	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
							ba08007.1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X61987.1 Mus musculus mRNA for TAA responsive element binding protein (MOUSE);
1294	14329		8.41	2.0E-58	BE208632.1	EST_HUMAN	ba08009.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2867704 3'
8409	16512	31390	0.76	2.0E-58	AW074831.1	EST_HUMAN	60149996FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 5'
5431	25938	31413	3.25	2.0E-58	BE907188.1	EST_HUMAN	60149996FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 5'
5431	25938	31441	3.25	2.0E-58	BE907188.1	EST_HUMAN	60149996FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901811 5'
8175	19250	32463	1.09	2.0E-58	BF510488.1	EST_HUMAN	UH-BW1-ams-g-T1-QJ1.81 NCI_CGAP_Su67 Homo sapiens cDNA clone IMAGE:3071060 3'
							am57602.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE06065 UBIQUITIN CONJUGATING ENZYME, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6244	19317	32547	1.85	2.0E-58	AI124874.1	EST_HUMAN	ba08006.1 Soares fetal liver spleen TNF.L5 Homo sapiens cDNA clone IMAGE:199379 5'
9278	19350	32894	0.83	2.0E-58	R92587.1	EST_HUMAN	ba08006.1 Soares fetal liver spleen TNF.L5 Homo sapiens cDNA clone IMAGE:199379 5'
7112	20046	33348	0.83	2.0E-58	AI291407.1	EST_HUMAN	gm84601.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1856424 3'
7394	20334	33983	2.98	2.0E-58	AF134836.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7394	20334	33984	2.98	2.0E-58	AF134836.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
11093	24033	37476	18.24	2.0E-58	BF307445.1	EST_HUMAN	601800812FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131897 5'
11312	24262	37768	1.48	2.0E-58	AW872644.1	EST_HUMAN	hm2508.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
723	13785	26719	0.88	1.0E-58	M65134.1	NT	Human complement component C3 mRNA, 3' end
							Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (23kD, B22) (NDUFB9), mRNA
1089	14114	27064	5.86	1.0E-58	6274549	NT	EST1369282 MAGE resources, MAGED Homo sapiens cDNA
1330	14365	27333	2.03	1.0E-58	AW957182.1	EST_HUMAN	EST1369282 MAGE resources, MAGED Homo sapiens cDNA
1330	14365	27334	2.03	1.0E-58	AW957182.1	EST_HUMAN	EST1369282 MAGE resources, MAGED Homo sapiens cDNA
1397	14431	27400	0.98	1.0E-58	AJ230603.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and A10 repeat elements
1672	14704	27651	0.95	1.0E-58	BE466132.1	EST_HUMAN	hy01008.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3196933 3'
2914	15806	28625	1.21	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
3548	16594	29520	1.19	1.0E-58	4759061	NT	Homo sapiens chondroin sulfate proteoglycan 2 (versican) [CSPG2] mRNA
3548	16594	29521	1.19	1.0E-58	4759061	NT	Homo sapiens chondroin sulfate proteoglycan 2 (versican) [CSPG2] mRNA
3733	16775	29887	0.7	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPI) mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5008	18020	30909	5.17	1.0E-58	AI141063.1	EST_HUMAN	oz4301.x1 Soares_NHMP-Pu_S1 Homo sapiens cDNA clone IMAGE:1878128 3'
5941	18027	32221	1.18	1.0E-58	BE01880.1	EST_HUMAN	RC1-18T0254-280100-075-40T BT0254 Homo sapiens cDNA
7046	20058	33374	0.64	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
8451	21420		0.5	1.0E-58	AW1973537.1	EST_HUMAN	EST306537 MAGE resequences, MAGE Homo sapiens cDNA
9221	22187	35819	0.59	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (1650) (MYOM2), mRNA
9333	22268	35727	0.84	1.0E-58	AV761001.1	EST_HUMAN	AV761001 NPC Homo sapiens cDNA clone NPCACH08 5'
9436	22400	35937	0.95	1.0E-58	AA412397.1	EST_HUMAN	259305.x1 Soares_Teslis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9436	22400	35938	0.55	1.0E-58	AA412397.1	EST_HUMAN	259305.x1 Soares_Teslis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10548	23468	36953	0.68	1.0E-58	11432984	NT	Homo sapiens discal, large (Discophila) homolog 2 (chapsyn-110) (DLG2), mRNA
12059	24942		2.61	1.0E-58	X63382.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2238	15252	28278	21.09	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
7016	20141	33463	0.71	8.0E-59	AA382291.1	EST_HUMAN	EST186583 Testis 1 Homo sapiens cDNA 5' end
7015	20141	33459	0.71	8.0E-59	AA382291.1	EST_HUMAN	EST186583 Testis 1 Homo sapiens cDNA 5' end
8521	21489	34904	3.74	8.0E-59	AT01865.1	EST_HUMAN	WHS006.x1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2384171 3'
179	16834		3.9	8.0E-59	BF035327.1	EST_HUMAN	63148633T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3602088 5'
							63148633T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3602088 5'
							SA GENE PRODUCT PRECURSOR ;
8151	21089	34489	1.64	6.0E-59	AA982431.1	EST_HUMAN	cn06102.y1 Normal Human, Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06102 random
8588	21658	34972	0.56	6.0E-59	AT760970.1	EST_HUMAN	au33045.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
1788	14787	27782	1.19	5.0E-59	AW157281.1	EST_HUMAN	TR-O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1. ;
1788	14787	27783	1.19	5.0E-59	AW157281.1	EST_HUMAN	au33045.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
3144	16201	28112	7.03	5.0E-59	AB07484.1	EST_HUMAN	TR-O75786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1. ;
4687	17708	30601	7.38	5.0E-59	X83497.1	NT	x48411.x1 Soares_NFL_T_CBG_S1 Homo sapiens cDNA clone IMAGE:2345836 3'
5796	18888	32070	0.58	6.0E-59	6005598	NT	H. sapiens DNA for ZNF60-linked ERV9 long terminal repeat
							Homo sapiens axadin 2 related protein (A2LP), mRNA
7182	18413	31215	7.97	5.0E-59	AW162304.1	EST_HUMAN	element TAR1 repetitive element ;
9158	22124	35553	0.56	5.0E-59	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (350D) (RPC39), mRNA
10093	22890	38459	1.94	5.0E-59	AV762869.1	EST_HUMAN	AV762869 MOS Homo sapiens cDNA clone MDSEIC12 5'
11253	24206	37728	3.1	5.0E-59	11434908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
784	13853	26801	3.22	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
							Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1242	14278	27239	0.75	4.0E-59	4505818	NT	

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1242	14278	27240	0.75	4.0E-59	4503818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5615	18711	31869	1.04	4.0E-59	11034810	NT	Homo sapiens calenlin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12107	24977	38578	1.5	4.0E-59	7657426	NT	Homo sapiens origin recognition complex, subunit 8 (yeast homolog)-like (ORC6L), mRNA
12492	25910		2.98	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13130		6.8	3.0E-59	AW66524.1	EST_HUMAN	EST1377582 IMAGE, resequences, VAGI Homo sapiens cDNA
228	13327	26250	4.47	3.0E-59	7662247	NT	Homo sapiens KIAA0980 gene product (KIAA0980), mRNA
1723	14753	27738	11.42	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLAT), mRNA
1723	14753	27738	11.42	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLAT), mRNA
2139	15159	28171	6.05	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2139	15159	28172	6.05	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3146	16203	29116	2.91	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3146	16203	29117	2.91	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3333	16878	29781	1.26	3.0E-59	4505044	NT	Homo sapiens zona pellucida glycoprotein 2 (sparm receptor) (ZP2), mRNA
4712	17732	30626	1.4	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4878	17895	30785	1.66	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5091	18101		1.05	3.0E-59	M65981.1	NT	Homo sapiens chromosome 21 segment HS21C084
6348	19415	32658	1.68	3.0E-59	8024074	NT	Human probomona converting enzyme (NEC2) gene, exon 2
7684	20646	33008	2.12	3.0E-59	5454137	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
8293	21292	34642	1.5	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
8293	21292	34643	1.5	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
10404	23328	36809	0.84	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10404	23328	36810	0.84	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12470	25219		1.37	3.0E-59	11417868	NT	H. sapiens gamma-glutamyltransferase-like activity 1 (GGTLAT), mRNA
12612	25311		7.97	3.0E-59	11417868	NT	H. sapiens gamma-glutamyltransferase-like activity 1 (GGTLAT), mRNA
5995	19070	32268	0.82	2.0E-59	BF503933.1	EST_HUMAN	U1-H-B1-ayp-b-02-QJ1 st NCI CGAP Subd Homo sapiens cDNA clone IMAGE:308522 3'
5995	19070	32269	0.82	2.0E-59	BF503933.1	EST_HUMAN	U1-H-B1-ayp-b-02-QJ1 st NCI CGAP Subd Homo sapiens cDNA clone IMAGE:308522 3'
6979	20022		0.61	2.0E-59	AA470073.1	EST_HUMAN	28B05 st Soares, Leslie, NHT Homo sapiens cDNA clone IMAGE:730377 3'
7272	20007	33307	0.57	2.0E-59	AF135187.1	NT	Human interferon-induced protein p78 (MX1) gene, complete cds
8025	21019		0.52	2.0E-59	BF373329.1	EST_HUMAN	MRO-F10144-280700-002-at10 F10144 Homo sapiens cDNA
6995	22922		4.8	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10893	23813		1.55	2.0E-59	BF385554.1	EST_HUMAN	RC0-NT0036-100700-032-407 NT0036 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
11180	24136	37667	2.34	2.0E-59	AW410898.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2951654 5'	
11180	24136	37668	2.34	2.0E-59	AW410898.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2951654 6'	
12373	26158	31857	6.06	2.0E-59	A6931809.1	EST_HUMAN	w865612.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR.Q86542	
12694	26836	31426	4.02	2.0E-59	L11645.1	EST_HUMAN	Q86542 RTVL-H-PROTEIN, contains LTR7 b1 LTR7 repetitive element;	
184	13267		18.92	1.0E-59	BE26841.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds	
2625	16824		3.89	1.0E-59	AA748488.1	EST_HUMAN	h0117875FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:33531927 5'	
7812	20761	34137	1.18	1.0E-59	AJ130894.1	NT	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;	
7896	20925	34319	1.07	1.0E-59	BE26814.1	EST_HUMAN	Homo sapiens mRNA for transcription factor	
7896	20925	34320	1.07	1.0E-59	BE26814.1	EST_HUMAN	h011105FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352692 5'	
9740	22768	36222	0.85	1.0E-59	11419830	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA	
9953	22880	36351	0.84	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	
9953	22880	36362	0.84	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA	
11201	20761	34137	0.85	1.0E-59	AJ130894.1	EST_HUMAN	EST386849 MAGE resequences, MAGEO Homo sapiens cDNA	
1487	14500	27474	2.85	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18KD) (SNRPD3) mRNA	
2182	15197	28217	2.65	8.0E-60	5174556	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA	
2182	15197	28218	2.65	8.0E-60	5174556	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA	
6094	19173	32389	0.94	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds	
6653	19710	32987	1.01	8.0E-60	S93182.1	NT	hyaluronan-binding protein=heparocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	
7692	20903	34265	0.89	8.0E-60	11420841	NT	Homo sapiens phosphatase cytidylate transferase 1, choline, beta isoenzyme [PCYT1B], mRNA	
8298	21267	34679	2.37	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit	
9291	22267	35687	2.68	8.0E-60	11428849	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA	
9826	22675	36130	1.2	8.0E-60	-	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9826	22675	36131	1.2	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA	
10638	23858	37373	0.68	8.0E-60	5453697	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA	
11182	24138	37670	4.65	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
11182	24138	37671	4.65	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
755	13816	26760	30.34	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region	
758	13816	26760	69.13	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region	
816	13874	28822	1.17	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA	
2193	15195	28170	1.04	7.0E-60	AF07188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds	



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2766	15788	28906	1.18	7.0E-60	AB011163.1	NT	Homo sapiens mRNA for KIA00687 protein, partial cds
4208	17237	30124	3.1	7.0E-60	4505498	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4608	17627	30519	0.72	7.0E-60	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9782	22703	36161	3.89	7.0E-60	H58041.1	EST_HUMAN	Y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR3 repetitive element ;
11692	24697	38235	1.57	7.0E-60	H58041.1	EST_HUMAN	Y1204.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR6 repetitive element ;
2189	15204	28224	1.01	6.0E-60	BE984974.2	EST_HUMAN	601658/51RT NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3890059 3'
8156	21094	34493	0.68	8.0E-60	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS1681.15.1), mRNA
8780	21747		8.33	8.0E-60	H52456.1	EST_HUMAN	Y17806.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201653 5' similar to contains ORF repetitive element ;
84	13200	26123	1.13	5.0E-60	AI807817.1	EST_HUMAN	W62607.XT Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
84	13200	26124	1.13	5.0E-60	AI807817.1	EST_HUMAN	W62607.XT Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2244	15288	28284	1.25	4.0E-60	AW503208.1	EST_HUMAN	U1HF-BNO-akt-a-07-0-J11 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078348 5'
2244	15288	28285	1.25	4.0E-60	AW503208.1	EST_HUMAN	U1HF-BNO-akt-a-07-0-J11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2984	19042		1.31	4.0E-60	AA209037.1	EST_HUMAN	EST11468 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7576	20538	33597	0.81	4.0E-60	BF190088.1	EST_HUMAN	h81105.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134813 3' similar to SWRHOP_MOUSE
9482	22446		0.59	4.0E-60	AI153278.2	NT	Homo sapiens chromosome 21, segment HS21C078
11628	24568	38127	1.7	4.0E-60	11433597	NT	Homo sapiens vraf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
11628	24568	38128	1.7	4.0E-60	11433597	NT	Homo sapiens vraf-1 murine leukemia viral oncogene homolog 1 (RAF1), mRNA
1876	14601	27900	4.44	3.0E-60	BE562811.1	EST_HUMAN	6013364/46FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1876	14601	27901	4.44	3.0E-60	BE562811.1	EST_HUMAN	6013364/46FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1685	14970		1.88	3.0E-60	6031180	NT	Homo sapiens prolidase (PHE) mRNA
4465	17570	30398	2.27	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5452	18554	31465	2.11	3.0E-60	BF365143.1	EST_HUMAN	QV44-NN114b-250000-423-101 NN1149 Homo sapiens cDNA
5724	18818	31997	2.11	3.0E-60	AW836195.1	EST_HUMAN	RC3-L10023-200100-012-a01 L70023 Homo sapiens cDNA
7143	18375	31263	0.95	3.0E-60	AI792814.1	EST_HUMAN	460H1.15 NCI CGAP_K43 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8745	21713	35135	5.22	3.0E-60	5174644	NT	P52624 URIDINE PHOSPHORYLASE ;
8745	21713	35136	5.22	3.0E-60	5174644	NT	Homo sapiens prolase dehydrogenase (proline addase) (PRODH) mRNA
8930	21806	35324	0.68	3.0E-60	AI040235.1	EST_HUMAN	ox56009.XT Soares_NHMPU_S11 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE_Q05960 FORMIN ;
9094	22000	35465	4.2	3.0E-60	5174644	NT	Homo sapiens prolase dehydrogenase (proline addase) (PRODH) mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10017	22944	38411	0.42	3.0E-60	BF102612.1	EST_HUMAN	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3830990 5'
12870	28971		1.53	3.0E-60	AA485286.1	EST_HUMAN	ab07804.r1 Stragelene lung (#637210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR1041 LTR10 repetitive element
33	13153	28054	1.7	2.0E-60	AY008235.1	NT	Homo sapiens scute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1421	14454	27428	2.76	2.0E-60	Z11694.1	NT	H sapiens 4102a protein kinase related to rat ERK2
1734	14764	2747	1.34	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
1743	14773	27758	1.01	2.0E-60	AY008285.1	NT	Homo sapiens scute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2492	15495	28520	1.76	2.0E-60	AW380450.1	EST_HUMAN	RC1-1170268-03/289-012-02 HT0268 Homo sapiens cDNA
2814	15812	28637	1.38	2.0E-60	7657228	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
2721	15715	28733	0.84	2.0E-60	AW978005.1	EST_HUMAN	EST380114 MAGE resequences, MAGE Homo sapiens cDNA
3652	16637	28657	1.49	2.0E-60	4757867	NT	Homo sapiens v-rif murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3935	16975	29889	0.83	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4151	17182		0.65	2.0E-60	BF513455.1	EST_HUMAN	U1H-BW1-ams-e-05-0-U1.s1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
6433	19499	32752	0.9	2.0E-60	AF191952.1	EST_HUMAN	nr01121.25 NCJ_CGAP_C08 Homo sapiens cDNA clone IMAGE:1078495 5' similar to contains THRL1 THR repetitive element
6840	19598	32974	1.49	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6874	19927	33224	0.82	2.0E-60	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
7027	18359	31279	2.05	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7027	18359	31280	2.05	2.0E-60	4603044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7317	20288	33630	6.6	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7317	20288	33631	6.6	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7434	20401	33755	0.93	2.0E-60	AI08124.1	EST_HUMAN	162400.x1 NCJ_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055185 3' similar to SW:GALR, RAT
7894	20837		1.06	2.0E-60	BF512808.1	EST_HUMAN	Q62806 GALANIN RECEPTOR
8338	21307	34722	1.06	2.0E-60	XB5597.1	EST_HUMAN	U1H-BW1-ams-e-02-0-U1.s1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
9219	22185	35618	4.86	2.0E-60	L36033.1	NT	H5165EST human adult testis Homo sapiens cDNA clone CAM_1EST15
10337	23281	36740	2.2	2.0E-60	11991659	NT	Human pro-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10337	23281	36741	2.2	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
12094	24955	38561	1.9	2.0E-60	AW751181.1	EST_HUMAN	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
12094	24955	38562	1.9	2.0E-60	AW751181.1	EST_HUMAN	CM0-CT0013-260569-017-03 CT0013 Homo sapiens cDNA
12094	24955	38562	1.9	2.0E-60	AW751181.1	EST_HUMAN	CM0-CT0013-260569-017-03 CT0013 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12647	25330		1.38	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12771	25900		1.82	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12773	25411		5.64		11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
12789	25421		2.38	2.0E-60	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
523	13564	26512	0.87	1.0E-60	BE178588.1	EST_HUMAN	PMO-110605-27020-001-c08 H1065 Homo sapiens cDNA
3920	16960	29573	1.46	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AAT1 Homo sapiens cDNA clone Y79AAT1007854 5'
4993	18008	30899	1.34	1.0E-60	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8280	21249	34861	0.88	1.0E-60	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011008 BT0311 Homo sapiens cDNA
9108	22074		3.08	1.0E-60	AA244041.1	EST_HUMAN	nc04612.11 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.1 L1
9134	27100	35526	1.38	1.0E-60	AV754081.1	EST_HUMAN	repetitive element;
1101	14145	27095	1.85	9.0E-61	AU119344.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED06 5'
8061	22027	35450	0.48	9.0E-61	4885546	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
8061	22027	35451	0.49	9.0E-61	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2878	15874	28594	1.17	8.0E-61	AW006478.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2878	15874	28595	1.17	8.0E-61	AW006478.1	EST_HUMAN	w08510.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2505555 3'
2882	16020		1.86	8.0E-61	X57147.1	NT	w08510.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2505555 3'
8227	21195	34804	0.73	8.0E-61	AA583968.1	EST_HUMAN	Human endogenous retrovirus pH-E.1 (ERV6)
11826	24807	38400	1.47	8.0E-61	H71225.1	EST_HUMAN	ms8906.at NCL_CGAP_Lart1 Homo sapiens cDNA clone IMAGE:1088218 3'
11826	24807	38401	1.47	8.0E-61	H71225.1	EST_HUMAN	ys12609.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:214600 5' similar to
128	13234	26163	0.67	7.0E-61	7706970	NT	SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
128	13234	26164	0.67	7.0E-61	7706970	NT	SP-C40H1.1 CE00109 OVARIAN PROTEIN ;
285	13361	26285	2.81	6.0E-61	BE409310.1	EST_HUMAN	Homo sapiens PXR2b protein (PXR2b), mRNA
812	13870	26919	2.17	6.0E-61	BE409310.1	EST_HUMAN	Homo sapiens PXR2b protein (PXR2b), mRNA
1324	14359	27328	13.5	6.0E-61	AF119880.1	NT	601300538F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1634	14636	27642	0.9	6.0E-61	BE257400.1	EST_HUMAN	601300538F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1655	14687	27652	2.32	6.0E-61	AA586033.1	EST_HUMAN	Homo sapiens PR02014 mRNA, complete cds
2137	15154	28169	0.91	6.0E-61	AY008285.1	NT	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
3317	16370	29290	8.07	6.0E-61	AU130689.1	EST_HUMAN	ms66109.st NCL_CGAP_Lart1 Homo sapiens cDNA clone IMAGE:1088897 3'
8147	19222	32452	3.08	6.0E-61	Y79248.1	NT	Homo sapiens solute carrier (SLC25A18), mRNA, complete cds; nuclear gene for mitochondrial product
7655	20528	33687	1.93	6.0E-61	U24498.1	NT	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
							ig-beta/CD7b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
							Human subcutaneous dominant polycystic kidney disease protein 1 (PKD1) gene

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Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7878	20822	34186	1.87	6.0E-61	AF037373.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds
221	13321	26246	1.14	5.0E-61	8922990	NT	Homo sapiens hypodermal protein FLJ11316 (FLJ11316), mRNA
221	13321	26247	1.14	5.0E-61	8922990	NT	Homo sapiens hypodermal protein FLJ11316 (FLJ11316), mRNA
1688	14719	27699	3.18	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3049	16106	28020	1.96	5.0E-61	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
4005	17045		1.87	5.0E-61	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
1774	14803	27768	1.17	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLACE200302.5'
5813	18860	32100	0.51	4.0E-61	7681637	EST_HUMAN	Homo sapiens DKFZP668B023 protein (DKFZP668B023), mRNA
12349	25143		2.27	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801.5'
8764	21731	35154	0.65	3.0E-61	AF150180.1	EST_HUMAN	AF150180 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAG804
469	13571	26493	1.74	2.0E-61	8922829	NT	Homo sapiens hypodermal protein FLJ11028 (FLJ11028), mRNA
1217	14255	27213	3.4	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1217	14255	27214	3.4	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1674	14706	27694	1.34	2.0E-61	N63039.1	EST_HUMAN	Y558T11.s1 Soares fetal liver spleen TNF $\alpha$ Homo sapiens cDNA clone IMAGE:246453 3' similar to
2849	15646		1.25	2.0E-61	N30397.1	EST_HUMAN	gbl.284444 603 RIBOSOMAL PROTEIN L35A (HUMAN);
6568	18626	32891	0.92	2.0E-61	11426166	NT	Y03111.1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270189 5'
9369	22334	35765	1.07	2.0E-61	AV694317.1	EST_HUMAN	Homo sapiens ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein
9820	22347		1.27	2.0E-61	AB011108.1	NT	1A (11011802) (ATP8A1A), mRNA
10282	22707	36992	1.61	2.0E-61	AW500256.1	EST_HUMAN	AV694317 GRG Homo sapiens cDNA clone GKCELO05 5'
10812	23534	37031	2.38	2.0E-61	11421778	NT	Homo sapiens mRNA for KIAA0593 protein, partial cds
11230	24183		6.91	2.0E-61	11419729	NT	UI-HF-BNO-akd-12-0-U1.7 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3076774 5'
13042	25593	31701	1.39	2.0E-61	AW995328.1	EST_HUMAN	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
435	13509		1.65	1.0E-61	AL163203.2	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
774	13533	26779	0.98	1.0E-61	5453929	NT	QV0-BNO042-170300-162-110 BNO042 Homo sapiens cDNA
1764	14813		0.95	1.0E-61	U32657.1	NT	Homo sapiens chromosome 21 segment HS21C003
1675	14900	27699	4.99	1.0E-61	6055863	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog-like) (ORC2L) mRNA
2206	15221	28241	1.52	1.0E-61	AW827281.1	EST_HUMAN	Human polymorphic pellucidolipide repeat in X-linked retinitis pigmentosa (RP3) gene region
2846	15506	28831	1.58	1.0E-61	BE398363.1	EST_HUMAN	Homo sapiens zeta pellucidolipide glycoprotein 3A (sperm receptor) (ZF3A), mRNA
3387	16436	29353	0.87	1.0E-61	7692319	NT	Homo sapiens zeta pellucidolipide glycoprotein 3A (sperm receptor) (ZF3A), mRNA
4268	17317	30196	1	1.0E-61	M68840.1	NT	Human monomannine oxidase A (MAOA) mRNA, complete cds
4468	17484	30381	1.02	1.0E-61	4769249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4468	17494	30382	1.02	1.0E-61	4756246	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4893	17910	30799	9.18	1.0E-61	AW28181.1	EST_HUMAN	U1-H-BWO-ajb-b-08-Q-U1 st NCI CGAP SJ08 Homo sapiens cDNA clone IMAGE:2732871 3'
4893	17910	30800	9.18	1.0E-61	AW28181.1	EST_HUMAN	U1-H-BWO-ajb-b-08-Q-U1 st NCI CGAP SJ08 Homo sapiens cDNA clone IMAGE:2732871 3'
4971	17988	30876	0.94	1.0E-61	7705898	NT	Homo sapiens flavohemoglobin B5+HSR (LOC51187), mRNA
4971	17988	30877	0.94	1.0E-61	7705898	NT	Homo sapiens flavohemoglobin B5+HSR (LOC51187), mRNA
5471	17859	31479	0.88	1.0E-61	M76423.1	NT	H. sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5773	18885	32046	0.72	1.0E-61	7662303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6884	19069	32287	1.02	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7085	20019	33321	7.83	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
7298	20270	33605	0.95	1.0E-61	4756171	NT	Homo sapiens SC35-interacting protein 1 (GRRP128), mRNA
7397	20365	33717	1.59	1.0E-61	8823130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7397	20365	33718	1.58	1.0E-61	8823130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8471	21440	34658	4.16	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8556	21624	35044	3.41	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9837	22581		2.94	1.0E-61	AW999726.1	EST_HUMAN	MRO-BN0070-0-00-00-010-H01 BN0070 Homo sapiens cDNA
9712	22965	36122	0.99	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10359	23311	36760	5.56	1.0E-61	11426822	NT	Homo sapiens KIAA0871 protein (KIAA0871), mRNA
10598	23584	37488	3.38	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11651	24597		3.58	1.0E-61	BE439409.1	EST_HUMAN	HTM1-025F1 HTMT Homo sapiens cDNA
12283	25846	31433	4.15	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12283	25846	31434	4.15	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12652	25335	31761	23.14	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chrt) variable region (subgroup V kappa I)
12842	25521	31711	10.09	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10722	23644	37137	2.13	9.0E-62	BE064388.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
4681	17503	30500	1.04	8.0E-62	AA930420.1	EST_HUMAN	ce56h11.st NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVVK
1109	14153	27103	1.8	7.0E-62	AV1714334.1	EST_HUMAN	P31795 POL POLYPROTEIN;
3517	16663	29488	0.7	7.0E-62	P17480	SWISSPROT	AV1714334 DGB Homo sapiens cDNA clone DGBAMA08.5'
6023	19106	32309	1.73	7.0E-62	11427965	NT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-60)
11878	24844	38221	9.39	7.0E-62	AI208681.1	EST_HUMAN	qp58a04.x1 Soares, Iestis, NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TRC018103
3012	16070		1.49	6.0E-62	U09410.1	NT	O18103 HYPOTHETICAL 27.3 KD PROTEIN, ; Human zinc finger protein ZNF131 mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3395	16444		4.9	6.0E-62	11418255	NT	Homo sapiens CGI-58 protein (CGI-58), mRNA
7887	20831	34209	3.27	6.0E-62	AT762801.1	EST_HUMAN	w04402.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
7887	20831	34210	3.27	6.0E-62	AT762801.1	EST_HUMAN	w04402.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8422	21391		0.72	6.0E-62	AW501124.1	EST_HUMAN	U1HF-BPop-til-4-9-9-4-J11 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8600	21588	34984	1.4	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9709	22662	38118	4.02	6.0E-62	AW1814393.1	EST_HUMAN	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
416	13489	28424	2.28	5.0E-62	AB50528.1	EST_HUMAN	w05167.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
2416	15423	28448	3.61	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2416	15423	28447	3.61	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2596	15597	28815	1.43	5.0E-62	U39487.1	NT	Homo sapiens xanthine dehydrogenase oxidase mRNA, complete cds
2596	15597	28816	1.43	5.0E-62	U39487.1	NT	Homo sapiens xanthine dehydrogenase oxidase mRNA, complete cds
3430	16478	28937	2.06	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
4355	17382	30284	1.91	5.0E-62	AA431083.1	EST_HUMAN	2v78000.s1 Scarae3 testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDQ_FAT
4689	17611		1.1	6.0E-62	AW905897.1	EST_HUMAN	P47243 NARDILysin ;
8894	21860	35283	0.64	5.0E-62	4506758	NT	RC5-NN1085-100500-021-H03 NN1088 Homo sapiens cDNA
9875	22828	36282	8.13	5.0E-62	AW410687.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
11586	24534	38090	2.18	5.0E-62	11425574	NT	R07609.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981616 5'
11586	24534	38091	2.18	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (MS), mRNA
841	13888	26953	2.29	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (MS), mRNA
841	13888	26954	2.29	4.0E-62	AW161479.1	EST_HUMAN	sa171003.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
842	13898	26953	1.27	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
842	13898	26954	1.27	4.0E-62	AW161479.1	EST_HUMAN	sa171003.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
1459	14491		1	4.0E-62	AA311281.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2464	15468	28491	2.85	4.0E-62	AB27800.1	EST_HUMAN	sa171003.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2464	15468	28492	2.85	4.0E-62	AB27800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3410	16459		6.48	4.0E-62	4507887	NT	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end
							wf12008.x1 Scarae3_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X37138.mat HISTONE H2B.2 (HUMAN);
							wf12008.x1 Scarae3_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
							gb:X37138.mat HISTONE H2B.2 (HUMAN);
							Homo sapiens keratin 18 (KRT18), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6032	19115	32318	1.63	4.0E-62	4509978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC19A2) mRNA
6429	19495	32748	2.53	4.0E-62	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7377	20347	33989	2.08	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
7896	20839	34219	2.59	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7896	20839	34220	2.59	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
8511	21478	34893	0.93	4.0E-62	11429973	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
9189	22164	35594	5.95	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
11353	24303	37830	3.05	4.0E-62	Z78786.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11353	24303	37831	3.05	4.0E-62	Z78786.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
11598	24536	38083	1.57	4.0E-62	AW023559.1	EST_HUMAN	diff5g04.yt Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487761 5'
12267	25090	39176	3.39	4.0E-62	11418038	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12491	25803		1.3	4.0E-62	11418182	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12871	25953	31709	1.96	4.0E-62	11418322	NT	Homo sapiens cathepin EGF LAG seven-pass C-type receptor 1 (CELST1), mRNA
12924	25950	31703	19.77	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12924	25950	31704	19.77	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12977	25542	31717	3.07	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13182	26114	0.68	3.0E-62	4557794	NT	Homo sapiens neurofascin 2 (bilateral acoustic neuroma) (NF2), mRNA
3059	16116	29239	1.02	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3059	16116	29030	1.02	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3712	18765	29669	3.52	3.0E-62	XG2858.1	NT	Human cyclophilin-related processed pseudogene
8985	21851	35272	4.65	3.0E-62	AI632733.1	EST_HUMAN	w633104.x1 NCI CGAP, Kd11 Homo sapiens cDNA clone IMAGE:2269803 3' similar to contains THR12
1235	14272	27232	2.78	2.0E-62	AI63284.2	EST_HUMAN	THR repetitive element
8142	21076	34479	0.88	2.0E-62	AA307490.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
9127	22093	35520	4.47	2.0E-62	BF329911.1	EST_HUMAN	HT176374 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9127	22093	35521	4.47	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300600-031-e05 BN0284 Homo sapiens cDNA
			4.47	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300600-031-e05 BN0284 Homo sapiens cDNA
10333	22455		4.96	2.0E-62	AF246868.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3' (UBE2D) genes, complete cds
11896	24873		20.5	2.0E-62	BF330876.1	EST_HUMAN	QV4-BT0257-081189-017-e03 BT0257 Homo sapiens cDNA
1045	14091	27044	1.88	1.0E-62	AF248540.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1547	14590	27552	12.74	1.0E-62	L79810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1816	14842	27633	1.18	1.0E-62	AA025207.1	EST_HUMAN	at70a11.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP-K01H12.1 CE03453;
2925	15983	28506	1.45	1.0E-62	AL030044.1	EST_HUMAN	DKFZp566F104.r1 598 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566F104 5'
3435	16482		1.15	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4556	17578	30470	1.43	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FL20212 (FL20212), mRNA
5169	18178	31056	0.88	1.0E-62	AA148822.1	EST_HUMAN	20608.r1 Soares_Pregnant uterus_NHPU Homo sapiens cDNA clone IMAGE:491611 5' similar to SW-C561 BOVIN P10897 CYTOCHROME B561;
5198	18205	31079	0.94	1.0E-62	L23503.1	NT	Human glucagon-like peptide-1 receptor (GLP-1) mRNA, complete cds
8421	19488	32738	2.84	1.0E-62	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RP-L18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7341	20312	33655	0.91	1.0E-62	AA490090.1	EST_HUMAN	ab0502.s1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839006 3'
7352	20322	33659	2.48	1.0E-62	AA722878.1	EST_HUMAN	2089f10.s1 Soares_fetal_heart_NH119W Homo sapiens cDNA clone IMAGE:409771 3'
7352	20322	33670	2.68	1.0E-62	AA722878.1	EST_HUMAN	2089f10.s1 Soares_fetal_heart_NH119W Homo sapiens cDNA clone IMAGE:409771 3'
9110	22078	35502	0.58	1.0E-62	AA280350.1	EST_HUMAN	2836a07.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705060 5'
9413	22378	35816	1.82	1.0E-62	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9413	22378	35817	1.82	1.0E-62	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9457	22421	35858	1.97	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EG 3.1.3.2) Exon 9
9457	22421	35859	1.97	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EG 3.1.3.2) Exon 9
9915	22738	36188	3.42	1.0E-62	AA465170.1	EST_HUMAN	aa330a08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11694	24659	38237	2.41	1.0E-62	Z76988.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC0PA14D8
12750	25397		2.22	1.0E-62	11418322	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12956	25520	31714	3.25	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
338	13427	26349	2.41	9.0E-63	AW818405.1	EST_HUMAN	QV4-ST0234-181189-037-005 ST0234 Homo sapiens cDNA
2353	15362		1.51	9.0E-63	C18189.1	EST_HUMAN	C18189 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-556C10 5'
4071	17107	30000	9.28	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4071	17107	30001	9.29	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5315	15331	38014	2.17	9.0E-63	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
5541	16638	31578	1.3	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7388	20357	33708	3.41	9.0E-63	11426985	NT	Homo sapiens nucleoprotein 88KD (NUP88), mRNA
8138	21075	34476	0.73	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8689	21937	35060	1.58	9.0E-63	11421160	NT	Homo sapiens Ras association (RASSF) domain family 2 (RASSF2), mRNA
11246	24199	37718	1.64	9.0E-63	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11246	24199	37720	1.54	9.0E-63	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA



Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15360	28382	1.1	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2353	15391	28416	2.49	8.0E-63	6031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3475	16521	28443	3.42	8.0E-63	AF198348.1	NT	Gallus gallus Dec2 protein (Dec2) mRNA, complete cds
3476	16521	28444	3.42	8.0E-63	AF198349.1	NT	Gallus gallus Dec2 protein (Dec2) mRNA, complete cds
4294	17523	30203	3.75	8.0E-63	AL163288.2	NT	Homo sapiens chromosome 21 segment HS2T068
929	13982		1.67	7.0E-63	AB72137.1	EST_HUMAN	wm5611.1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2436008 3'
5412	18516		23.22	6.0E-63	AA420803.1	EST_HUMAN	nc5302.1 NCL CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361.60S
9226	22192	35622	0.83	5.0E-63	11528484	NT	RIBOSOMAL PROTEIN (HUMAN);
3332	16393	28305	0.7	4.0E-63	AL163278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3821	16861	28764	1.16	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS2T078
3821	16861	28765	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6588	16048	32917	2.92	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-003 BT0595 Homo sapiens cDNA
6588	16048	32918	2.92	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-003 BT0595 Homo sapiens cDNA
11467	24410	37693	2.12	4.0E-63	AW134709.1	EST_HUMAN	UIH-B1-abq-a-02-Q-UI.s1 NCL CGAP_Su33 Homo sapiens cDNA clone IMAGE:2712482 3'
11467	24410	37699	2.12	4.0E-63	AW134709.1	EST_HUMAN	UIH-B1-abq-a-02-Q-UI.s1 NCL CGAP_Su33 Homo sapiens cDNA clone IMAGE:2712482 3'
13023	26571		1.49	4.0E-63	AA628058.1	EST_HUMAN	zu84501.s1 Scoville's testis_NHT Homo sapiens cDNA clone IMAGE:744849 3' similar to contains L1.H L1
1952	14875	27975	2.52	3.0E-63	AB018260.1	NT	repetitive element;
2760	15782	28798	1.95	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2832	14280	27243	15.82	3.0E-63	6005663	NT	Human Met-RNA-1 gene 1
6619	19877	32554	32.28	3.0E-63	11545810	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
10064	22991	35460	0.51	3.0E-63	BE876158.1	EST_HUMAN	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC39323), mRNA
10064	22991	35461	0.61	3.0E-63	BE876158.1	EST_HUMAN	601485566F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3888253 5'
193	13294	29221	1.91	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
199	13300	28228	1.91	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
498	13570		3.08	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
827	13895	28936	1.7	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1599	14502	27577	4.18	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for R1 blood CE group antigen polypeptide, complete cds
1599	14502	27578	4.18	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for R1 blood CE group antigen polypeptide, complete cds
1781	14810	27798	1.33	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3288	16351	28271	2.77	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3925	16865	29878	3.64	2.0E-63	U60891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4901	17918	30810	0.95	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5188	18197	31070	1.19	2.0E-63	BE146928.1	EST_HUMAN	QV4-HT0222-0.1159-018-01 HT0222 Homo sapiens cDNA
5222	18240	31112	1.89	2.0E-63	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5334	26635	31192	0.57	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
5686	16071	32270	2.49	2.0E-63	BF373641.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5866	19071	32271	2.49	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6310	16381	32620	0.83	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6310	16381	32621	0.83	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2M1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6860	19913	33209	1.23	2.0E-63	U60059.1	NT	Homo sapiens MIST mRNA, partial cds
6911	19963	33258	0.81	2.0E-63	AB032399.1	NT	Homo sapiens MIST mRNA, partial cds
6911	19963	33260	0.81	2.0E-63	AB032399.1	NT	Homo sapiens MIST mRNA, partial cds
7278	20012	33315	1.46	2.0E-63	8910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7278	20012	33316	1.46	2.0E-63	8910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
8058	20965	34391	0.82	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8878	21845	35287	3.81	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9409	22374	35810	1.08	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9409	22374	35811	1.08	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10269	23224	38707	0.98	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11008	24058	37582	13.74	2.0E-63	N78945.1	EST_HUMAN	2518005.t1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE302385 3' similar to gbX17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
11127	24087	37614	2.32	2.0E-63	AF098910.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
11127	24087	37616	2.32	2.0E-63	AF098910.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
12381	25747	37635	8.02	2.0E-63	11416185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
1615	14647	27618	0.83	1.0E-63	F08485.1	EST_HUMAN	HS2ZV0111 normalized infant brain cDNA Homo sapiens cDNA clone c-2cd11
1515	14547	27519	0.93	1.0E-63	F08485.1	EST_HUMAN	HS2ZV0111 normalized infant brain cDNA Homo sapiens cDNA clone c-2cd11
4370	17397	30276	3.4	1.0E-63	F08485.1	EST_HUMAN	HS2ZV0111 normalized infant brain cDNA Homo sapiens cDNA clone c-2cd11
4370	17397	30277	3.4	1.0E-63	F08485.1	EST_HUMAN	HS2ZV0111 normalized infant brain cDNA Homo sapiens cDNA clone c-2cd11
5426	18529	31408	1.89	1.0E-63	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5884	18553	32140	97.84	1.0E-63	AW682868.1	EST_HUMAN	QV0:ST0215-060100-053-b09 ST0215 Homo sapiens cDNA
6531	19594	32856	0.72	1.0E-63	AW451950.1	EST_HUMAN	UI-H-B13-alk-h-02-0-U1st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3058763 3'
6531	19594	32856	0.72	1.0E-63	AW451950.1	EST_HUMAN	UI-H-B13-alk-h-02-0-U1st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3058763 3'
8816	21583		2.64	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13020	25659		5.16	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C047
6078	19159	32370	0.96	9.0E-64	AW401433.1	EST_HUMAN	UI-HF-BKO-ead-b-09-Q-U1st NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053193 5'
8199	21169	34579	4.61	9.0E-64	AW178186.1	EST_HUMAN	bm5007.xt NCI_CGAP_Kf11 Homo sapiens cDNA clone IMAGE:2161525 3'
1048	14094		2.71	8.0E-64	BE280796.1	EST_HUMAN	bm155232.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6263	18335	32566	3.26	8.0E-64	BE865755.1	EST_HUMAN	60150898.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
12187	25034		8.22	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12239	25070		2.63	8.0E-64	T00651.1	EST_HUMAN	y68b02.1 Strategene lung (6937210) Homo sapiens cDNA clone IMAGE:79179 5'
3540	16566		0.8	7.0E-64	BE394321.1	EST_HUMAN	601311455.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3933204 5'
4763	17763	30678	3.2	7.0E-64	4507480	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4763	17763	30678	3.2	7.0E-64	4507480	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
8098	21032	34430	0.84	7.0E-64	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
10363	23315	36784	4.76	7.0E-64	V07848.1	NT	Homo sapiens EWS, gcr22, rrp22 and bcr22 genes
1735	14765	27748	3.86	8.0E-64	AI651992.1	EST_HUMAN	w651607.xt NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1735	14765	27748	3.86	8.0E-64	AI651992.1	EST_HUMAN	w651607.xt NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3139	19166	29105	4.25	8.0E-64	AW028445.1	EST_HUMAN	wv13603.xt NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3139	19166	29106	4.25	8.0E-64	AW028445.1	EST_HUMAN	wv13603.xt NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
6703	18768	31973	2.43	8.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5703	18798	31974	2.43	8.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5725	18819	31898	6.33	8.0E-64	M13976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5929	19015	32206	0.71	8.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
5929	19015	32206	0.71	8.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
7446	20412	33764	2.85	8.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7446	20412	33765	2.85	8.0E-64	11525878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9862	22635	36091	7.07	8.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9864	22900	36254	1.78	8.0E-64	AF174753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
10076	23003	36473	2.44	8.0E-64	S76475.1	NT	bKc1 human, brain, mRNA, 2716 nt
11121	24081	37605	4.48	8.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11121	24081	37606	4.48	8.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11358	16196	29105	1.73	6.0E-64	AW026445.1	EST_HUMAN	wr13603.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2629436 3'
11358	16196	29106	1.73	6.0E-64	AW026445.1	EST_HUMAN	wr13603.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2629436 3'
12398	25172	31818	9.28	6.0E-64	11526198	NT	Homo sapiens interferin 10 receptor, beta (IL10RB), mRNA
821	13879	26929	3.68	5.0E-64	AF221918.1	NT	Homo sapiens chromosome 21 unknown mRNA
821	13879	26930	3.68	5.0E-64	AF221918.1	NT	Homo sapiens chromosome 21 unknown mRNA
1341	14376	27345	0.93	5.0E-64	AB020191.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1724	14764	27740	1.7	5.0E-64	U99358.1	NT	Human [(3)mb] protein homolog mRNA, complete cds
2637	14509	27483	3.52	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2637	14509	27484	3.52	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3983	17023	29934	7.14	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
4132	17184	30053	0.93	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
8125	21082	34480	0.57	4.0E-64	BE794607.1	EST_HUMAN	G01560382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3644397 5'
11164	24122	37650	1.55	4.0E-64	AW813763.1	EST_HUMAN	RC3-ST0197-120200-015-403 ST0197 Homo sapiens cDNA
11164	24122	37651	1.55	4.0E-64	AW813763.1	EST_HUMAN	RC3-ST0197-120200-015-403 ST0197 Homo sapiens cDNA
2208	15223	28243	6.32	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (T1-jlwara) Homo sapiens cDNA clone GEN-565E02 5'
3268	18322	28244	0.72	3.0E-64	BE794381.1	EST_HUMAN	G01589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3643577 5'
3457	18503	29422	1.85	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3457	18503	29423	1.85	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6200	19274	32608	1.35	3.0E-64	Z28273.1	NT	H sapiens tadinin 1 gene for L-type calcium channel, exon 28
6475	19540	32786	0.64	3.0E-64	AW500661.1	EST_HUMAN	UHF-BP0p-ak-c-05-Q-U1.1 NIH_MGC_5T Homo sapiens cDNA clone IMAGE:3073101 5'
6641	19599	32876	2.78	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-230600-011-G11 FN0019 Homo sapiens cDNA
8609	21176	35201	1.78	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8609	21176	35202	1.78	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8840	21807	35225	2.73	3.0E-64	BE206521.1	EST_HUMAN	b572h12.Y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:L08068 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
8840	21807	35226	2.73	3.0E-64	BE206521.1	EST_HUMAN	b572h12.Y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:L08068 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9782	22723	36177	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9782	22723	36178	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9872	22825	36278	0.8	3.0E-64	AW977384.1	EST_HUMAN	EST389463 IMAGE:389463 MAGO Homo sapiens cDNA
9872	22825	36279	0.8	3.0E-64	AW977384.1	EST_HUMAN	EST389463 IMAGE:389463 MAGO Homo sapiens cDNA
11988	24875	38471	1.87	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1090	14134	27088	0.95	2.0E-64	AA060940.1	EST_HUMAN	af08d08.s1 Soares, Jessica_NHT Homo sapiens cDNA clone IMAGE:1031161 3'
1398	14432	27401	1.2	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2530	15533		2.05	2.0E-64	AI927030.1	EST_HUMAN	w087601.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2492281 3' similar to contains element L1 repetitive element;
2536	15538	28590	3.13	2.0E-64	AI163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2536	15538	28590	3.13	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3801	16841	29748	0.87	2.0E-64	AW658145.1	EST_HUMAN	EST1370215 MAGE resequences, MAGE Homo sapiens cDNA
3801	16841	29748	0.87	2.0E-64	AW658145.1	EST_HUMAN	EST1370215 MAGE resequences, MAGE Homo sapiens cDNA
6121	19169	32424	2.2	2.0E-64	AI124387.1	EST_HUMAN	AI124387 NT2RM2 Homo sapiens cDNA clone NT2RM2023113 5'
6370	19438	32681	1.38	2.0E-64	AF112438.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
6532	19690	32689	4.02	2.0E-64	BF668337.1	EST_HUMAN	602723474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280395 5'
8745	19800	33080	1.5	2.0E-64	AI076387.1	EST_HUMAN	oz28b03.x1 Soares, total, testis, NB2HFB, gw Homo sapiens cDNA clone IMAGE:1676717 3'
8856	19912	33208	3.88	2.0E-64	M77185.1	NT	H sapiens dopamine receptor D5 pseudogene 1, partial cds
8108	21043	34442	0.57	2.0E-64	11431054	NT	Homo sapiens alxin 2-binding protein 1 (A2BP1), mRNA
8164	21102	34501	0.56	2.0E-64	AW608785.1	EST_HUMAN	QV1-HT0413-010200-059-112 HT0413 Homo sapiens cDNA
9016	21682	35400	5.69	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin) (LCP1), mRNA
9016	21682	35401	5.69	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plestin) (LCP1), mRNA
9405	22459	35899	0.43	2.0E-64	11423508	NT	Homo sapiens hypothetical protein SBB167 (LOC57115), mRNA
9586	22548	35900	0.96	2.0E-64	AI132570.1	EST_HUMAN	AI132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
11114	24074	37597	3.74	2.0E-64	BF528114.1	EST_HUMAN	602342882F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4180556 5'
11391	24337	37896	4.59	2.0E-64	AI922811.1	EST_HUMAN	w087606.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2462271 3'
11391	24337	37897	4.59	2.0E-64	AI922811.1	EST_HUMAN	w087606.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2462271 3'
11833	24716	38301	1.89	2.0E-64	BE268660.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
11833	24716	38302	1.89	2.0E-64	BE268660.1	EST_HUMAN	601185078F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3542922 5'
12316	25122	31844	1.47	2.0E-64	8587387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12744	25393		3.64	2.0E-64	H65162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
256	13355	26279	1.48	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1794	14823	27807	17.02	1.0E-64	AI929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gbl-21.696, cds1 PROTHYMOSIN ALPHA (HUMAN)/contains element MSR1 repetitive element ;
3024	18081	29004	0.81	1.0E-64	4507334	NT	Homo sapiens synaptophysin 1 (SYN1), mRNA
3822	19598	29492	5.73	1.0E-64	AF106779.1	NT	Homo sapiens transcription factor 1GIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
3598	16643	29562	1.38	1.0E-64	AF228527.1	NT	Homo sapiens TRAC3 mRNA, partial cds
3598	16643	29563	1.38	1.0E-64	AF228527.1	NT	Homo sapiens TRAC3 mRNA, partial cds
3917	16657	29670	2	1.0E-64	8022829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10424	23346	38931	0.88	1.0E-64	AA042976.1	EST_HUMAN	z65308.t1 Soares_pregnant_uterus_NBHFU Homo sapiens cDNA clone IMAGE:486587 3'
12286	25104		2.03	1.0E-44	AA163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2284	15297	28321	1.64	9.0E-45	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
2284	15297	28322	1.64	9.0E-46	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
11853	24745		35.25	9.0E-45	BF530678.1	EST_HUMAN	QV4-B-T0257.081189-017-603 BT0257 Homo sapiens cDNA
11837	24720	38305	7.27	8.0E-46	A1029244.1	EST_HUMAN	au68H07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to
10515	23437	36936	2.13	7.0E-45	BE081653.1	EST_HUMAN	SW-RL21_HUMAN P.46719.60S RIBOSOMAL PROTEIN L21.;
1059	14105	27056	2.73	9.0E-46	AV721898.1	EST_HUMAN	QV2-B-T0635-240400-162-502 BT0635 Homo sapiens cDNA
							AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1938	14962		12.23	9.0E-46	AA550629.1	EST_HUMAN	RI88R0.0.t1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:989379 similar to gb:K03002 60S
6721	19777	33056	0.87	6.0E-45	AA503892.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
							nh37607.st1 NCI_CGAP_P15 Homo sapiens cDNA clone IMAGE:954517
9098	22064	35489	2.49	6.0E-45	AW083252.1	EST_HUMAN	xc07609.x1 NCI_CGAP_Cox21 Homo sapiens cDNA clone IMAGE:2583645 3' similar to TR:Q83306 Q83306
9085	27330	35759	4.16	6.0E-45	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF.S.; contains L1.82 L1 repetitive element;
9365	22330	35760	4.16	6.0E-46	AA427878.1	EST_HUMAN	z65308.st1 Soares_total_fetus_NB2HF8_5w Homo sapiens cDNA clone IMAGE:773747 3'
9429	22383	35832	1.08	6.0E-46	A1085314.1	EST_HUMAN	z65308.st1 Soares_total_fetus_NB2HF8_5w Homo sapiens cDNA clone IMAGE:773747 3'
9429	22383	35833	1.08	6.0E-46	A1085314.1	EST_HUMAN	qf18105.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1750425 3'
11220	24773	37669	2.69	6.0E-46	BE667816.1	EST_HUMAN	qf18105.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1750425 3'
11378	24925	37654	1.51	6.0E-46	BF340825.1	EST_HUMAN	601340465F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
11825	24708	39291	1.8	6.0E-45	AL163210.2	NT	602037721F1 NCI_CGAP_Bm43 Homo sapiens cDNA clone IMAGE:4185977 5'
632	13697	29817	1.92	5.0E-46	AF064604.1	NT	Homo sapiens chromosome 21 segment HS21C010
1355	14390	27369	1.22	5.0E-46	AF064604.1	NT	Homo sapiens KEG3 protein mRNA, partial cds
1355	14390	27369	1.22	5.0E-46	AF064604.1	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1355	14390	27369	1.22	5.0E-46	AF064604.1	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2164	15180	28200	1.61	6.0E-46	AB033768.1	NT	Homo sapiens HPAD-coxny10 mRNA for peptidylarginine deiminase type I, complete cds
3269	16523	29245	2.13	5.0E-46	4507848.NT	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
3269	16523	29246	2.13	5.0E-46	4507848.NT	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
7052	20074	33361	1.18	5.0E-46	4504603.NT	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10533	23754	37253	1.28	5.0E-46	AF090868.1	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
195	13296	28224	2.33	4.0E-45	AL120419.1	EST_HUMAN	Multiple sclerosis associated retrovirus polyprotein (psl) mRNA, partial cds
							DKFZp761G103.J1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761G108 5'
747	13808	28748	1.29	4.0E-45	AJ208488.1	EST_HUMAN	qmk4801.x1 Soares_placenta_8to8weeks_2NH-HP8aGW Homo sapiens cDNA clone IMAGE:1891800 3'

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Table 4

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13808	26749	1.29	4.0E-65	AI268468.1	EST_HUMAN	qtm4601.x1 Soares_placenta_806weeks_ZNH-PEt69W Homo sapiens cDNA clone IMAGE:1891800 3'
1080	14124	27077	1.51	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1482	14515	27488	15.68	4.0E-65	4506638	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
3871	17011	28925	0.97	4.0E-65	AW993185.1	EST_HUMAN	RC3-BN033-160200-013-403 BN033 Homo sapiens cDNA
8278	18351	32585	4.17	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
8278	18351	32588	4.17	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7289	20261	33595	0.82	4.0E-65	AY008372.1	NT	Homo sapiens cysylated binding protein-related protein 3 (ORE3) mRNA, complete cds
7324	20295	33638	0.84	4.0E-65	AY008372.1	NT	Human clathrin 27 gene, exons 10 and 11, and L1 and A1 repeats
7429	20396	33748	2.48	4.0E-65	U18879.1	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7797	20749	34124	0.58	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE(C3A) mRNA, partial cds
7797	20749	34125	0.58	4.0E-65	U40372.1	NT	Human 3',5' cyclic nucleotide phosphodiesterase (HSPDE(C3A) mRNA, partial cds
8118	21055	34452	0.81	4.0E-65	U39556.1	NT	Human MAP kinase kinase 5 (MKK5) mRNA, complete cds
8174	21144	34549	0.78	4.0E-65	5453765	NT	Homo sapiens nei (GNCN)-like 2 (NELL2) mRNA
8174	21144	34550	0.78	4.0E-65	5453765	NT	Homo sapiens nei (GNCN)-like 2 (NELL2) mRNA
9501	22465	35605	1.34	4.0E-65	U78932.1	NT	Homo sapiens Junus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10946	23865		2.65	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11301	24251	37777	2.69	4.0E-65	AV738764.1	EST_HUMAN	AY738764 CB Homo sapiens cDNA clone CBCCBE05 5'
11434	24378	37518	6.02	4.0E-65	AF118846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12606	14124	27077	1.79	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13091	13266	20224	1.8	4.0E-65	AL120416.1	EST_HUMAN	DKFZp781G103.r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G103 5'
97	13214	28139	3.16	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
98	13214	28139	5.52	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1236	15519		22.13	3.0E-65	X78932.1	NT	H. sapiens HZF6 mRNA for zinc finger protein
1840	14897	27666	1.7	3.0E-65	A1000692.1	EST_HUMAN	ox23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3003	18061	28979	0.74	3.0E-65	DB7078.2	NT	MSR1 repetitive element
3260	15343	29294	0.68	3.0E-65	4504950	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3260	15343	29294	0.68	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3734	16776	29688	1.61	3.0E-65	A1000692.1	EST_HUMAN	ox23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
4672	17700	30588	1.33	3.0E-65	8912385	NT	MSR1 repetitive element
10429	23351	38635	1.42	3.0E-65	BE787368.1	EST_HUMAN	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
10429	23351	38635	1.42	3.0E-65	BE787368.1	EST_HUMAN	601479686F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3882405 5'

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11719	23816	37433	8.57	3.0E-05	AA439006.1	EST_HUMAN	zw6506.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3415	18483	28384	6.08	2.0E-05	BF680284.1	EST_HUMAN	602115502.F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4295866 5'
6883	19743		4.55	2.0E-05	BE25373.1	EST_HUMAN	801190383.F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534741 5'
7338	20310	33653	27.64	2.0E-05	BF176922.1	EST_HUMAN	602154359.F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4282205 5'
9197	22163	35592	1.26	2.0E-05	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9197	22163	35593	1.26	2.0E-05	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
12288	26069		2.76	2.0E-05	AA307904.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous
12708	25728		1.95	2.0E-05	BP246088.1	EST_HUMAN	retrovirus
540	13611	28530	1.54	1.0E-05	7957495.1	EST_HUMAN	801854033.F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4073766 5'
2056	18075	28095	1.07	1.0E-05	AB040948.1	NT	Homo sapiens putative Rab5 GDI/GTP exchange factor homologue (RABEX6), mRNA
3365	18434	28361	0.8	1.0E-05	BE466981.1	EST_HUMAN	Homo sapiens mRNA for KIAA1513 protein, partial cds
4023	17061	28662	1.71	1.0E-05	4504082	NT	h224409.x1 NCI_CGAP_G028 Homo sapiens cDNA clone IMAGE:3208888 3'
4023	17061	28663	1.71	1.0E-05	4504082	NT	Homo sapiens glycine 4 (GPC4) mRNA
4234	17263	30147	2.4	1.0E-05	AW028340.1	EST_HUMAN	Homo sapiens glycine 4 (GPC4) mRNA
4234	17263	30148	2.4	1.0E-05	AW028340.1	EST_HUMAN	w09609.x1 NCI_CGAP_G044 Homo sapiens cDNA clone IMAGE:2643162 3'
5368	18463	31332	0.64	1.0E-05	BE086509.1	EST_HUMAN	w09609.x1 NCI_CGAP_G044 Homo sapiens cDNA clone IMAGE:2543162 3'
5358	18463	31333	0.64	1.0E-05	BE086509.1	EST_HUMAN	QV0-B10702-170400-194-009 B10702 Homo sapiens cDNA
5554	18851	31595	0.61	1.0E-05	AI24738.1	EST_HUMAN	QV0-B10702-170400-194-008 B10702 Homo sapiens cDNA
8597	21565	34690	5.47	1.0E-05	AW820481.1	EST_HUMAN	q08907.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR-07823
8597	21565	34691	5.47	1.0E-05	AW820481.1	EST_HUMAN	QV2-S10708-140200-042412 ST0288 Homo sapiens cDNA
8623	21591	35009	2.16	1.0E-05	BE732118.1	EST_HUMAN	QV2-S10708-140200-042412 ST0288 Homo sapiens cDNA
8623	21591	35010	2.16	1.0E-05	BE732118.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
8662	21630	35050	2.14	1.0E-05	AW141295.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
8662	21630	35051	2.14	1.0E-05	AW141295.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
9192	22158	35596	1.94	1.0E-05	BF688707.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
9374	22336	35799	2.25	1.0E-05	AW129040.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
9374	22336	35799	2.25	1.0E-05	AW129040.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
9385	22351		2.52	1.0E-05	11431994	NT	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
9832	22081	36196	5.48	1.0E-05	AI191716.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
10245	23170	36836	1.28	1.0E-05	AW163783.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'
10855	23687	37096	0.84	1.0E-05	AA069599.1	EST_HUMAN	801566124.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3841012 5'



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10635	23955	37371	1.02	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11011	23976	37501	7.57	1.0E-65	M28107.1	NT	Human platelet factor 4 variation 1 (PF4-variant) gene, complete cds
11131	24091	37620	10.37	1.0E-65	4306630	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11465	24408	37855	2.43	1.0E-65	BF693707.1	EST_HUMAN	60212623BF1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4283313.5
11546	24486	38040	1.89	1.0E-65	AI621017.1	EST_HUMAN	ts76d06xt NCI_CGAP_GG8 Homo sapiens cDNA clone IMAGE:2237170.3 similar to gbL15533_mn1
12280	25105		3.13	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HOMO);
12391	25168	31815	7.2	1.0E-65	11416322	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12780	25427		1.87	1.0E-65	11418248	NT	Homo sapiens cadherin EGF-LAG seven-pass G-type receptor 1 (CELSR1), mRNA
72	13160	26110	0.94	9.0E-68	AL160311.1	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
72	13160	26111	0.94	9.0E-68	AL160311.1	NT	Novel human gene mapping to chromosome 22
1356	14391	27351	0.93	9.0E-66	5031680	NT	Novel human gene mapping to chromosome 22
1356	14391	27362	0.93	9.0E-66	5031680	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1480	14513		6.17	9.0E-66	M72393.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
3916	16958	29868	0.74	9.0E-66	M72393.1	NT	Human transposon-like element, partial
3916	16958	29869	0.74	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4717	17739	30831	0.73	9.0E-66	AL137183.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4717	17737	30829	1.59	8.0E-69	AA424304.1	EST_HUMAN	Novel human gene mapping to chromosome X
11675	24841		1.48	7.0E-66	BE064410.1	EST_HUMAN	Novel human gene mapping to chromosome X
4393	17421	30304	1.01	6.0E-66	AI924653.1	EST_HUMAN	Novel human gene mapping to chromosome X
4393	17421	30305	1.01	6.0E-66	AI924653.1	EST_HUMAN	Novel human gene mapping to chromosome X
4393	17421	30306	1.01	6.0E-66	AI924653.1	EST_HUMAN	Novel human gene mapping to chromosome X
8777	21744		0.52	6.0E-66	BE178593.1	EST_HUMAN	Novel human gene mapping to chromosome X
11463	24436	37853	4.18	6.0E-66	X69181.1	NT	Novel human gene mapping to chromosome X
1368	14403	27373	1.94	5.0E-66	BE094410.1	EST_HUMAN	Novel human gene mapping to chromosome X
9549	22593	35041	15.54	5.0E-66	11420557	NT	Novel human gene mapping to chromosome X
791	13650	26787	1.39	4.0E-68	6870816	EST	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
1760	14779	27764	1.15	4.0E-68	AW697768.1	EST_HUMAN	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
2288	15301	28325	1.84	4.0E-66	X69211.1	NT	Human endogenous retrovirus 1 homolog (Fint1), mRNA
2481	15485		2.82	4.0E-68	AJ223384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4823	17840		3.19	4.0E-68	5935487	NT	Human endogenous retrovirus, complete genome



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11838	24721	38308	5.1	3.0E-08	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
13109	29529	31847	1.38	3.0E-06	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
63	13173	26082	1.94	2.0E-06	7857334	NT	Homo sapiens Mtschapan/NIK-related kinase (MINK), mRNA
53	13173	26083	1.94	2.0E-06	7857334	NT	Homo sapiens Mtschapan/NIK-related kinase (MINK), mRNA
422	13117	26015	0.7	2.0E-06	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
422	13117	26016	0.7	2.0E-06	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORCSL) mRNA, and translated products
1843	14869	27807	2.18	2.0E-06	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2241	15265	28278	2.33	2.0E-06	X69859.1	NT	H sapiens pseudogene for the low affinity L-8 receptor
2886	18044	28965	1.39	2.0E-06	X69399.1	NT	H sapiens pseudogene for the low affinity L-8 receptor
3532	16578	29501	0.79	2.0E-06	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3777	16816	29727	0.9	2.0E-06	AL117233.1	NT	Novel human gene mapping to chromosome 1
4655	17708	30598	38.02	2.0E-06	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4985	17708	30599	38.62	2.0E-06	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5914	19000	32191	0.82	2.0E-06	AW98854.1	EST_HUMAN	EST1380930 MAGE sequences, MAGJ Homo sapiens cDNA
5914	19000	32192	0.82	2.0E-06	AW98854.1	EST_HUMAN	EST1380930 MAGE sequences, MAGJ Homo sapiens cDNA
9180	22165	35595	2.88	2.0E-06	N45480.1	EST_HUMAN	h5602.1 Soares_multigene_sclerosis_2NBHMSF Homo sapiens cDNA IMAGE:277826 5'
12614	25941		2.81	2.0E-06	11416318	NT	Homo sapiens C-2 and S-phase expressed 1 (GTSE1), mRNA
2804	15933	28885	1.56	1.0E-06	AV177817.1	EST_HUMAN	AV177817 DGB Homo sapiens cDNA clone DGBAD007 5'
2804	15933	28886	1.58	1.0E-06	AV177817.1	EST_HUMAN	AV177817 DGB Homo sapiens cDNA clone DGBAD007 5'
4412	15933	28885	3.59	1.0E-06	AV177817.1	EST_HUMAN	AV177817 DGB Homo sapiens cDNA clone DGBAD007 5'
4412	15933	28886	3.59	1.0E-06	AV177817.1	EST_HUMAN	AV177817 DGB Homo sapiens cDNA clone DGBAD007 5'
6455	16557	31468	5.82	1.0E-06	BF873088.1	EST_HUMAN	602162996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
6875	19894	32154	0.64	1.0E-06	BE765232.1	EST_HUMAN	IL2NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
6875	19894	32155	0.64	1.0E-06	BE765232.1	EST_HUMAN	IL2NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
7126	20058	33364	1.09	1.0E-06	BF32623.1	EST_HUMAN	RC5-BJ0183-010900-034-G08 BN0193 Homo sapiens cDNA
8901	21768	35192	1.2	1.0E-06	AA638855.1	EST_HUMAN	es8004.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827282 3'
9781	22722	36718	0.7	1.0E-06	AA018823.1	EST_HUMAN	z857161.21 Soares retina Z854HR Homo sapiens cDNA clone IMAGE:363118 5'
10737	23659	37163	0.9	1.0E-06	AV1748749	EST_HUMAN	AV1748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10737	23659	37164	0.9	1.0E-06	AV1748749	EST_HUMAN	AV1748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10993	23913	37429	0.44	1.0E-06	BE044595.1	EST_HUMAN	hc47m02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:3049563 3'

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11290	24240	37767	2.47	1.0E-06	AF11187.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds, and unknown gene
11863	24735	38322	1.69	1.0E-08	AW968744.1	EST_HUMAN	EST1380920 IMAGE ressequencs, MAGJ Homo sapiens cDNA
12368	25170		2.76	9.0E-07	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
380	13493	28425	2.51	7.0E-07	AW162232.1	EST_HUMAN	au7502.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
1382	14416	27368	1.23	7.0E-07	AA3383416.1	EST_HUMAN	NT106812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK3933
1558	14580	27561	1.19	7.0E-07	W85947.1	EST_HUMAN	2558003.1 Sources_fetal_liver_spleen_INFELS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1658	14590	27662	1.19	7.0E-07	W85947.1	EST_HUMAN	2558003.1 Sources_fetal_liver_spleen_INFELS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2048	15097	28088	1.02	7.0E-07	7857243	NT	Homo sapiens lincalot 1,3,4-triphosphate 5'G kinase (TPK1), mRNA
2048	15097	28087	1.02	7.0E-07	7857243	NT	Homo sapiens lincalot 1,3,4-triphosphate 5'G kinase (TPK1), mRNA
2821	13493	28425	2.78	7.0E-07	AW162232.1	EST_HUMAN	au7502.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 8, MITOCHONDRIAL PRECURSOR (HUMAN);
6189	19273	32507	0.96	7.0E-07	10190696	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6401	19469	32716	1.92	7.0E-07	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6401	19469	32717	1.92	7.0E-07	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6886	19637	33233	1.14	7.0E-07	4885084	NT	Homo sapiens ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110116KD) (ATP9M1A), mRNA
7693	20596	34216	1.13	7.0E-07	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC555972), mRNA
7693	20596	34217	1.13	7.0E-07	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC555972), mRNA
8666	21634	35055	0.69	7.0E-07	4957132	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8284	22260	35681	0.73	7.0E-07	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11985	24882	35458	2.43	7.0E-07	UB2488.1	NT	Human cyclochrome oxidase subunit 1/a (COX6A1P) pseudogene, complete cds
12169	25016	38819	1.92	7.0E-07	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12169	25016	38820	1.92	7.0E-07	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12639	25323	31769	1.66	7.0E-07	AB011395.1	NT	Homo sapiens gene for AF-6, complete cds
13009	25581		1.44	7.0E-07	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2 (delta subunit 1 (CACNA2D1), mRNA
581	16631	29546	1.19	6.0E-07	X58968.1	NT	H sapiens mRNA for acetyl-CoA carboxylase
786	13855	28802	1.7	6.0E-07	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1278	14313	27274	2.06	6.0E-07	Y14320.1	NT	Homo sapiens PMP68 gene, exons 3,4,5,6 & 7
3183	16238	29168	1.19	6.0E-07	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3451	16487	28414	1.33	6.0E-07	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3451	16487	28415	1.33	6.0E-07	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products

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4162	17183	30069	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4162	17183	30070	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4734	17764	30647	3.56	6.0E-67	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4734	17764	30648	3.56	6.0E-67	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4242	18250	31121	0.99	6.0E-67	AF018698.1	NT	Homo sapiens B-ATF gene, complete cds
5242	18250	31122	0.99	6.0E-67	AF018698.1	NT	Homo sapiens B-ATF gene, complete cds
3235	18290	28212	2.02	5.0E-67	AF008960.1	NT	Homo sapiens T cell receptor beta locus, TCRBV753A2 to TCRBV1252 region
11039	24279	31391	13.19	5.0E-67	BE510038.1	EST_HUMAN	PMS3.BN0176-105400-001-004.BN01176.Homo sapiens cDNA
1331	13496	27335	2.25	4.0E-67	R90819.1	EST_HUMAN	YNU241.1.1 Soares adult brain N244H855Y Homo sapiens cDNA clone IMAGE:167263 5'
8355	21324	34736	0.89	4.0E-67	AT733032.1	EST_HUMAN	Q26065.5X NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1493288 3' similar to SW_Z33A_HUMAN
8725	21693	21693	1.18	4.0E-67	BF357821.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ;
11403	24347	24347	1.46	4.0E-67	AA714294.1	EST_HUMAN	RC0-H10634-150900-028-003 HT0934 Homo sapiens cDNA
2824	13669	28620	1.16	3.0E-67	AA333768.1	EST_HUMAN	pro0601.at NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR.O10385 O10385
4723	17743	30634	2.62	3.0E-67	AW669159.1	EST_HUMAN	ESTS17803 Embryo, 9 week Homo sapiens cDNA 5' end
4733	17713	30634	1.08	3.0E-67	AL163276.2	NT	MR3-SN0068-040500-008-001 SN0058 Homo sapiens cDNA
8522	21490	34805	1.15	3.0E-67	BF196068.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
11568	24526	24526	15.35	3.0E-67	AA927874.1	EST_HUMAN	hr87105.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
190	13281	28217	0.87	2.0E-67	BE548354.1	EST_HUMAN	OR01895 GTP-RHO BINDING PROTEIN 1 ;
848	13502	28680	6.48	2.0E-67	AF1816405.1	EST_HUMAN	cmt1807.at1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541385 3'
1107	14151	14151	1.26	2.0E-67	AF167460.1	NT	hw1609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP.F23H11.9
14925	14925	27822	1.28	2.0E-67	BE5303037.1	EST_HUMAN	GE08917 ;
1901	14925	27823	1.28	2.0E-67	BE5303037.1	EST_HUMAN	QV4-S10234-161190-037-05 S10234 Homo sapiens cDNA
2251	15265	28281	0.9	2.0E-67	11422948	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 2a, 2, 3, and 4
2251	15265	28282	0.9	2.0E-67	11422948	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 2a, 2, 3, and 4
2394	15401	28428	1.16	2.0E-67	AF309561.1	NT	ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892
2394	15445	28463	1.36	2.0E-67	AA623755.1	EST_HUMAN	KIA0798 PROTEIN ;
3481	16327	29452	3.78	2.0E-67	AA623755.1	EST_HUMAN	ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	KIA0798 PROTEIN ;
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	Homo sapiens hypothetical protein dJ462023.2 (DJA62023.2), mRNA
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	Homo sapiens hypothetical protein dJ462023.2 (DJA62023.2), mRNA
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	Homo sapiens KIRAB zinc finger protein ZFQ97 mRNA, complete cds
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	zlu97g01.at1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:746382 3'
4027	17065	29466	2.7	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6190	19264	32500	0.77	2.0E-67	AL049784.1	NT	Novel human gene mapping to chromosome 13
6247	19320	32550	4.91	2.0E-67	BF240738.1	EST_HUMAN	60187535.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4091880 5'
6428	19464	32746	2.19	2.0E-67	AB051783.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6428	19464	32747	2.19	2.0E-67	AB051783.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
6789	19652	33137	0.77	2.0E-67	AL120542.1	EST_HUMAN	DKFZB761A229.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229.5'
8894	21870	32925	0.83	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
8904	21870	33236	0.83	2.0E-67	AA334603.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to cerebellin
8348	22313	35737	1.11	2.0E-67	AW062835.1	EST_HUMAN	RC4-BT0568-770100-011-c07 BT0568 Homo sapiens cDNA
9348	22313	35738	1.11	2.0E-67	AW062835.1	EST_HUMAN	RC4-BT0568-770100-011-c07 BT0568 Homo sapiens cDNA
9625	22800	36261	1.05	2.0E-67	AV1791333.1	EST_HUMAN	U7131333 HIT Homo sapiens cDNA clone HTFAR003 5'
10057	22964	36463	1.01	2.0E-67	AV129324.1	EST_HUMAN	U11-B12-htc-e-10-Q1.a1 NCI_OGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
10984	23804	37418	0.44	2.0E-67	AA629089.1	EST_HUMAN	on68603.F1 Scanes, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
11290	24202	37724	1.47	2.0E-67	BF685788.1	EST_HUMAN	602140470.F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'
11340	24327	37656	1.59	2.0E-67	BF034485.1	EST_HUMAN	601462825.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3368878 5'
11359	28011		2.57	2.0E-67	111438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11562	24502	38060	1.83	2.0E-67	BE206714.1	EST_HUMAN	601175762.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11764	23939	37461	1.63	2.0E-67	BF377168.1	EST_HUMAN	PM2:TN0103-040600-001-c02 TN0103 Homo sapiens cDNA
12805	25434	37741	1.73	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
263	13350	26278	1.92	1.0E-67	45021066	NT	Homo sapiens enoyl beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
709	13771	25705	1.34	1.0E-67	AA702794.1	EST_HUMAN	Z86004.41 Scanes, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
10587	23509	37001	0.44	1.0E-67	CG3075	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0218
10587	23509	37002	0.44	1.0E-67	CG3075	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0218
2186	15201	28221	2.37	8.0E-68	BE870732.1	EST_HUMAN	z86210.1_r1 Striatogene NNT neuron (#637233) Homo sapiens cDNA clone IMAGE:3852254 5'
3983	16923	29831	4.26	8.0E-68	AA209458.1	EST_HUMAN	SW-SAV_SULAC Q07590 SAV PROTEIN, 1
3983	16923	29832	4.26	8.0E-68	AA209458.1	EST_HUMAN	z86210.1_r1 Striatogene NNT neuron (#637233) Homo sapiens cDNA clone IMAGE:348163 5' similar to
8438	21407	34819	0.57	7.0E-68	AB181050.1	EST_HUMAN	SW-SAV_SULAC Q07590 SAV PROTEIN, 1
10816	29373	37240	2.48	6.0E-68	11422088	NT	SW-SAV_SULAC Q07590 SAV PROTEIN, 1
12811	25436		2.18	6.0E-68	BE612564.1	EST_HUMAN	Homo sapiens bromelain A-inhibited, guanine nucleotide-exchange protein 2 (BIG2), mRNA
13058	25584	37688	1.52	6.0E-68	BF310875.1	EST_HUMAN	601462067.F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5855761 5'
803	15815	26810	0.69	5.0E-68	AF2319719.1	NT	60194365.F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124141 5'
803	15815	26811	0.69	5.0E-68	AF2319719.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Table 4  
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
820	13878	28927	4.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	13878	28928	4.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2791	15793	29799	1.23	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3162	16218	29133	3.08	5.0E-68	AB037892.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4210	17298		0.8	5.0E-68	4628987	EST_HUMAN	Homo sapiens retinoblastoma-binding protein 2 (RBP2) mRNA
4518	17543	30429	0.76	5.0E-68	AL157945.1	EST_HUMAN	DKFZp467D207.1 547 (synonym: rib1) Homo sapiens cDNA clone DKFZp467D207.5
6889	19941	33236	0.67	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3i)-like 1 (RAB3IL1), mRNA
6889	19941	33237	0.67	5.0E-68	7019512	NT	Homo sapiens RAB3A interacting protein (rab3i)-like 1 (RAB3IL1), mRNA
2532	15535	29455	0.94	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2532	15535	29556	0.94	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5011	18026		7.63	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6075	19156	32369	0.67	4.0E-68	AF197963.1	NT	Homo sapiens sedlin (SEDL) gene, exon 4
6939	20163	33485	5.5	4.0E-68	11055891	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6939	20163	33496	5.6	4.0E-68	11055891	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7948	20887	34278	0.72	4.0E-68	7561963	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
9395	22360	35790	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9395	22360	35791	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9395	22360	35791	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9395	22360	35791	5.91	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11345	24295	37821	1.55	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11345	24295	37822	1.56	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
3673	18716	29630	5.02	3.0E-68	AF236092.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
5299	18303	31164	0.93	3.0E-68	AF236092.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9812	21135		5.47	3.0E-68	A1342323.1	EST_HUMAN	q38a02.x1 Soares, fetal, lung, NIH-L16W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains
10968	23788	37288	2.01	3.0E-68	F28784.1	EST_HUMAN	THR2-TH2 repetitive element;
13012	25725		1.99	3.0E-68	AW939485.1	EST_HUMAN	HSPD1878 HMG3 Homo sapiens cDNA clone s3000023D69
2873	18321		27.6	2.0E-68	D00522.1	NT	QV1-DT0072-010200-056-H06 DT0072 Homo sapiens cDNA
2873	18321		27.6	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4055	17092	20987	0.75	2.0E-68	BE675768.1	EST_HUMAN	T11502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR-O60328 O60328
4708	17729	30623	1.88	2.0E-68	AB006881.1	NT	HYPOTHETICAL 88.8 KD PROTEIN. ;
7059	20081		9.21	2.0E-68	R45068.1	EST_HUMAN	Homo sapiens gene for actin receptor type IIB, complete cds
7265	20000	33269	4.51	2.0E-68	BF05316.1	EST_HUMAN	Y939G04.x1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:34895 3'
7425	20392		0.61	2.0E-68	11525737	NT	60145551AF1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
							Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:poly(epsilon-D-glucose) N-acetylglucosaminyltransferase 8 (Gulnac-T8) (GALNT8), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7595	20358	33916	0.61	2.0E-68	BF336745.1	EST_HUMAN	IL3-CT0344-180900-273-A01 CT0834 Homo sapiens cDNA
6301	22265	35565	0.87	2.0E-68	Q08559	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
80	13195	28120	0.75	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT1), mRNA
288	13390	26318	17.65	1.0E-68	AW1816403.1	EST_HUMAN	GV4-5T0234-181199-037-005 ST0234 Homo sapiens cDNA
2293	15277	26301	1.27	1.0E-68	AB011148.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2293	15277	26302	1.27	1.0E-68	AB011146.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2767	15759	28781	1.04	1.0E-68	AW451832.1	EST_HUMAN	U1-H3B-alk-107-5-U1a1 NC1_GCAP_Sub5 Homo sapiens cDNA clone IMAGE:3552344.5
4037	17075	28975	1.01	1.0E-68	BE268032.1	EST_HUMAN	01117002F1NH_MGC_17 Homo sapiens cDNA clone IMAGE:3552344.5
5066	18078	30957	0.69	1.0E-68	AA987343.1	EST_HUMAN	g47g12.a1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480518.3
5395	19498	31376	1.6	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0668), mRNA
7638	20860	34270	0.95	1.0E-68	11436716	NT	Homo sapiens sentrin/SUMO-specific protease (SENPT1), mRNA
11166	24153	37894	1.48	1.0E-68	11418859	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11166	24153	37895	1.48	1.0E-68	11418859	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11250	24203	37725	3.37	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSM13) mRNA, complete cds
11631	24568	38131	2.13	1.0E-68	U50318.1	NT	Human protein kinase C substrate 80K-H (PRKC8H) gene, exon 4-5
11631	24568	38132	2.13	1.0E-68	U50318.1	NT	Human protein kinase C substrate 80K-H (PRKC8H) gene, exon 4-5
11975	24852	38449	1.73	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11975	24852	38450	1.73	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12790	13198	28120	2.19	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT1), mRNA
13005	25866	31419	2.07	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13037	25593		2.01	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13142	26040	5.15	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
22	13142	26041	5.15	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1029	14076	27025	0.76	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated padf homolog (POH1) mRNA
1029	14075	27026	0.76	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated padf homolog (POH1) mRNA
4155	17186	30074	0.97	9.0E-69	4757697	NT	Homo sapiens v-rel murine sarcoma viral oncogene homolog B1 (BRAP) mRNA
4175	17208	30082	1.02	9.0E-69	4504010	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8KD) (GLCLR) mRNA
8241	18246	31120	0.93	9.0E-69	AU057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
11236	24186		5.51	9.0E-69	AJ117241.1	EST_HUMAN	AU117241 HEMK1 Homo sapiens cDNA clone HEMK1A1000668.5
3397	18446		1.77	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
8487	18552	32802	5.65	7.0E-69	6966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
8195	21185	34574	16.42	8.0E-69	A182784.1	EST_HUMAN	g62201.X1 Soares_fetal_lung_NH4L10W Homo sapiens cDNA clone IMAGE:1743601.3 similar to gbL11569.603 RIBOSOMAL PROTEIN L18 (HUMAN);



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[illegible]

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
128	13477	26411	1.06	2.0E-69	AF160282.1	NT	Homo sapiens KIA0553 protein gene, complete cds, and alpha1b protein gene, partial cds
129	13477	26412	1.06	2.0E-69	AF160282.1	NT	Homo sapiens KIA0553 protein gene, complete cds, and alpha1b protein gene, partial cds
404	13477	26411	4.75	2.0E-69	AF160282.1	NT	Homo sapiens KIA0553 protein gene, complete cds, and alpha1b protein gene, partial cds
404	13477	26412	4.76	2.0E-69	AF160282.1	NT	Homo sapiens KIA0553 protein gene, complete cds, and alpha1b protein gene, partial cds
1802	14928	27824	1.46	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360074 5'
2856	18916		3.9	2.0E-69	AA431157.1	EST_HUMAN	zwf1062.1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:3635781 5'
8900	27688	35289	0.97	2.0E-69	AA114270.1	EST_HUMAN	zn28091.1 Stralagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:527088 5'
1714	14744	27728	2.69	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
5059	18069		0.73	1.0E-69	BE409094.1	EST_HUMAN	801301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
8168	19243	32474	0.78	1.0E-69	BE502501.1	EST_HUMAN	801675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3698632 5'
8168	19243	32475	0.78	1.0E-69	BE502501.1	EST_HUMAN	801675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3698632 5'
6768	19812	33062	4.09	1.0E-69	AV335969.1	EST_HUMAN	QV0-1T0019-031198-045-e07 T10010 Homo sapiens cDNA
6992	20215	33545	1.4	1.0E-69	7662293	NT	Homo sapiens KIA00716 gene product (KIA00716), mRNA
7011	20137	33453	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7011	20137	33454	2.78	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7065	20087	33399	0.62	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610814 5'
7065	20087	33397	0.62	1.0E-69	BE531007.1	EST_HUMAN	601278532F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610814 5'
10534	23459	36952	4.31	1.0E-69	BE246070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10534	23459	36953	4.31	1.0E-69	BE246070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10631	23563	37053	1.46	1.0E-69	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10779	23700	37198	0.53	1.0E-69	BF528429.1	EST_HUMAN	602043782F1 NCI_CGAP_Brim7 Homo sapiens cDNA clone IMAGE:4181325 5'
11219	24172		2.78	1.0E-69	4504918	NT	Homo sapiens koratlin 8 (KRT8) mRNA
12234	25066	38167	1.89	1.0E-69	BF125987.1	EST_HUMAN	60176502F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12648	25331		6.78	1.0E-69	AB069694.1	EST_HUMAN	wf6408.v1 Scores, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:4025785 5'
2339	15590	28370	1.61	8.0E-70	AA230303.1	EST_HUMAN	nc130121.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:108023
4401	17429	30314	2.11	8.0E-70	L77566.1	NT	nc130121.1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:108023
1830	14857	27854	2.28	7.0E-70	AI467807.1	EST_HUMAN	hm8301.v1 NCI_CGAP_Brim25 Homo sapiens cDNA clone IMAGE:27165305 3'
1830	14857	27854	2.28	7.0E-70	AI467807.1	EST_HUMAN	hm8301.v1 NCI_CGAP_Brim25 Homo sapiens cDNA clone IMAGE:27165305 3'
1947	14971	27968	1.87	7.0E-70	AA282966.1	EST_HUMAN	z11604.v1 NCI_CGAP_OCB1 Homo sapiens cDNA clone IMAGE:713339 5'
2078	15095		2.97	7.0E-70	5031069	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA.

Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4252	17281	30162	4.29	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5550	18687	31802	5.38	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5560	18697	31803	5.38	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7110	20044	33346	2.38	7.0E-70	AJ000082.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
8046	20982	34379	0.74	7.0E-70	11417306	NT	Homo sapiens thin immunoglobulin domain protein (myosin) (TITD), mRNA
8774	21741	35162	2.43	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
8774	21741	35163	2.43	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
8072	22038	35462	4.26	7.0E-70	M74059.1	NT	Human displacement protein (CCAA1) mRNA
8072	22038	35463	4.26	7.0E-70	M74059.1	NT	Human displacement protein (CCAA1) mRNA
9512	22475	35919	2.79	7.0E-70	X68841.1	NT	Human PBX3 mRNA
9512	22475	35920	2.79	7.0E-70	X68841.1	NT	Human PBX3 mRNA
9780	21113	34513	3.51	7.0E-70	AF163715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5 flanking region
8816	21138	34542	2.05	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transport (TRN2), mRNA
8816	21138	34543	2.05	7.0E-70	11525984	NT	Homo sapiens karyopherin beta 2b, transport (TRN2), mRNA
10014	22941	36407	0.93	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
10591	23583	37078	0.6	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
10591	23583	37080	0.6	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
11923	24804	35358	2.36	7.0E-70	11528316	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11923	24804	35397	2.36	7.0E-70	11528316	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
12893	25382	31414	13.53	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
13071	25505	31698	34.82	7.0E-70	Z00040.1	NT	Human kappa-immunoglobulin germ line pseudogene variable region (subgroup V kappa I)
872	13929	28986	2.38	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2147	16163	28178	1.7	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2516	15518	28542	1.17	6.0E-70	8822899	NT	Homo sapiens CYP-N-acetylneuraminate acid synthase (LOC555907), mRNA
2560	15897	29577	1.76	5.0E-70	7692307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2559	15997	29578	1.76	5.0E-70	7692307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12243	28073	32285	2.62	5.0E-70	BE166034.1	EST	MR3-H10487-150200-115-05 H10487 Homo sapiens cDNA
6918	19695	32285	1.24	4.0E-70	T06837.1	EST	EST03824 Fetal brain, Staphylococcus (Gef838206) Homo sapiens cDNA
8961	20186	33510	0.78	4.0E-70	AW769228.1	EST	CH44-UM0003-016300-105-008 UM0003 Homo sapiens cDNA
6961	20186	33511	0.78	4.0E-70	AW769228.1	EST	CH44-UM0003-016300-105-008 UM0003 Homo sapiens cDNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1593	14625	27698	1.95	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-at12 BT0522 Homo sapiens cDNA
1593	14625	27599	1.56	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071299-011-at12 BT0522 Homo sapiens cDNA
5701	18796	31970	0.63	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5701	18796	31971	0.63	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6055	18736	32346	1.1	3.0E-70	AB31975.1	EST_HUMAN	W60003.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2388065 3'
6509	19573	32826	1.27	3.0E-70	BF685233.1	EST_HUMAN	60214165FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6509	19573	32827	1.27	3.0E-70	BF685233.1	EST_HUMAN	60214165FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10467	23369	36883	0.55	3.0E-70	BE502973.1	EST_HUMAN	h281102.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
407	13160	28063	2.14	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
690	13753	26680	14.23	2.0E-70	N42161.1	EST_HUMAN	Y07A10.11 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
690	13753	26681	14.23	2.0E-70	N42161.1	EST_HUMAN	Y07A10.11 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
708	13768	28704	1.39	2.0E-70	AI246899.1	EST_HUMAN	g3f101.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1023	14069	27020	1.23	2.0E-70	892968	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1188	14228	27184	1.73	2.0E-70	7691863	NT	Homo sapiens KIAA0163 gene product (KIAA0163), mRNA
1188	14228	27185	1.73	2.0E-70	7691863	NT	Homo sapiens KIAA0163 gene product (KIAA0163), mRNA
1684	14686	27671	1.53	2.0E-70	AA180093.1	EST_HUMAN	TR-G1041293 G1041293 D2085.5 ;
1684	14686	27672	1.53	2.0E-70	AA180093.1	EST_HUMAN	TR-G1041293 G1041293 D2085.5 ;
1757	14786	27771	1.73	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2328	15339		5.47	2.0E-70	AA054010.1	EST_HUMAN	P03345 GAG POLYPEPTIDE ;
3641	16684	29900	1.06	2.0E-70	H37688.1	EST_HUMAN	yc58B04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:191569 5'
3833	16873	29774	0.86	2.0E-70	AL133207.2	NT	Novel human gene mapping to chromosome X
4079	17114	30010	5.83	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-3 (MYH10) mRNA, partial cds
4221	17250	30735	0.96	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4221	17250	30739	0.96	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
5593	18659	31658	9.14	2.0E-70	X72692.1	NT	H. sapiens gene for schwannomin (CS9)
5593	18659	31659	9.14	2.0E-70	X72692.1	NT	H. sapiens gene for schwannomin (CS9)
6328	19398	32640	1.1	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6780	19944	33128	3.84	2.0E-70	D12825.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
8824	19878	33167	11.3	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dyenin intermediate chain 1 mRNA, complete cds



Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9026	21992	35412	1.61	7.0E-71	AA705457.1	EST_HUMAN	291a06.s1 Soares_fetal_liver_spleen_1NF.LS_51 Homo sapiens cDNA clone IMAGE:462228 3'
11656	24594	39168	1.76	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2220	10234	28238	8.79	5.0E-71	AF058322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4146	17177	30056	1.1	5.0E-71	AW818403.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
5991	19056	32264	2.02	6.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6519	18873	33162	1.15	5.0E-71	11941408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7105	20039	33341	0.72	5.0E-71	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7197	19398	31243	0.64	5.0E-71	AB033106.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
7353	20323	33671	0.69	5.0E-71	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7753	20708	34075	1.62	5.0E-71	M38108.1	NT	Homo sapiens neurofibromatosis protein type 1 mRNA, 3' end of cds
7974	20913	34304	0.84	5.0E-71	11528445	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8007	20945	34340	22.85	5.0E-71	AF072810.1	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8688	21835	35256	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8898	21835	35257	0.61	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
10271	22196		2.45	5.0E-71	X13407.1	NT	Homo sapiens gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
11329	24279	37803	7.5	5.0E-71	11439514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11525	24466	38020	2.01	5.0E-71	11438089	NT	Homo sapiens similar to hypothetical protein FLJ20763 (H. sapiens) (LOC553325), mRNA
12198	26043	38624	1.81	5.0E-71	11417692	NT	Homo sapiens calcitriol binding protein 1 (KIAA0330), mRNA
104	13220	26145	1.04	4.0E-71	4607592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
350	13439	26363	58.4	4.0E-71	AF167626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
350	13439	26364	58.4	4.0E-71	AF167626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2897	15955	26973	1.9	4.0E-71	4605880	NT	Homo sapiens plasminogen (PLG) mRNA
4459	17495	30372	4.75	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100), complete cds
6022	18036	30621	6.04	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
8308	21337		1.34	3.0E-71	AU135734.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5
11061	24014	37538	2.84	3.0E-71	AA557683.1	EST_HUMAN	repetitive element
1234	14271	27231	5.56	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
5393	19496	31374	8.35	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5393	19496	31375	8.35	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7160	18392	31236	0.57	2.0E-71	AL042493.1	EST_HUMAN	DKFZ434D1721.1 434 (synonym: hncs) Homo sapiens cDNA clone DKFZ434D1721 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6350	22324	35752	0.5	2.0E-71	BF195585.1	EST_HUMAN	7n55611.x1 NCL_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3671221 3' similar to TR-Q82165 Q82165 PUTATIVE FOUR REPEAT ION CHANNEL ;
10860	23870	37382	4.19	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10950	23870	37383	4.19	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
11053	24018	37539	3.41	2.0E-71	BE018477.1	EST_HUMAN	bb51a05.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P64727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B ;
11907	24788	38377	2.27	2.0E-71	R56526.1	EST_HUMAN	317611.1 Scores breast ZNF681 Homo sapiens cDNA clone IMAGE:154772 5'
12316	25121		7.13	2.0E-71	T85489.1	EST_HUMAN	ye43603.1 Scores fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:120520 5'
639	13705	26926	1.69	1.0E-71	AI077927.1	EST_HUMAN	oy15603.1 Scores senescent fibroblasts NIHHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.52 LOR1 repetitive element ;
840	13893	26945	1.68	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1102	14140	27098	0.21	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exon 2 through 15 and complete cds
1343	14378	27347	9.86	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 200 (p4K230) mRNA, complete cds
2084	15111	28131	1.29	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2084	15111	28132	1.29	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2703	15699	28714	4.81	1.0E-71	7697193	NT	Homo sapiens hairpin/hairpin-of-split related with YRPW motif-like (HEY1), mRNA
3610	16855	29572	5.11	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3610	16855	29573	5.11	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3682	16705	29610	1.19	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3682	16705	29620	1.18	1.0E-71	BE122850.1	EST_HUMAN	clone 02_15 5' similar to Homo sapiens chromosome 19
3764	16768	29707	1.56	1.0E-71	AF218604.1	NT	Homo sapiens epidermal keratinocyte subtraction library: Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
4497	17522	30409	2.16	1.0E-71	D28478.1	NT	Homo sapiens atrial natriuretic precursor (ATRN) gene, exon 19
4622	17643	30531	0.68	1.0E-71	H23176.1	EST_HUMAN	Homo sapiens mRNA for KIAA0045 gene, complete cds
6308	18658	33256	1.38	1.0E-71	11426182	NT	ym5h10.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
7292	20264	33598	1.28	1.0E-71	AB011131.1	NT	Homo sapiens GON5 (general control of amino-acid synthesis, yeast, homolog-like 2 (GON5L2), mRNA
7533	20486	33957	12.67	1.0E-71	U60753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8486	21454	34371	0.76	1.0E-71	AF105287.1	NT	Homo sapiens glycican-8 (GPO8) mRNA, complete cds
8503	21477	34890	2.14	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (195SD) (MYOM2), mRNA
8786	21766	35177	4.49	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10598 (FLJ10598), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8790	21756	35178	4.49	1.0E-71	8822811	NT	Homo sapiens hypothetical protein FLJ10988 (FLJ10988), mRNA
9594	22546	35607	0.83	1.0E-71	S72352.1	NT	CSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
10387	23220	36767	9.49	1.0E-71	AY007643.1	NT	Homo sapiens cyclochrome c oxidase subunit VII-related protein gene, complete cds
10428	23360		3.08	1.0E-71	AY761217.1	EST_HUMAN	AY761217 MDS Homo sapiens cDNA clone MDSEIA03.5'
10804	23824	37338	1.52	1.0E-71	U1433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11137	24097		2.43	1.0E-71	AY761217.1	EST_HUMAN	AY761217 MDS Homo sapiens cDNA clone MDSEIA03.5'
11228	24181	37706	2.12	1.0E-71	U1418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11481	24424	37973	2.27	1.0E-71	U1417181	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11481	24424	37974	2.27	1.0E-71	U1417181	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12831	25349		3.13	1.0E-71	AB011369.1	NT	Homo sapiens gene for AP-6, complete cds
407	13480	26414	1.23	9.0E-72	AB87685.1	EST_HUMAN	w85503.x1 NCI CGAP Lu10 Homo sapiens cDNA clone IMAGE:2423188.3' similar to TR:O86705 O86705
407	13480	26415	1.23	9.0E-72	AB87685.1	EST_HUMAN	w85503.x1 NCI CGAP Lu10 Homo sapiens cDNA clone IMAGE:2423188.3' similar to TR:O86705 O86705
6232	19306	32538	0.89	8.0E-72	BF035752.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
11444	24387	37927	2.55	8.0E-72	U1424480	NT	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
11444	24387	37928	2.55	8.0E-72	U1424480	NT	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element
11444	24387	37929	2.55	8.0E-72	U1424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
11444	24387	37929	2.55	8.0E-72	U1424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4139	17170	30056	1.24	7.0E-72	4501868	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30057	1.24	7.0E-72	4501868	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4139	17170	30058	1.24	7.0E-72	4501868	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7331	20302	33846	2.87	7.0E-72	S41894.1	NT	(pseudo gene) PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12800	25628		1.52	7.0E-72	F20259.1	EST_HUMAN	HSPD13970 H33 Homo sapiens cDNA clone s4000051G02
8727	21695		4.9	6.0E-72	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C048
65	13184	28102	4.86	5.0E-72	BF333707.1	EST_HUMAN	QVQ-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
65	13184	28103	4.86	5.0E-72	BF333707.1	EST_HUMAN	QVQ-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
66	13184	28102	13.05	5.0E-72	BF333707.1	EST_HUMAN	QVQ-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
68	13184	28103	13.05	5.0E-72	BF333707.1	EST_HUMAN	QVQ-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1141	14184		2.78	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7138	20114	33427	1.95	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003761.5'



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Table 4  
Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8163	21101	34500	0.65	5.0E-72	AA316632.1	EST_HUMAN	EST188312 HCC cell line (metastasis to liver in mouse)    Homo sapiens cDNA 5' end similar to similar to FAC1
9129	22065	35523	4.14	5.0E-72	AW161274.1	EST_HUMAN	au08003.y1 Schneider field brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to
10320	23244	35724	0.56	5.0E-72	AV724632.1	EST_HUMAN	TRQ89788 Qsar845 HYPOTHETICAL 32.4 KD PROTEIN, contains element MSR1 repetitive element ;
11573	24511	38067	2.74	5.0E-72	BF331571.1	EST_HUMAN	ATV24632 HTB Homo sapiens cDNA clone HTBARK01 5'
11573	24511	38068	2.74	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT05998-010800-005-405 BT05998 Homo sapiens cDNA
12389	25929		2.52	5.0E-72	BE926645.1	EST_HUMAN	MR4-BT05998-010800-005-405 BT05998 Homo sapiens cDNA
4890	17877		1.12	4.0E-72	11034844	NT	QV1-BT05932-283800-342-410 BT0532 Homo sapiens cDNA
5540	18637	31677	0.75	4.0E-72	AF170025.1	NT	Homo sapiens hypothetical protein dJ107520.2 (DJ107520.2), mRNA
6709	19765	33046	0.83	4.0E-72	T87947.1	EST_HUMAN	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
7639	20569	33063	1.28	4.0E-72	5728857	NT	Y683a01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
10143	23069	36546	1.24	4.0E-72	8923659	NT	SP-A44282 A44282 RETROVIRUS-RELATED POL. POLYPEPTIDE, HUMAN ;
10758	23679	37174	0.49	4.0E-72	AW836230.1	EST_HUMAN	Homo sapiens hct1 domain and RLD 2 (HERC2), mRNA
10758	23679	37175	0.49	4.0E-72	AW836230.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20768 (FLJ20768), mRNA
							RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
							RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
							q87c02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848730 3' similar to
10786	23707	37206	1.24	4.0E-72	A1248796.1	EST_HUMAN	TRQ14498 Q14498 SPLICING FACTOR, [1] contains Alu repetitive element, contains element L1 repetitive element ;
11616	24554	38116	1.54	4.0E-72	AA465388.1	EST_HUMAN	aa23009.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR
11616	24554	38116	1.54	4.0E-72	AA465388.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
11857	24739	38324	5.09	4.0E-72	H79421.1	EST_HUMAN	aa23009.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR
11988	24865	38461	1.72	4.0E-72	T81910.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR. ;
							yJ28403.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:23684 5'
							yJ28403.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
12728	25382	31748	4.28	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
21	13141	26039	1.89	3.0E-72	5031876	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
904	13959		1.23	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.a1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1159	14201	27152	5.57	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1159	14201	27163	5.57	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1188	14238	27193	0.71	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1188	14238	27194	0.71	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1523	14555	27528	1.45	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) BAYLOR-HGSC projectTCAA Homo sapiens cDNA clone TCAAP1252
3090	16148	29052	13.29	3.0E-72	AJ239483.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3292	16345	29255	2.41	3.0E-72	8823548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3636	16676	29778	2.82	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha alpha T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4578	17568	30482	3.77	3.0E-72	11416196	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4800	17817	30710	1.31	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4800	17817	30711	1.31	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
5149	18168	31037	1.02	3.0E-72	AW958677.1	EST_HUMAN	EST371747 MAGE resequences, MAGF Homo sapiens cDNA
5558	18684	31037	1.06	3.0E-72	4759063	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6092	19171	32386	1.91	3.0E-72	AF073567.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6092	19171	32387	1.91	3.0E-72	AF073567.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6290	19362	32600	4.78	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6290	19362	32601	4.78	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6767	19821	33103	3.89	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7838	20785	34160	1.87	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (bTF2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
8516	21484	34698	1.07	3.0E-72	5031862	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
10797	23718	37220	7.09	3.0E-72	X98269.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
11912	24783	38383	3.23	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
11912	24783	38384	3.23	3.0E-72	11424091	NT	Homo sapiens CD37 antigen (CD37), mRNA
12078	24950	39546	3.56	3.0E-72	AF190864.1	NT	Homo sapiens ADP-ribosylation factor binding protein GGA3 (GGA3) mRNA, complete cds
6059	19160	32362	1.53	2.0E-72	11426871	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
8451	22415	35852	0.82	2.0E-72	BF308560.1	EST_HUMAN	60180419F1 NIH_MGC-17 Homo sapiens cDNA clone IMAGE:4131461.5'
8451	22415	35853	0.82	2.0E-72	BF308560.1	EST_HUMAN	60180419F1 NIH_MGC-17 Homo sapiens cDNA clone IMAGE:4131461.5'
11092	24052	37575	2.4	2.0E-72	AA789277.1	EST_HUMAN	q26b09.e7 Soares, tests, NHT Homo sapiens cDNA clone 1391609.3' similar to gb-X02067.H.sapiens mRNA for TSL RNA pseudogene (HUMAN);
12726	25379	31745	6.47	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylcholine transferase (PCAT) mRNA, complete cds
9861	18950	32136	3.76	1.0E-72	7657878	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6711	18767	33046	1.24	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORT SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6711	19767	33047	1.24	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6768	25693	33126	1.3	1.0E-72	AV761618.1	EST_HUMAN	AV761618 NP2 Homo sapiens cDNA clone NP2A1E11 5'
7899	20842	34224	3.72	1.0E-72	BE175434.1	EST_HUMAN	RC4-H10578-170300-072-002 HT0578 Homo sapiens cDNA
7899	20842	34225	3.72	1.0E-72	BE175434.1	EST_HUMAN	RC4-H10578-170300-072-002 HT0578 Homo sapiens cDNA
8949	22876	36338	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2), mRNA, complete cds
8949	22876	36339	7.79	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2), complete cds
1455	14488	27463	1.53	9.0E-73	AW374968.1	EST_HUMAN	MRQ-GT0063-071099-002-H11 CT0063 Homo sapiens cDNA
6166	19231	32462	0.94	9.0E-73	11625893	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGLIP, p55 subfamily member 3) (MPP3), mRNA
11297	24247		18.46	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L16a (RPL16A), mRNA
1039	14084	27035	0.93	8.0E-73	AW071755.1	EST_HUMAN	ws5506.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501068 3' similar to TR:Q59050
9660	18766	31924	0.79	8.0E-73	4505798	NT	Q59050 HYPOTHETICAL PROTEIN MJ1656.
6724	19780	33059	5.01	8.0E-73	11426469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A), mRNA
8432	21401	34814	2.3	8.0E-73	AF113129.1	NT	Homo sapiens lysosome homolog (LOC57151), mRNA
							Homo sapiens vacuolar ATPase isoform V46B mRNA, complete cds
8708	22661	38117	7.24	8.0E-73	BE019000.1	EST_HUMAN	bb62a08.Y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:XD4098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
10097	23023	39497	2.34	8.0E-73	11626037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10097	23023	39498	2.34	8.0E-73	11626037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12010	24687	36463	3.64	8.0E-73	AF084520.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12765	25416	37353	3.45	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
11336	14179	27130	1.3	7.0E-73	8923260	NT	Homo sapiens hypothetical protein FL20309 (FL20309), mRNA
3312	19365	29285	1	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4681	17896		1.74	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C008
159	13982		2.28	8.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7378	20348	33699	3.68	8.0E-73	BE166574.1	EST_HUMAN	QY0-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5326	18432	31184	2.11	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM44A1), mRNA
1344	14378	27346	1.19	3.0E-73	AW843789.1	EST_HUMAN	CMO-CH0044-260100-164-408 CN0044 Homo sapiens cDNA
1879	14804	27604	1.34	3.0E-73	11435913	NT	Homo sapiens home-binding protein (HEBP), mRNA
1879	14804	27605	1.34	3.0E-73	11435913	NT	Homo sapiens home-binding protein (HEBP), mRNA
6656	19809	33204	0.86	3.0E-73	AA135403.1	EST_HUMAN	zn95d4.5t Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565650 3' similar to
9111	22077	35503	0.54	3.0E-73	AV729428.1	EST_HUMAN	gb:223084_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
							AV729428 HTC Homo sapiens cDNA clone HTCAA071 5'

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9111	22077	35504	0.54	3.0E-73	AV728428.1	EST_HUMAN	AY728428 HTG Homo sapiens cDNA clone HTCAAF071 5'
11047	24011		1.65	3.0E-73	XQ9680.1	NT	H. sapiens SH3GLP2 pseudogene, 5' end
13017	25567		1.35	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13021	25559		1.97	3.0E-73	AW868081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
852	13908	26868	1.9	2.0E-73	AF138697.1	NT	Homo sapiens BASST (BASS1) mRNA, partial cds
1563	14955		2.95	2.0E-73	AW868081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2308	18318		1.58	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3166	16251	28170	3.89	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3561	16607	28527	0.77	2.0E-73	7659539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile 2, parkin (PARK2), transcript variant 3, mRNA
3561	18607	26528	0.77	2.0E-73	7659539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile 2, parkin (PARK2), transcript variant 3, mRNA
6577	19537	32902	0.7	2.0E-73	AF085824.1	NT	Mus musculus rhodoc-interacting citron kinase (Crik) mRNA, complete cds
6577	19537	32903	0.7	2.0E-73	AF085824.1	NT	Mus musculus rhodoc-interacting citron kinase (Crik) mRNA, complete cds
6527	19695	32964	6.38	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1597 protein, partial cds
6558	19911	33206	1.82	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6558	19911	33207	1.52	2.0E-73	11431471	NT	Human peripheral myelin protein 22 mRNA, complete cds
8092	21028	34427	0.58	2.0E-73	M94048.1	NT	Homo sapiens mRNA for KIAA1529 protein, partial cds
8099	21035	34435	0.77	2.0E-73	AB037760.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
8890	22843	36256	0.55	2.0E-73	AF198349.1	NT	Ovis aries Dach2 protein (Dach2) mRNA, complete cds
8890	22843	36300	0.65	2.0E-73	AF198349.1	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10788	23709	37211	1.12	2.0E-73	4504165	NT	Homo sapiens superinilin (SVIL), transcript variant 1, mRNA
10893	23783	37284	1.69	2.0E-73	11456980	NT	Homo sapiens superinilin (SVIL), transcript variant 1, mRNA
10893	23783	37285	1.69	2.0E-73	11456980	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
11107	24067	37599	1.49	2.0E-73	11431598	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
11395	24341	37872	2.84	2.0E-73	4576712	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11395	24341	37873	2.84	2.0E-73	4576712	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11420	24364	37869	1.81	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12691	14885		1.81	2.0E-73	AB028982.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1798	14827	27814	2.91	1.0E-73	AJ121585.1	EST_HUMAN	AJ121585 MAMMA1 Homo sapiens cDNA clone MAMMA100490 5'
6495	19559	32810	1.2	1.0E-73	BE151283.1	EST_HUMAN	CM1-110282-11189-042h10 HT0282 Homo sapiens cDNA
9557	22793	38244	1.47	1.0E-73	AJ147427.1	EST_HUMAN	cg61007.1 Scores: testis, NHT Homo sapiens cDNA clone IMAGE1839637 5' similar to contains element 1MER22 repetitive element:

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value:	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11779	23334	37455	2.1	1.0E-73	BE38477.1	EST_HUMAN	601276073F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:361705 5'
742	13303	26742	1.47	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6021	19104	32309	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
6021	19104	32307	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1968	14789	27989	4.33	7.0E-74	AJ001689.1	NT	Homo sapiens NKX2-2 gene, exon 10
3339	16350	29311	2.01	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9598	22902	36051	2.25	7.0E-74	BE907432.1	EST_HUMAN	601649294F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3922997 5'
12784	25417	31734	4.84	7.0E-74	BE266305.1	EST_HUMAN	601181927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:333855 5'
1124	14168	27120	5.19	6.0E-74	AF109607.1	NT	Homo sapiens S164 gene, partial cds, PST and hypothetical protein genes, complete cds, and S171 gene, partial cds
1631	14684	27639	1.03	6.0E-74	AW263177.1	EST_HUMAN	x078g07.xt Soares_NFL_T_OBC_ST Homo sapiens cDNA clone IMAGE:2700888 3'
2324	15335	28357	7.92	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2324	15335	28358	7.92	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2875	15934	28852	1.12	6.0E-74	AW014039.1	EST_HUMAN	U1H-B10-aah-h-03-01-1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2875	15934	28853	1.12	6.0E-74	AW014039.1	EST_HUMAN	U1H-B10-aah-h-03-01-1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3726	16768	28679	1.28	6.0E-74	BE048846.1	EST_HUMAN	h54e11.xt NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3726	16768	28680	1.28	6.0E-74	BE048846.1	EST_HUMAN	h54e11.xt NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5065	18075	30955	4.18	6.0E-74	4759135	NT	Homo sapiens DEAD/1H (Asp-Glu-Ala-Asp-His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5065	18075	30956	4.18	6.0E-74	4759135	NT	Homo sapiens DEAD/1H (Asp-Glu-Ala-Asp-His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5439	18541	31451	3.08	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
808	13691	28617	2.09	5.0E-74	AW020988.1	EST_HUMAN	dfr7c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2713	15707	31492	3.88	6.0E-74	AW362768.1	EST_HUMAN	PMO-CT0269-271099-001-H07 CT0269 Homo sapiens cDNA
5481	18591	31492	1.76	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5887	18976	32168	12.05	6.0E-74	X89970.1	NT	H.sapiens mRNA for TPOR16 protein
5838	18024	32218	7.23	5.0E-74	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6013	18098	32256	2.71	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6013	18098	32297	2.71	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7080	20101	33412	2.18	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7832	20101	33412	0.54	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8371	21340	34751	3.05	5.0E-74	11349483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
11097	24048	37670	4.06	6.0E-74	Y00420.1	NT	H.sapiens mRNA for HIP-1

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11087	24048	37571	4.08	5.0E-74	Y08420.1	NT	H sapiens mRNA for HIP-1
279	13374	28303	1.85	4.0E-74	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
853	13309	28987	5.8	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1978	15000	28902	2.21	4.0E-74	AB028988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1979	15000	28903	2.21	4.0E-74	AB028988.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2088	15103	28120	2.38	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2088	15103	28121	2.38	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2142	15159	28175	1.91	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2434	15441	28459	0.91	4.0E-74	ALJ006976.1	NT	Homo sapiens PTP gene
3107	16184	29076	5.45	4.0E-74	ALJ006978.1	NT	Homo sapiens PTP gene
4091	17123	30018	1.23	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4697	17609	30504	2.08	4.0E-74	7662183	NT	Homo sapiens KIAA0668 gene product (KIAA0668), mRNA
4646	17987	30654	0.99	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5055	18067	30949	0.74	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
8895	21881		21.81	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
9727	22755	36208	2.57	3.0E-74	M78884.1	EST_HUMAN	EST01132 Subcloned Hippocampus, Striatum (cat. #939205) Homo sapiens cDNA clone HHOPF51
10703	23625	37122	2.89	3.0E-74	AA001493.1	EST_HUMAN	hot7805.s1 NCI CGAP_Phot1 Homo sapiens cDNA clone IMAGE:100984.3
959	14012	28965	58.94	2.0E-74	7669481	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
959	14012	28966	58.94	2.0E-74	7669481	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1178	14220	27176	0.9	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-147D
1249	14285	27251	1.32	2.0E-74	AB060528.1	EST_HUMAN	wo61607.x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204.3 similar to SW:GG95_HUMAN
1599	14631	27806	3.54	2.0E-74	4885198	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element; homolog (EGF) mRNA
1599	14631	27806	3.54	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1599	14631	27807	3.54	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2600	15008	28532	3.02	2.0E-74	AL557280.1	EST_HUMAN	PT2.1_16_G11.7 tumor2 Homo sapiens cDNA 3'
5042	18055	30933	3.67	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5042	18055	30934	3.67	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5046	18059	30936	0.93	2.0E-74	J02883.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5896	25647	32174	2.03	2.0E-74	BE711134.1	EST_HUMAN	RC8-H10078-220500-011-C03 H10078 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5999	25650	32280	1.83	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5999	25650	32281	1.93	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6077	25650	32280	2.58	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6077	25650	32281	2.58	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7310	20281	33621	1.14	2.0E-74	BF030788.1	EST_HUMAN	301557624F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8272	12141	34652	1.35	2.0E-74	AB0307816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9737	22765	36220	8.08	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12058	24631	38528	1.72	2.0E-74	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
12621	26252		3.11	2.0E-74	7657334	EST_HUMAN	z98406.s1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:628018 3'
65	13175	26098	2.22	1.0E-74	7657334	NT	Homo sapiens Meschazepin/NIK-related kinase (MINK), mRNA
337	13428	26348	3.95	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA
500	13572	26494	1.1	1.0E-74	8022828	NT	Homo sapiens hypothetical protein FLJ11025 (FLJ11028), mRNA
507	13578	26495	8.16	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
603	13670	26584	2.15	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2235	15249	28273	2.21	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
3156	16212	29127	3.56	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3391	16893	28688	2.83	1.0E-74	4759937	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3943	16993	28689	0.79	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3943	16993	28689	0.79	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3982	17032	29941	5.75	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4052	17126	30019	0.98	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0542-270300-019-005 BT0542 Homo sapiens cDNA
4296	17325	30205	0.71	1.0E-74	BE46769.1	EST_HUMAN	h27308.s1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP-B0311.12
5217	18226	31100	1.36	1.0E-74	D83327.1	NT	CE17561.1
6803	19916	33210	0.97	1.0E-74	M89914.1	NT	Homo sapiens DORR1 mRNA, partial cds
7888	20832	34211	1.17	1.0E-74	1141797	NT	Homo sapiens neurofibromin (NF1) gene, complete cds
8391	21360	34769	1.1	1.0E-74	BE549105.1	EST_HUMAN	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8391	21360	34769	1.1	1.0E-74	BE549105.1	EST_HUMAN	301070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9157	22123	35552	3.85	1.0E-74	AF214562.1	NT	301070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9186	22162	35581	0.71	1.0E-74	BF351951.1	EST_HUMAN	Homo sapiens tracheal epithelium enriched protein (TLPUNC) gene, complete cds
10800	23522	37015	0.65	1.0E-74	AL251650.1	NT	MFO-HT0559-230600-021-a03 HT0559 Homo sapiens cDNA
10800	23522	37015	0.65	1.0E-74	AL251650.1	NT	Homo sapiens partial AK155 gene for AK 155 protein, exons 1-3 and joined CDS
10847	23767	37268	1.51	1.0E-74	11420549	NT	Homo sapiens partial AK155 gene for AK 155 protein, exons 1-3 and joined CDS
12100	24871	38568	1.5	1.0E-74	AB007641.1	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
							Homo sapiens mRNA for KIAA0472 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12154	25012	38616	3.9	1.0E-74	11417858	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12235	25067		7.14	1.0E-74	11417858	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12848	25458		1.52	1.0E-74	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2852	15849		6.34	8.0E-76	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12843	25265		1.81	8.0E-76	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2229	15340	28382	1.16	8.0E-76	AB17415.1	EST_HUMAN	W438a03.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
5201	18210	31084	0.91	5.0E-76	AB814305.1	EST_HUMAN	MRU-SN0040-08000-006-008 SN0040 Homo sapiens cDNA
8075	21012	34411	0.51	5.0E-76	AA573448.1	EST_HUMAN	hM89d03.s1 NCI CGAP_C63 Homo sapiens cDNA clone IMAGE:1028933 3'
8075	21012	34412	0.51	5.0E-76	AA573448.1	EST_HUMAN	hM89d03.s1 NCI CGAP_C63 Homo sapiens cDNA clone IMAGE:1028933 3'
8259	22225	35654	1.13	5.0E-76	BE272325.1	EST_HUMAN	601126068F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
9472	22436	35874	0.94	5.0E-76	AA13261.1	EST_HUMAN	z017e08.r1 Stralagene colon (#337204) Homo sapiens cDNA clone IMAGE:387174 5'
9549	22512	35961	0.89	5.0E-76	BE661655.1	EST_HUMAN	601346909F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3687458 5'
9549	22512	35962	0.89	5.0E-76	BE661655.1	EST_HUMAN	601346909F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3687458 5'
9728	22756	38209	1.42	5.0E-76	BF690254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10594	23516	37007	2.9	5.0E-76	AG39823.1	EST_HUMAN	h31c12.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2242380 3' similar to Tr:P07361 P07361
1112	13223	28147	1.68	4.0E-76	BE081333.1	EST_HUMAN	HYPOPHYSICAL 20.1 KD PROTEIN
459	15332		2.86	4.0E-76	BE081333.1	EST_HUMAN	QY1-BT0632-210260-079-e02 BT0632 Homo sapiens cDNA
1780	14809	27706	1.73	4.0E-76	AW697230.1	EST_HUMAN	Y89H08.r1 Soera melanocyte ZNH1M Homo sapiens cDNA clone IMAGE:269055 5'
2881	15521	28841	4.5	4.0E-76	BE409464.1	EST_HUMAN	601303666F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636344 5'
3912	16558	29482	0.93	4.0E-76	8922837	NT	Homo sapiens hypochelated protein FLJ10747 (FLJ10747), mRNA
5907	18703	31850	0.65	4.0E-76	11417846	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5907	18703	31860	0.65	4.0E-76	11417846	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6400	19468	32716	6.35	4.0E-76	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110d) (EIF3S8), mRNA
6923	18973	33270	1.81	4.0E-76	11417846	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6923	18973	33271	1.81	4.0E-76	11417846	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6923	18973	33272	1.81	4.0E-76	11417846	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1004	14055	27007	4.38	3.0E-76	AF157623.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
1005	14055	27007	3.22	3.0E-76	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1853	14879	27875	2.36	3.0E-76	AB011153.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2430	15437	28454	5.12	3.0E-76	4759103	NT	Homo sapiens mRNA for KIA0581 protein, partial cds
3034	16092	29010	1.09	3.0E-76	AL169201.2	NT	Homo sapiens synaptosomal-associated protein, 25kD (SNAP25) mRNA
							Homo sapiens chromosome 21 segment HS21C001



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3203	16258	281177	1.13	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0881 protein, partial cds
3381	16411	283334	0.85	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3391	16411	283335	0.85	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3752	16784	28705	0.78	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4197	17228	301118	1.03	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4468	17492	30379	0.71	3.0E-75	7662421	NT	Homo sapiens KIAA0871 protein (KIAA0871), mRNA
5323	18428	31178	1.15	3.0E-75	11420356	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5323	18428	31180	1.15	3.0E-75	11420356	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6537	18714	32681	0.51	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6537	18714	32692	0.51	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6835	20159	33479	1.78	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6835	20159	33480	1.78	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7342	20313	33656	4.47	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7342	20313	33657	4.47	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7884	20828	34204	2.82	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7884	20828	34205	2.82	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8336	22301	35730	1.21	3.0E-75	11420304	NT	Homo sapiens enal 1 (Grosophilin homolog), zinc finger protein (SNF1), mRNA
10037	22584	36431	0.85	3.0E-75	11420222	NT	Homo sapiens Drepanella Kelch like protein (DKELCH), mRNA
10908	23828	37241	4.16	3.0E-75	11436430	NT	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
12085	24857	38552	1.73	3.0E-75	6715598	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
12085	24857	38553	1.73	3.0E-75	6715598	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
5755	18850		1.41	2.0E-76	AV734860.1	EST_HUMAN	AV734860 cDNA Homo sapiens cDNA clone cDABED02 5'
9103	22069	35495	2.55	2.0E-76	AI311783.1	EST_HUMAN	q9r1602.x1 NCL CGAP_K46 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POLYOMV GENE;
2311	15223	28346	7.79	1.0E-76	AW168195.1	EST_HUMAN	x60602.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains P1R7.11
2357	16015	28943	3.35	1.0E-75	X52221.1	NT	P1R7 repetitive element;
4718	17738	30630	0.65	1.0E-76	BE276301.1	EST_HUMAN	H.sapiens ERCC22 gene, exons 1 & 2 (partial)
5224	18232	31107	0.7	1.0E-76	BE694192.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
7843	20790	34165	0.78	1.0E-76	BE082528.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
7843	20790	34166	0.78	1.0E-76	BE082528.1	EST_HUMAN	IC5-B10640-020300-031-H03 B10640 Homo sapiens cDNA
7843	20790	34166	0.78	1.0E-76	BE092528.1	EST_HUMAN	IC5-B10640-020300-031-H03 B10640 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8757	21724		12.42	1.0E-75	AA398270.1	EST_HUMAN	z57803.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gbM13932.40S
9783	22724	36178	4.03	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
9783	22724	36180	4.03	1.0E-75	BF313645.1	EST_HUMAN	60160294F1 NIH_MGC.19 Homo sapiens cDNA clone IMAGE:4126678 5'
11229	24182		3.78	1.0E-75	AA664377.1	EST_HUMAN	60160294F1 NIH_MGC.19 Homo sapiens cDNA clone IMAGE:4126678 5'
11428	24372	37910	2.13	1.0E-75	AF223391.1	NT	ac77008.s1 Stragene lung (9837210) Homo sapiens cDNA clone IMAGE:368593 3'
12438	18232	31107	1.72	1.0E-75	BE894182.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
46	13109	28070	2.23	9.0E-76	A1652948.1	EST_HUMAN	601437130F1 NIH_MGC.72 Homo sapiens cDNA clone IMAGE:3922303 6'
46	13169	28071	2.23	9.0E-76	A1652948.1	EST_HUMAN	w630010.x1 NCL_OGAP_G008 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR-O75235 O75235
2425	15432		0.95	8.0E-76	AA702415.1	EST_HUMAN	TRAP1:
10281	23185	36870	37.43	9.0E-76	M12937.1	NT	TRAP1:
837	13960	28041	0.98	8.0E-76	4504374	NT	285507.s1 Scores_fetal_liver脾脾_1NF.LS.S1 Homo sapiens cDNA clone IMAGE:447541 3'
837	13960	28542	0.98	8.0E-76	4504374	NT	Human ferritin Heavy subunit mRNA, complete cds
2921	15979	28904	1.28	8.0E-76	7706724	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
6285	18387	32808	4.79	8.0E-76	11421442	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
7731	20986	34049	1.41	8.0E-76	11435215	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7816	20765	34141	0.97	8.0E-76	11419212	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8639	21807	35230	0.84	8.0E-76	11416981	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
9453	22417	35855	0.45	8.0E-76	A5046784.1	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
10744	23668	37161	1.41	8.0E-76	M13792.1	NT	Homo sapiens mRNA for KIAA1544 protein, partial cds
11028	23991	37519	4.09	8.0E-76	10442821	NT	Homo sapiens adenosine deaminase (ADA) gene, complete cds
12767	25408		2.29	8.0E-76	11417862	NT	Homo sapiens baculoviral IAP repeat-containing 8 (BIRC8), mRNA
777	13638	28782	1.41	7.0E-76	5016002	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3305	16358	29277	28.65	7.0E-76	A056490.1	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3311	16364	29284	8.23	7.0E-76	4505032	NT	Homo sapiens cAMP-specific phosphodiesterase 6A (PDE6A) mRNA, partial cds
4399	17427	30311	4.82	7.0E-76	4507184	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4399	17427	30312	4.62	7.0E-76	4507184	NT	Homo sapiens septalactin reductase (7.8-dihydropteridin-NADP+ oxidoreductase) (SPR) mRNA
1238	14274		12.96	6.0E-76	BE398253.1	EST_HUMAN	Homo sapiens septalactin reductase (7.8-dihydropteridin-NADP+ oxidoreductase) (SPR) mRNA
11763	23946	37469	2.36	6.0E-76	BE273201.1	EST_HUMAN	601312018F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3658767 5'
							801142253F1 NIH_MGC.14 Homo sapiens cDNA clone IMAGE:3509029 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1960	14682	27683	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1960	14682	27684	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1960	14682	27685	8.97	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3220	16275	28199	1.01	4.0E-76	BE814098.1	EST_HUMAN	Q15-BN0047-270700-283-q06 BN0047 Homo sapiens cDNA
5342	18447	31200	1.08	4.0E-76	BE783412.1	EST_HUMAN	60147725F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3874470.5'
10384	23305	36783	6.69	4.0E-76	D81025.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujikawa) Homo sapiens cDNA clone GEN-178G01.5'
10384	23306	36784	6.69	4.0E-76	D81025.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujikawa) Homo sapiens cDNA clone GEN-178G01.5'
630	13695	26814	1.94	3.0E-76	BF516262.1	EST_HUMAN	U1H-BW1-anz-b-04-04U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862.3'
630	13695	26815	1.94	3.0E-76	BF516262.1	EST_HUMAN	U1H-BW1-anz-b-04-04U1.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862.3'
1603	14635	27612	9.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1603	14635	27612	9.36	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3442	16488	29407	5.03	3.0E-76	BF375689.1	EST_HUMAN	RC5-S10300-180100-033-A03 S10300 Homo sapiens cDNA
3442	16489	29408	5.03	3.0E-76	BF375689.1	EST_HUMAN	RC5-S10300-180100-033-A03 S10300 Homo sapiens cDNA
4105	17139	30034	14.72	3.0E-76	BE348693.1	EST_HUMAN	R67H12.x1 NCL CGAP_Luz4 Homo sapiens cDNA clone IMAGE:3151823.3' similar to TR:09-4686 O94886 KIAA0792 PROTEIN. ;
5301	18304	31165	0.68	3.0E-76	AV702891.1	EST_HUMAN	AV702891 ADB Homo sapiens cDNA clone ADBBSC02.5'
5308	18327	38612	2.12	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04.3'
6822	18912	32085	1	3.0E-76	AA160611.1	EST_HUMAN	gbl329r78 MIXED LINEAGE KINASE 1 (HUMAN);
6102	19181	32400	0.71	3.0E-76	AF027705.1	EST_HUMAN	z78c07.r1 Stratiotes panacea (8837208) Homo sapiens cDNA clone IMAGE:2565668.3'
6504	19568	32820	8.03	3.0E-76	AF286598.1	NT	ww75005.x1 Soares, thymus, NHFth Homo sapiens cDNA clone IMAGE:2565668.3'
8460	27498	34876	0.83	3.0E-76	N42871.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
10074	23001	36471	3.32	3.0E-76	AW299383.1	EST_HUMAN	x20g10.r1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:271842.5'
10068	23024	39499	1.08	3.0E-76	AA442309.1	EST_HUMAN	x46901.x1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2773009.3'
10068	23024	39500	1.08	3.0E-76	AA442309.1	EST_HUMAN	z564d11.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:757481.5'
12143	25760	31519	2.43	3.0E-76	AW687984.1	EST_HUMAN	EST138059 MAGC resequences, MAGC Homo sapiens cDNA
12248	25971	31301	4.4	3.0E-76	AW69465.1	EST_HUMAN	EST138828 MAGC resequences, MAGC Homo sapiens cDNA
281	13376	26305	1.46	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
342	13431	26352	2.6	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
342	13431	26353	2.6	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
461	13534	26573	1.14	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD78A) binding protein 1 (IGBP1) mRNA
592	13559	26573	1.12	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1032	14078	27031	1.37	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1637	14570	27542	1.74	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1337	14570	27543	1.74	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1945	14969	27687	1.03	2.0E-76	AA2363954.1	EST_HUMAN	zs00111.s1 Straglene schizo brain 311 Homo sapiens cDNA clone IMAGE:701925 3'
2854	15914	28837	3.73	2.0E-76	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3308	16361	29281	1.87	2.0E-76	AA445892.1	EST_HUMAN	zxc4602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780366 3' similar to SW:ITB5_HUMAN
3308	16361	29282	1.87	2.0E-76	AA445892.1	EST_HUMAN	P18004 INTEGRIN BETA-3 SUBUNIT PRECURSOR. ;
4651	17584	30476	1.01	2.0E-76	AL163263.2	NT	zxc4602.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780366 3' similar to SW:ITB5_HUMAN
4684	17669	30688	7.6	2.0E-76	AW876618.1	EST_HUMAN	P18004 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
5382	18486		0.87	2.0E-76	AF127845.1	NT	
5700	18795	31963	5.35	2.0E-76	AB028004.1	NT	Homo sapiens cDNA clone 21 segment HS21C083
7843	20603	33668	0.55	2.0E-76	11421326	NT	GV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
7698	20627	33681	0.76	2.0E-76	11426308	NT	Garilla gorilla olfactory receptor (GGO18) gene, partial cds
7924	20867	34255	1.65	2.0E-76	11427410	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10645	23567	37054	7.03	2.0E-76	11437211	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11265	24218	37742	2.84	2.0E-76	7549807	NT	Homo sapiens TPOCR68 protein (HSTPCR68P), mRNA
4328	17355	30241	3.37	1.0E-76	D63874.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
4328	17355	30242	3.37	1.0E-76	D63874.1	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
5523	18622	31957	6.74	1.0E-76	BE766537.1	EST_HUMAN	Human mRNA for HMG-1, complete cds
6372	19440		0.64	1.0E-76	AA333207.1	EST_HUMAN	601589808F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3944302 5'
7109	20043	33345	4.09	9.0E-77	BE889525.1	EST_HUMAN	EST737901 Embryo 8 week Homo sapiens cDNA 5' end
12823	25469		1.36	9.0E-77	BE410354.1	EST_HUMAN	601512435F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3913737 5'
							601302333F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3936753 5'
189	13289	28215	1.35	8.0E-77	R83144.1	EST_HUMAN	yp1102.r1 Soares breast 3NB-Hib2 Homo sapiens cDNA clone IMAGE:187165 5' similar to
4550	17573	30463	1.26	8.0E-77	BF205181.1	EST_HUMAN	SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1 ;
5528	18827	31663	1.83	8.0E-77	4506230	NT	601669282F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4109503 5'
11716	24679	38257	1.82	8.0E-77	AA019770.1	EST_HUMAN	mRNA
11716	24679	38258	1.82	8.0E-77	AA019770.1	EST_HUMAN	zxc6202.r1 Soares retina N26-4HR Homo sapiens cDNA clone IMAGE:363578 5'
							zxc62602.r1 Soares retina N26-4HR Homo sapiens cDNA clone IMAGE:363578 5'
12900	25484	31732	4.66	8.0E-77	R00245.1	EST_HUMAN	ye6904.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains
1946	14970	27968	2.43	7.0E-77	AA825755.1	EST_HUMAN	ye6904.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2421	15428	28451	1.88	7.0E-77	4505944	NT	zxc1071.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2421	15428	28452	1.88	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
262	13358	26283	4.64	6.0E-77	4504800	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (FNAR2) mRNA
1144	14187	27138	20.18	6.0E-77	AW957753.1	EST_HUMAN	EST396923 IMAGE resequences, IMAGE Homo sapiens cDNA
1545	14578	27551	3.97	6.0E-77	AI204066.1	EST_HUMAN	q97h12.x1 Soares, fetal_lung, Nbr-HL19W Homo sapiens cDNA IMAGE:1745063 3'
1240	14216	27236	2.34	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
2935	14398	27387	1.41	5.0E-77	4357260	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2935	15091	28709	1.03	5.0E-77	AF162688.1	NT	Homo sapiens tau-like kinase 1 (TLK1) mRNA, complete cds
2774	15760	28780	0.99	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3534	16580	29504	0.64	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4732	17752	30644	0.92	5.0E-77	5031680	NT	Homo sapiens EGF-like repeats and discordin-like domains 3 (EDIL3), mRNA
4732	17752	30645	0.92	5.0E-77	5031680	NT	Homo sapiens EGF-like repeats and discordin-like domains 3 (EDIL3), mRNA
4975	17990	30890	3.64	5.0E-77	AL043983.1	EST_HUMAN	DKFZp434G1728.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G1728 5'
6951	20175	33459	0.84	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7948	20511	33858	0.52	5.0E-77	X85295.1	NT	H. sapiens mRNA for ubiquitin hydrolase
7849	20511	33859	0.87	5.0E-77	X85295.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8711	21579	35104	1.22	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8711	21579	35105	1.22	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9028	22811	36284	3	5.0E-77	11421828	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9028	22811	36285	3	5.0E-77	11421828	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10857	23777	37276	0.82	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
10857	23777	37277	0.82	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
10857	23777	37277	0.82	5.0E-77	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
1989	15010	28015	1.26	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1989	15010	28016	1.26	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10952	23574	37069	0.71	3.0E-77	H65167.1	EST_HUMAN	y064g01.t1 Wellmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to
10952	23574	37070	0.71	3.0E-77	H65167.1	EST_HUMAN	SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -;
10958	23888	37599	0.56	3.0E-77	A017333.1	EST_HUMAN	y064g01.t1 Wellmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to
10958	23888	37599	0.56	3.0E-77	A017333.1	EST_HUMAN	SP-S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -;
11222	24175	37701	3.68	3.0E-77	BF359917.1	EST_HUMAN	oa31h07.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1638973 3'
1354	14389	27598	1.68	2.0E-77	AV764617.1	EST_HUMAN	oa31h07.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1638973 3'
1428	14462	27439	2.31	2.0E-77	AW992712.1	EST_HUMAN	PM3-M10078-006800-005-g03 MT0078 Homo sapiens cDNA
2102	15119	28140	1.01	2.0E-77	L41825.1	NT	AV764617 MOD5 Homo sapiens cDNA clone MOSBT10 5'
2102	15119	28140	1.01	2.0E-77	L41825.1	NT	AV764617 MOD5 Homo sapiens cDNA clone MOSBT10 5'
2600	15898	28520	2.28	2.0E-77	AB037836.1	NT	Homo sapiens CYP17 gene, 5' end
2600	15898	28520	2.28	2.0E-77	AB037836.1	NT	Homo sapiens CYP17 gene, 5' end
2600	15898	28520	2.28	2.0E-77	AB037836.1	NT	Homo sapiens CGL-7a protein (LOC51634), mRNA
2600	15898	28520	2.28	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2600	15868	26821	2.26	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4064	17100	29892	1.25	2.0E-77	BE044318.1	EST_HUMAN	h343b05.x1 Scanes_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW-GAG2 HUMAN P1024 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4442	17468	30357	0.68	2.0E-77	AI613519.1	EST_HUMAN	W22602.x1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR-O65245
4442	17468	30358	0.68	2.0E-77	AI613519.1	EST_HUMAN	W22602.x1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR-O65245
4802	17819	30713	2.32	2.0E-77	AA653025.1	EST_HUMAN	ns66g12.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1188938 similar to SW.RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1] contains element MSR1 repetitive element ;
5169	17468	30357	0.65	2.0E-77	AI613519.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
5169	17468	30358	0.65	2.0E-77	AI613519.1	EST_HUMAN	W22602.x1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR-O65245
6065	19146	32358	2.06	2.0E-77	BE298940.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
6256	19368	32607	1.62	2.0E-77	BE787143.1	EST_HUMAN	W22602.x1 NCL CGAP Bm52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR-O65245
7390	20350	33701	14.21	2.0E-77	AI833003.1	EST_HUMAN	Q13311 TAX1-BINDING PROTEIN TXBP151, [1] ;
8874	21841	35284	0.75	2.0E-77	AB62707.1	EST_HUMAN	Q70609.x1 NCL CGAP Bm25 Homo sapiens cDNA clone IMAGE:2017390 3' similar to WP-F29D11.1
8886	22839	36296	5.94	2.0E-77	U60321.1	NT	CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
8886	22839	36296	5.64	2.0E-77	U60321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10354	23278	36753	0.5	2.0E-77	BF310349.1	EST_HUMAN	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10354	23278	36754	0.5	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
45	13165	26058	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
45	13165	26059	0.94	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
272	13368	26294	1.33	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
272	13368	26295	1.33	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	15853	26891	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	15853	26892	2.31	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	15455	28477	1.73	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3058	16115	26028	2.01	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEOR1), mRNA
4380	17408	30288	3.92	1.0E-77	7708269	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4525	17550	30438	0.73	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA
4552	17575	30465	18.98	1.0E-77	AJ229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4880	17701	30589	2.11	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4721	17741	30832	0.72	1.0E-77	AJ273014.1	EST_HUMAN	g03g04.x1 NCJ CGAP_K48 Homo sapiens cDNA clone IMAGE1981110 3'
5000	17550	30438	0.85	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA
5219	17550	30438	0.88	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1), mRNA
5245	18254		1.12	1.0E-77	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21Q47
6038	19120	32324	1.61	1.0E-77	AJ086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6038	19120	32325	1.61	1.0E-77	AJ086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6165	19240	32471	1.39	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6590	19650	32621	1.26	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7254	19889	33285	14.51	1.0E-77	5881412	NT	Homo sapiens elastin (supraaortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7828	20871	34280	0.91	1.0E-77	11420159	NT	Homo sapiens cullin 1 (CUL1), mRNA
8040	20977	34373	0.89	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9820	22564	36013	0.65	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
9820	22564	36014	0.65	1.0E-77	X94354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10850	23810	37316	0.92	1.0E-77	AB029396.1	NT	Homo sapiens hu-GleAT-P mRNA for glucuronyltransferase, complete cds
10850	23810	37317	0.92	1.0E-77	AB029396.1	NT	Homo sapiens hu-GleAT-P mRNA for glucuronyltransferase, complete cds
10916	23598	37552	3	9.0E-78	AW75302.1	EST_HUMAN	RC2-CT0254-280698-011-b05 CT0254 Homo sapiens cDNA
6589	16649	32919	2.83	8.0E-78	AW647081.1	EST_HUMAN	RC2-ET10023-080503-012-e05 ET10023 Homo sapiens cDNA
6589	16649	32920	2.83	8.0E-78	AW647081.1	EST_HUMAN	RC2-ET10023-080503-012-e05 ET10023 Homo sapiens cDNA
86	13202	26126	2.14	6.0E-78	AJ118789.1	EST_HUMAN	AJ118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004364 5'
86	13202	26127	2.14	6.0E-78	AJ118789.1	EST_HUMAN	AJ118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004364 5'
3325	16378	29297	8.65	6.0E-78	BF344101.1	EST_HUMAN	602016028F1 NCJ CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4152511 5'
6712	19768		2.34	6.0E-78		NT	Homo sapiens GDNF family receptor alpha 1 (GFRAL), mRNA
219	13319	26244	1.78	5.0E-78	11422496	NT	Homo sapiens hypothetical protein FLJ11318 (FLJ11318), mRNA
						NT	h44h03.03 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP:Y4856A.6
2589	15570	28560	5.49	5.0E-78	AW673424.1	EST_HUMAN	CE22121
3356	16445	28372	3.84	5.0E-78	M95586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5485	18586	31467	2.45	5.0E-78	AF038536.1	NT	Homo sapiens Beal's macular dystrophy related protein mRNA, partial cds
5635	18751	31917	24.78	5.0E-78	11416595	NT	Homo sapiens transforming growth factor, beta-induced, 88kD (TGFB), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7361	20331	33681	2.22	5.0E-78	AW958320.1	EST_HUMAN	EST365160 MAGE resequences, MAGE Homo sapiens cDNA
8438	22402	35940	6.95	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
8439	22403	35941	3.51	5.0E-78	BE660896.1	EST_HUMAN	507648051F1 NIH_MGC 82 Homo sapiens cDNA clone IMAGE:3931887 5'
11614	24552	38112	1.84	5.0E-78	BE241639.1	EST_HUMAN	TCAAP/EO686 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0686
11614	24552	38113	1.84	5.0E-78	BE241639.1	EST_HUMAN	TCAAP/EO686 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0686
1139	14182	27733	1.88	4.0E-78	AL043914.2	EST_HUMAN	DKFZ434N0323_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ434N0323 5'
1521	14553	27624	2.74	4.0E-78	AL353841.1	NT	Novel human gene mapping to chromosome 22
1659	14688	27663	1.11	4.0E-78	AI985094.1	EST_HUMAN	w97b12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2466515 3' similar to SW:WAP_PIG
2326	15337	28360	3.31	4.0E-78	AF107405.1	NT	O46055 WHEATY ACIDIC PROTEIN PRECURSOR ;
4350	17377	30258	1.47	4.0E-78	7656376	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4807	17824	30719	2.16	4.0E-78	4505806	NT	Homo sapiens synovial (LOC30816) mRNA
4807	17824	30720	2.16	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5802	18651	32137	1.13	4.0E-78	11420732	NT	Homo sapiens SFRS protein kinase 2 (SRPK2) mRNA
6297	19369	32908	0.81	4.0E-78	7652109	NT	Homo sapiens KIAA0426 gene product (KIAA0426) mRNA
6297	19369	32909	0.81	4.0E-78	7652109	NT	Homo sapiens KIAA0426 gene product (KIAA0426) mRNA
6725	19761	33060	0.59	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S8 kinase, 70kD, polypeptide 1 (RPS8K1) mRNA
7733	20698	34052	0.93	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S8 kinase, 70kD, polypeptide 1 (RPS8K1) mRNA
9205	22171	35601	1.68	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4k230) mRNA, complete cds
9205	22171	35602	1.68	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4k230) mRNA, complete cds
9723	22751	36204	0.84	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4) mRNA
10811	23732	37233	1.97	4.0E-78	11660151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22604 (FLJ22604) mRNA
10811	23732	37234	1.97	4.0E-78	11660151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22604 (FLJ22604) mRNA
11749	24634	38213	1.85	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
11883	24764	38550	5.69	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12126	24955	38559	2.38	4.0E-78	...	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12977	25426	31739	3.89	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
162	13265	26169	2.77	3.0E-78	AF005901.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4) mRNA
162	13265	26169	2.77	3.0E-78	AF005901.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4) mRNA
3776	16818	29771	0.94	3.0E-78	AF140804.1	EST_HUMAN	Homo sapiens sRF1 gene, complete cds
3829	16869	29771	0.88	3.0E-78	4507334	NT	Homo sapiens sRF1 gene, complete cds
							AL140804 PLAC33 Homo sapiens cDNA clone PLACE300373 5'
							Homo sapiens synaptotagmin 1 (STN1) mRNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	16699	29771	0.79	3.0E-78	4507334	NT	Homo sapiens synaptobin 1 (SYNJ1), mRNA
10640	23571		6.79	3.0E-78	BE144758.1	EST_HUMAN	QV0-HT0180-041069-065-c07 HT0180 Homo sapiens cDNA
11326	24276	37604	1.8	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0397-150200-114-g09 HT0397 Homo sapiens cDNA
3138	16195		4.1	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4042	17060		1.43	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
7705	20602	34027	1.24	2.0E-78	AW402306.1	EST_HUMAN	UHFH-BKO-aa1-g-10-UJ11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7705	20652	34026	1.24	2.0E-78	AW402306.1	EST_HUMAN	UHFH-BKO-aa1-g-10-UJ11 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3054139 5'
8003	20942	34335	3.2	2.0E-78	BF689800.1	EST_HUMAN	902186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
8376	21344	34766	2.64	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DGBAWF08 5'
8795	21762	35183	1.51	2.0E-78	AB57509.1	EST_HUMAN	Pt2.1_16_B07.7 tumor2 Homo sapiens cDNA 3'
8795	21762	35184	1.51	2.0E-78	AB57509.1	EST_HUMAN	Pt2.1_16_B07.7 tumor2 Homo sapiens cDNA 3'
11416	24360		2.5	2.0E-78	AK07637.1	EST_HUMAN	g16005.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1859361 3' similar to WP:R80.1
11458	24401	37995	2.03	2.0E-78	N06951.1	EST_HUMAN	CE06325 PROTEIN KINASE :
5378	18482	31357	3.22	1.0E-78	11417304	NT	Zs48f12.s1 Soares fetal liver spleen 1NF.S Homo sapiens cDNA clone IMAGE:265823 3'
7144	18376	31264	0.87	1.0E-78	AV649699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC31308), mRNA
8498	21487		2.95	1.0E-78	U52373.1	NT	AV649699 GLC Homo sapiens cDNA clone GLCBMCD1 3'
12323	26125	31847	1.81	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (rmb) mRNA, complete cds
4727	17747	30638	3.81	9.0E-78	11625891	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4859	17916	30807	3.55	9.0E-78	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
6507	18607	31537	18.13	9.0E-79	AB028070.1	NT	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
							Homo sapiens mRNA for activator of S phase Kinase, complete cds
6474	19539	32765	2.49	9.0E-78	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/f5) (UBE2E3) mRNA
6772	19927	33109	0.87	9.0E-78	11430822	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11234), mRNA
7573	25684		1.05	9.0E-78	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7825	20773	34150	0.84	9.0E-78	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L16.1), mRNA
7825	20773	34151	0.84	9.0E-78	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7875	20819	34167	0.66	9.0E-78	D30856.1	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8659	21657	35079	0.5	9.0E-78	11417260	NT	Human T-cell mRNA for glycyl RNA synthetase (TARS), mRNA
8659	21657	35080	0.5	9.0E-78	11417260	NT	Homo sapiens threonyl-RNA synthetase (TARS), mRNA
9416	22303	36821	5.63	9.0E-79	102853.1	NT	Homo sapiens threonyl-RNA synthetase (TARS), complete cds
9416	22303	36822	5.53	9.0E-79	102853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9736	22763	36218	0.66	9.0E-79	D87875.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
10730	23652	37145	0.66	9.0E-79	11439843	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
							Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10784	23706	37204	1.53	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10784	23706	37205	1.53	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11408	24350	37882	4.27	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11841	24724	38310	2.97	9.0E-79	11423827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
11841	24724	38311	2.97	9.0E-79	11423827	NT	Homo sapiens suppressor of white apical homolog 2 (SWAP2), mRNA
12115	24865	38586	2.71	9.0E-79	7682451	NT	Homo sapiens KIAA1035 protein (KAA1035), mRNA
13000	25556	31720	1.55	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3765	16767	29708	1.33	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5185	18204	31078	0.66	8.0E-79	8567387	NT	Homo sapiens perlecan (Drosophila) homolog 3 (PER3), mRNA
3266	16320	29242	7.24	7.0E-79	BE618948.1	EST_HUMAN	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3975657 3'
12170	25020		2.63	6.0E-79	AA659829.1	EST_HUMAN	Z94604.s1 Soares_fetal_liver_spleen_1.INFLS_31 Homo sapiens cDNA clone IMAGE:492568 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT
11824	24707	38280	4.57	9.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3191	18248		1.35	4.0E-79	8622325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
313	13405	26331	1.46	3.0E-79	AF114488.1	NT	Homo sapiens interactin short isoform (ITSN) mRNA, complete cds
979	14030	29984	2.02	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cln) gene, complete cds
3115	16172	29082	1.82	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5435	18637	37446	6.05	3.0E-79	AF110322.1	NT	Homo sapiens MSTP018 (MST018) mRNA, complete cds
5812	18902	32085	1.81	3.0E-79	AB020689.1	NT	Homo sapiens mRNA for KIAA0882 protein, partial cds
5841	18931	32116	0.95	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5841	18931	32116	0.95	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5863	18952	32158	4.05	3.0E-79	11426770	NT	Homo sapiens neirin 1 (NTN1), mRNA
6803	18952	32159	4.05	3.0E-79	11426770	NT	Homo sapiens neirin 1 (NTN1), mRNA
6909	19981	33257	0.8	3.0E-79	BE256993.1	EST_HUMAN	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7262	18997	33294	3.31	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0520 protein, partial cds
7262	18997	33295	3.31	3.0E-79	AB014520.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
8504	21472	34866	1.58	3.0E-79	AF249273.1	NT	Homo sapiens tetraicosapeptide repeat domain 3 (TTG3), mRNA
9758	22869	36156	0.57	3.0E-79	10835038	NT	Homo sapiens tetraicosapeptide repeat domain 3 (TTG3), mRNA
10712	23634		0.94	3.0E-79	AV598115.1	EST_HUMAN	AV598115 GKX Homo sapiens cDNA clone GKCAHET11 5'
287	13382		2.05	2.0E-79	H63129.1	EST_HUMAN	Y48033.s1 Soares_fetal_liver_spleen_1.INFLS Homo sapiens cDNA clone IMAGE:208541 3'
635	13701	26822	1.29	2.0E-79	BE376928.1	EST_HUMAN	601159418F2 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3511107 5'
928	13981	26935	1.35	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
885	14036	26960	4.78	2.0E-79	4885234	NT	Homo sapiens Gardier-Rastfeld feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
885	14036	26991	4.78	2.0E-79	4885234	NT	Homo sapiens Gardier-Rastfeld feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1036	14082		1.02	2.0E-79	AI923747.1	EST_HUMAN	h18H07.X1 NC1_GGAP_P128 Homo sapiens cDNA clone IMAGE:2118885 3'
1804	14832	27819	0.87	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1804	14832	27820	0.87	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1893	14818	27814	0.92	2.0E-79	7657235	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2198	15174	28163	4.97	2.0E-79	4685863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2168	15174	28194	4.97	2.0E-79	4685863	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2202	16217	29237	0.91	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
3633	16973	29887	0.83	2.0E-79	AJ170492.1	NT	Homo sapiens chondroitin channel GLC4 (GLC4) mRNA, complete cds
4193	17224	30113	1.15	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4716	17736	30628	0.97	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
5754	18848		1.25	2.0E-79	AA312223.1	EST_HUMAN	EST182928 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
5815	18805	32088	0.88	2.0E-79	11161769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6371	19439	32692	1.07	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
7163	18385	31273	0.7	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7373	20343	35684	1.74	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7973	20343	35695	1.74	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8437	21406	34818	1.13	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8882	21826	35252	2.55	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9118	22084	35512	0.46	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9118	22084	35513	0.46	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9357	23232	35749	1.1	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) membrane occluder associated protein Mb-9 (H. sapiens) (LOC33861), mRNA
10452	23374	36885	3.12	2.0E-79	S72869.1	NT	H4(DT03170)-putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10452	23374	36886	3.12	2.0E-79	S72869.1	NT	H4(DT03170)-putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
11368	24315	37840	3.86	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-410 B T0310 Homo sapiens cDNA
11368	24315	37841	3.86	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-410 B T0310 Homo sapiens cDNA
11668	24602		2.62	2.0E-79	AB035632.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8 and complete cds
12207	18350	31295	3.21	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12293	25107	31837	4.8	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12524	25254	31804	2.41	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6739	25666		3.26	1.0E-79	BF363071.1	EST_HUMAN	MRD-NN0087-296000-017-B10 NND087 Homo sapiens cDNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6862	16905	33200	0.51	1.0E-79	AJ613480.1	EST_HUMAN	h37c08.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623 TEXTIN C1 ;
6862	16905	33201	0.51	1.0E-79	AJ613480.1	EST_HUMAN	TEXTIN C1 ;
6867	21555	34671	0.73	1.0E-79	BE394271.1	EST_HUMAN	601311517FI NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632903 5'
11944	24524	38419	2.64	1.0E-79	BF087406.1	EST_HUMAN	QV22-H10540-120300-358-ac05 HT0540 Homo sapiens cDNA
3161	16217	29131	6.25	9.0E-80	AA725848.1	EST_HUMAN	a129a05.e1 Soares testis, NHT Homo sapiens cDNA clone 1343648 3'
3161	16217	29132	6.25	9.0E-80	AA725848.1	EST_HUMAN	a129a05.e1 Soares testis, NHT Homo sapiens cDNA clone 1343648 3'
10373	23296	36772	1.02	9.0E-80	BE709603.1	EST_HUMAN	601581652FI NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3336081 5'
11606	24544	38104	8.28	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system), member 8 (SLC7A8), mRNA
11606	24544	38105	8.28	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system), member 8 (SLC7A8), mRNA
3816	16660		1.22	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7862	20606	34183	2.95	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7862	20606	34184	2.95	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8757	22698	38154	1.14	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9757	22698	38155	1.14	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7166	18397	31242	0.55	7.0E-80	AF127892.1	NT	Caellitnrl jacchus olfactory receptor (CJA80) gene, partial cds
801	13856	28613				EST_HUMAN	h59402.x1 NC1_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
1650	14882	27655	2.17	6.0E-80	U64898.1	NT	Q16765 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
2307	15319	28338	1.17	6.0E-80	6831094	NT	Homo sapiens NRD convertase mRNA, complete cds
2307	15319	28339	1.17	6.0E-80	6831094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4314	17043	30228	1.1	6.0E-80	AB032981.1	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4314	17043	30228	1.1	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5859	18986	32177	1.32	6.0E-80	11421462	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6194	19268	32603	3.12	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dyx1c1 heavy chain (DNAH9 gene)
6355	19424	32668	3.81	6.0E-80	11438736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6403	19471		0.93	6.0E-80	MT8533.1	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6455	19520	32770	0.88	6.0E-80	MT8533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
9176	22142	35568	3.06	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9176	22142	35569	3.08	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 61 (GPR61), mRNA
9373	22387	35798	1.55	6.0E-80	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9714	22698	36125	0.84	6.0E-80	AF181466.1	NT	Homo sapiens HSPC146 mRNA, complete cds
9841	22777	36233	0.474	6.0E-80	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
10220	23145	36834	2.93	6.0E-80	U02021.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11289	24239	37766	2.43	6.0E-80	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11556	24498	38034	20.37	6.0E-80	AF226730.1	NT	Homo sapiens Cyf19 mRNA, complete cds
12051	24624	38521	1.64	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
12304	25787		2.39	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) gene, complete cds
12506	25243		6.41	6.0E-80	AB028900.1	NT	Homo sapiens CST gene for carbodiimide sulfoxidase, exon 1, 2, 3, 4, 5
12594	26914		4.47	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
580	13657	26572	2.89	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
836	13853	26848	1.49	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
836	13853	26849	1.49	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1183	14233		0.66	5.0E-80	X91647.1	NT	H. sapiens rox1 gene (exon 12)
1450	14483		2.21	5.0E-80	AL183263.2	NT	Homo sapiens chromosome 21 segment HS21C083
2368	15377	29400	1.92	5.0E-80	U89358.1	NT	Human K3 mbl protein homolog mRNA, complete cds
2437	18444	29462	6.37	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2809	15798	29816	5	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4069	17105	29968	1.28	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4069	17105	29968	1.28	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4891	18066	30894	1.53	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8700	21668	35091	1.14	5.0E-80		NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9613	22617	39059	15.19	4.0E-80	F26916.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s400004503
2138	13318		9.37	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4738	17768	30683	1.45	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4945	17961		3.11	3.0E-80	BE817465.1	EST_HUMAN	QV4-5N0283-040600-241-g10 BN0263 Homo sapiens cDNA
5919	19005	32197	2.02	3.0E-80	A091675.1	EST_HUMAN	cc23a12.x1 Soares NSF_F8_gw_OT_PA_p_51 Homo sapiens cDNA clone IMAGE:1687054 3' similar to
1814	14841	27632	4.7	2.0E-80	R35321.1	EST_HUMAN	Xp55a08.1 Soares infant brain, IN1B Homo sapiens cDNA clone IMAGE:38060 5'
1877	14902	27602	1.49	2.0E-80	A1446821.1	EST_HUMAN	RET4B1 subtracted rat cDNA library Homo sapiens cDNA clone RE1487
2071	15086	28106	5.1	2.0E-80	AL043116.2	EST_HUMAN	DKFZP434D1323.J1 434 (synonym: hta33) Homo sapiens cDNA clone DKFZP434D1323 5'
8374	19442	32694	0.69	2.0E-80	A023972.1	EST_HUMAN	wn49c10.x1 NCI_OGAP_Lu19 Homo sapiens cDNA clone IMAGE:244878 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Database BLAST E Value	Top Hit Accession No.	Top Hit Source	Top Hit Descriptor
6374	19442	32685	0.69	2.0E-80	AB23972.1	EST_HUMAN	w49c10.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:248786 3'
6977	20200	33530	1.01	2.0E-80	AA592952.1	EST_HUMAN	nm00601.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1090177 3'
7098	20032	33535	1.51	2.0E-80	11421630	NT	nm00601.s1 NCI_CGAP_Go1 transport complex protein (80 kDa) (GTC90), mRNA
7463	20429	33788	0.81	2.0E-80	175215.1	EST_HUMAN	y689f1.2.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to
8514	22477	35922	1.22	2.0E-80	AV1964270.1	EST_HUMAN	SP-1/CR_XENLA_P08082 KERATIN, TYPE I CYTOSKELETAL ENDO B;
10126	23062	36530	0.97	2.0E-80	AJ0072761.1	NT	EST1376343 MAGE resequencing, MAGE Homo sapiens cDNA
11216	24169	37697	8.05	2.0E-80	AJ369362.1	EST_HUMAN	z70f12.r1 Soares, testis, N1H Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
340	13429	26806	2.11	1.0E-80	AL163003.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN.;
800	13859	26806	1.95	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS27C103
1971	14992		2.92	1.0E-80	AT732559.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
4857	17874	30762	0.78	1.0E-80	N99520.1	EST_HUMAN	nm0111235 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR
5400	18503		3.92	1.0E-80	BE386815.1	EST_HUMAN	repetitive element.;
6083	19163	32375	6.24	1.0E-80	L10347.1	NT	z839g07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:294972 5' similar to contains
6948	19704	32980	1.3	1.0E-80	5174640	NT	Alu repetitive element.
7414	20381	33732	1.08	1.0E-80	AJ24172.1	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
7824	20772	34148	2.6	1.0E-80	AJ948731.1	EST_HUMAN	Homo pro-alpha1 type I collagen (COLA1) gene exons 1-54, complete cds
7824	20772	34149	2.6	1.0E-80	AJ948731.1	EST_HUMAN	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial
8573	21541	34861	1.17	1.0E-80	11421211	NT	protein, mRNA
9048	22014	35437	0.92	1.0E-80	11421211	NT	Homo sapiens mRNA for lipophilin B
9048	22014	35439	0.92	1.0E-80	11421211	NT	wq25c05.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2472286 3'
9840	22584	36032	1.26	1.0E-80	AF245219.1	NT	wq25c05.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2472286 3'
9840	22584	36033	1.26	1.0E-80	AF245219.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
10791	23712	37214	1.72	1.0E-80	058478.2	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
11013	23978	37503	1.72	1.0E-80	11641276	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
11013	23978	37504	1.72	1.0E-80	11641276	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
11443	24066	37926	1.67	1.0E-80	BE394325.1	EST_HUMAN	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
12578	25287	31779	2.27	1.0E-80	11417901	NT	Homo sapiens similar to KIA00145 protein, partial cds
14683	24431	37980	9.7	8.0E-81	BE394325.1	EST_HUMAN	Homo sapiens similar to rat myomegalin (LOC84182), mRNA
7464	20430	33787	2.97	7.0E-81	AJ822115.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
							Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
							Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
							601310331F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							zab1c08.x8 Soares, fetal_lung_Nb1L18W Homo sapiens cDNA clone IMAGE:289918 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4414	17441	30331	4.98	6.0E-81	BE266929.1	EST_HUMAN	601111970F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3352840 5'
4414	17441	30332	4.08	6.0E-81	BE266929.1	EST_HUMAN	601111970F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3352840 5'
5365	18460	31329	1.65	6.0E-81	4501848	NT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5365	18460	31330	1.65	6.0E-81	4501848	NT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7845	20792	34168	0.56	6.0E-81	AF038860.1	NT	Homo sapiens chromosome 1p33-p34 beta-1.4-galactosyltransferase mRNA, complete cds
8592	22564	36004	1.17	6.0E-81	AA390017.1	EST_HUMAN	EST169129 Fetal lung II Homo sapiens cDNA 5' end
12707	25364	31768	2.68	6.0E-81	BF676022.1	EST_HUMAN	602153665F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284601 5'
12707	25364	31769	2.68	6.0E-81	BF676022.1	EST_HUMAN	602153665F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284601 5'
2228	15240	28285	2.27	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3344480 5'
8755	21723	35147	1.57	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10009	22533	36356	0.81	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
10006	22533	36357	0.81	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11008	24780	38378	1.84	5.0E-81	8506834	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
703	13765	26700	1.21	4.0E-81	AI521435.1	EST_HUMAN	th60912.x1 NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2127202 3' similar to TR:Q85560 Q85560
1839	14866	27665	1.36	4.0E-81	AW776912.1	EST_HUMAN	th98d02.x1 NC1_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:GOPQ_BOVIN
3186	18241	29156	4.49	4.0E-81	AB037769.1	NT	P83620 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1346 protein, partial cds
3644	16687	26602	0.89	4.0E-81	AW004608.1	EST_HUMAN	ws50103.x1 NC1_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:Q43815 Q43815
4187	17218	30104	1.85	4.0E-81	AF263306.1	NT	Homo sapiens rat3 interacting protein variant 2 mRNA, partial cds
4187	17218	30105	1.85	4.0E-81	AF263306.1	NT	Homo sapiens rat3 interacting protein variant 2 mRNA, partial cds
4419	17446	30337	1.1	4.0E-81	8923209	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
7492	20457	33815	0.93	4.0E-81	4757853	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
7629	20589	33952	0.89	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8630	21598	35018	2	4.0E-81	X06886.1	NT	Human cDNA for amyloid A4(751) protein
8690	21856	35276	3.34	4.0E-81	U20197.1	NT	Human core photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
8690	21856	35277	3.34	4.0E-81	U20197.1	NT	Human core photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9581	22543	35604	3.82	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10461	23383	36976	1.82	4.0E-81	11425281	NT	Homo sapiens ligase 1, DNA, ATP-dependent (LIG1), mRNA
10531	23453	36950	0.67	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10531	23453	36951	0.67	4.0E-81	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11519	24460	38010	3.39	4.0E-81	4769085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
11519	24460	38011	3.39	4.0E-81	4769085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
12200	25653	31439	3.45	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIA0330) mRNA
12200	25653	31439	3.45	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIA0330) mRNA
12737	25389	31754	1.71	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733) mRNA
12737	25389	31754	1.71	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733) mRNA
12878	25472	31726	3.69	4.0E-81	11417974	NT	Homo sapiens transcalcabin II, macrocytic anemia (TCN2) mRNA
1272	14307	27266	10.2	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1272	14307	27267	10.2	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2290	15388	28412	1.65	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3004	16062	28680	5.19	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3004	16062	28681	5.19	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2844	15904	28626	2.48	2.0E-81	BE784636.1	EST_HUMAN	601474072FT NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3877121 5'
2844	15904	28626	2.48	2.0E-81	BE784636.1	EST_HUMAN	601474072FT NIH_MGC 88 Homo sapiens cDNA clone IMAGE:3877121 5'
3787	16928	29735	0.88	2.0E-81	AW611542.1	EST_HUMAN	hg8500.1x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2652384 3'
8290	21269	34970	0.53	2.0E-81	8223839	NT	Homo sapiens hypothetical protein (LOC55588) mRNA
13032	16928	29735	2.55	2.0E-81	AW611542.1	EST_HUMAN	hg8500.1x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2652384 3'
4543	17568	30453	3.12	1.0E-81	AA040370.1	EST_HUMAN	z44508.r1 Soares_pregnant_uterus NHGPU Homo sapiens cDNA clone IMAGE:465925 5' similar to PIR.S52437 S52437 CDP-diacylglycerol synthase - full ty.
4675	17568	30583	9.34	1.0E-81	BE047966.1	EST_HUMAN	z45604.y1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2201526 5'
5308	18326	36611	3.31	1.0E-81	U67928.1	NT	Homo sapiens scintilla hydrolase (ACO2) gene, exon 3
5427	18530	31409	3.6	1.0E-81	11432666	NT	Homo sapiens polymerase (DNA directed), gamma (POLG) mRNA
5427	18530	31410	3.6	1.0E-81	11432666	NT	Homo sapiens polymerase (DNA directed), gamma (POLG) mRNA
5580	18676	31639	0.83	1.0E-81	AA255569.1	EST_HUMAN	z48600.r1 Soares NIHMPu.S1 Homo sapiens cDNA clone IMAGE:682476 5' similar to SW:PR12_HUMAN
6737	18631	32006	3.37	1.0E-81	U52351.1	NT	P48943 DNA PRIMASE 59 KD SUBUNIT
5737	18631	32010	3.37	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurotrophin (GTND2) mRNA, partial cds
6269	19342	32575	1.55	1.0E-81	BF674641.1	EST_HUMAN	Homo sapiens arm-repeat protein NPRAP/neurotrophin (GTND2) mRNA, partial cds
6609	19756	33032	0.59	1.0E-81	11420965	NT	602137664FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4274635 5'
6609	19756	33033	0.59	1.0E-81	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C) mRNA
6902	16954	33251	1.26	1.0E-81	AJ133269.1	NT	Homo sapiens cavolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)



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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	20886	34392	7.53	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
10134	23060	36537	7.65	1.0E-81	BE686278.1	EST_HUMAN	601645051F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3930228 5'
10134	23060	36538	7.65	1.0E-81	BE686278.1	EST_HUMAN	601645051F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3930228 5'
10328	23352	35731	4.53	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:3665483 5'
							ac1406.s1 Strategene HeLa cell s3 537216 Homo sapiens cDNA clone IMAGE:566427 3' similar to SW:YB36_YEAST P39126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION 1:
10463	23385	36878	1.09	1.0E-81	AA630784.1	EST_HUMAN	60157339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3538280 5'
10465	23387	36880	3.01	1.0E-81	BE744545.1	EST_HUMAN	60157339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3538280 5'
10485	23387	36881	3.01	1.0E-81	BE744545.1	EST_HUMAN	60157339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3538280 5'
10874	23794	37295	1.7	1.0E-81	AW897550.1	EST_HUMAN	CN3-NN0065-140400-147-at2 NN0059 Homo sapiens cDNA
11425	24360	37005	2.9	1.0E-81	AW844988.1	EST_HUMAN	MR0-CT0005-250595-019 CT0008 Homo sapiens cDNA
11425	24360	37006	2.9	1.0E-81	AW844988.1	EST_HUMAN	MR0-CT0005-250595-019 CT0008 Homo sapiens cDNA
11428	24373	37911	6.55	1.0E-81	AW798187.1	EST_HUMAN	RC3-UM0046-290200-011-a05 UM0046 Homo sapiens cDNA
11429	24373	37912	6.55	1.0E-81	AW798187.1	EST_HUMAN	RC3-UM0046-290200-011-a05 UM0046 Homo sapiens cDNA
11851	24734	38321	2.11	1.0E-81	BF204283.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12414	25185	31822	4.59	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to epolipoprotein B mRNA editing protein) (DU742C19.2). mRNA
13	13133	28031	0.94	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
107	13133	26031	2.07	8.0E-82	AF161408.1	NT	Homo sapiens HSPC288 mRNA, partial cds
263	13359	26284	2.7	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
815	13673	26821	14.95	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
898	13943	26501	1.44	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1487	14520	27493	1.36	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1666	14698	27674	1.7	8.0E-82	6719601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4114	17148	30040	0.82	8.0E-82	4504116	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4272	17501	30181	0.75	8.0E-82	8923432	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
1444	14477	28789	2.93	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3862088 5'
2777	16769	28769	2.93	7.0E-82	AF144050.1	EST_HUMAN	AU144050 HELM1A Homo sapiens cDNA clone IMAGE:1000752 3'
12053	24926	38524	1.75	7.0E-82	AA663747.1	EST_HUMAN	ae68604.s1 Strategene embry brain ST1 Homo sapiens cDNA clone IMAGE:968342 3'
1680	14712	27890	25.07	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5574	18070	31632	0.89	4.0E-82	BF351691.1	EST_HUMAN	QV2-H10540-120900-362-f08 HT0540 Homo sapiens cDNA
5574	18070	31633	0.89	4.0E-82	BF351691.1	EST_HUMAN	QV2-H10540-120900-362-f08 HT0540 Homo sapiens cDNA
5851	18941	32126	0.59	4.0E-82	M25933.1	NT	Human von Willebrand factor gene, exon 9

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12025	24801	38468	7.32	4.0E-82	AB37300.1	EST_HUMAN	wp75609.x1 NQ1_QGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR-O75276
12657	26337		3.96	4.0E-82	AF026701.2	NT	O75276 PKO1 ;
277	13373	26301	16.94	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
704	13769	26701	2.76	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010-00-013-02 BN0120 Homo sapiens cDNA
788	13847	26794	10.4	3.0E-82	6174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
871	13927	26885	6.11	3.0E-82	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1062	14108		53.62	3.0E-82	AA728848.1	EST_HUMAN	a23e05.g1 Soares_testis_NHT Homo sapiens cDNA clone T343648 3'
1357	14392	27363	1.01	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1462	14468	27469	2.51	3.0E-82	AL163265.2	NT	Homo sapiens chromosome 21 segment HS21C085
1677	14641	27937	1.95	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-280706-018-g04 BN0005 Homo sapiens cDNA
2023	15043	28096	1.2	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
3265	16339		2.31	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8492	21460	34877	2.7	3.0E-82	114252016	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8902	21668	35292	0.771	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8902	21668	35293	0.771	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10183	23103	36590	3.89	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10183	23103	36591	3.98	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
12108	24978	36577	1.9	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
12108	24978	36578	1.6	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
569	13699	26579	1.95	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
569	13699	26580	1.86	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
1694	14724	27707	2.13	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117.1 434 (synonym: hiaz3) Homo sapiens cDNA clone DKFZp434M117 5'
2891	16049	28970	0.78	2.0E-82	AL165201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3850	16889	29802	1.07	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4032	17089	29884	0.65	2.0E-82	U76633.1	NT	Homo sapiens integral membrane serine protease Seprease mRNA, complete cds
4261	17250	30171	1.07	2.0E-82	4504116	NT	Homo sapiens glial fibrillary acidic protein, kairate 1 (GFAP) mRNA
4588	17610	30505	1.08	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1036 protein, partial cds
4588	17610	30506	1.09	2.0E-82	AB029019.1	NT	Homo sapiens wiscr1 (WBSOR1) and wiscr2 (WBSOR2) genes, complete cds, alternatively spliced and
4904	17921	30813	3.21	2.0E-82	AF045555.1	NT	replication factor C subunit 2 (RFC2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5117	18127	31002	1.53	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5117	18127	31003	1.53	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5948	18943	31583	3.46	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIA0727 protein, partial cds
6269	19371	32610	4.99	2.0E-82	AF234862.1	NT	Homo sapiens FAM441 splice variant a (FAM441) mRNA, complete cds
7845	26204		0.88	2.0E-82	AF234862.1	EST_HUMAN	tm21005.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
8104	21041	34440	0.99	2.0E-82	8523130	NT	Homo sapiens hypodermal protein FLJ20128 (FLJ20128), mRNA
8589	21557	34973	0.48	2.0E-82	11431845	NT	Homo sapiens nucleotide binding protein 1 (E.coli MinD like) (NUBP1), mRNA
8848	21816	35038	1.94	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
9017	21983	35402	0.47	2.0E-82	7657340	NT	Homo sapiens microchitin (mouse) homolog (MORC), mRNA
9017	21983	35403	0.47	2.0E-82	7657340	NT	Homo sapiens microchitin (mouse) homolog (MORC), mRNA
10468	23390	36584	1.66	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10468	23390	36585	1.66	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11600	24538	38096	3.95	2.0E-82	11417191	NT	Homo sapiens leucyl/leucyl aminopeptidase (LNP2P), mRNA
11600	24538	38096	3.95	2.0E-82	11417191	NT	Homo sapiens leucyl/leucyl aminopeptidase (LNP2P), mRNA
11638	24575	38140	2.31	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11638	24575	38141	2.31	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12227	25062		1.84	2.0E-82	NP4950.1	EST_HUMAN	2631d10.s1 Soares_papillary thyroid tumor_NHPPA Homo sapiens cDNA clone IMAGE:305203 3'
12790	25403		4.39	2.0E-82	AA011278.1	EST_HUMAN	207p09.r1 Soares_fetal_liver_spleen_1NFL.S_S1 Homo sapiens cDNA clone IMAGE:429568 5'
13084	25598		1.93	2.0E-82	11418037	NT	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
584	13651	26574	1.27	1.0E-82	11645921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1213	14251		1.09	1.0E-82	BE885108.1	EST_HUMAN	801510859FT NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3912207 5'
1280	14325	27286	2.11	1.0E-82	BE004388.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1291	14326	27287	1.07	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIA0538 protein, partial cds
9294	22260	35689	1.09	1.0E-82	AB037638.1	NT	Homo sapiens mRNA for KIA01477 protein, partial cds
10011	22938	38403	0.69	1.0E-82	AB014592.1	NT	Homo sapiens mRNA for KIA0662 protein, partial cds
10009	23528		1.24	1.0E-82	BF518938.1	EST_HUMAN	U1H.BW1-acca-f-03-9-U1.s1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
11097	24057	37681	1.87	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9055	22031	35454	4.87	9.0E-83	BF72220.1	EST_HUMAN	802150403FT NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4291561 5'
10637	23569	37058	0.62	9.0E-83	BE233347.1	EST_HUMAN	801117160FT NIH_MGC 16 Homo sapiens cDNA clone IMAGE:335734 5'
1412	14445	27147	1.55	8.0E-83	BE383973.1	EST_HUMAN	801273349FT NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3614362 5'
1691	19820	27702	4.08	8.0E-83	NP6951.1	EST_HUMAN	2a48f12.s1 Soares_fetal_liver_spleen_1NFL.S Homo sapiens cDNA clone IMAGE:289823 3'
1356	14354	27364	0.89	7.0E-83	AW385528.1	EST_HUMAN	QY4.LT0016-271289-068-h11 LT0016 Homo sapiens cDNA
2876	16935		1.92	7.0E-83	AA564655.1	EST_HUMAN	nc012h01.s1 NCL CGAP_Pho1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4853	17870		7.64	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TRQ9Y316 Q9Y316
6169	19244	32478	0.73	7.0E-83	11426857	NT	DJ207H1.1
403	13476	29410	3.07	6.0E-83	M33320.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
							Human platelet glycoprotein Ila (GP1Ib) gene, exon 2-29
1802	14830	27617	1.08	6.0E-83	AW573088.1	EST_HUMAN	h3H03X1 Soares_NFL1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to
3030	16088	29008	0.64	6.0E-83	AW816405.1	EST_HUMAN	SW:YBBB_HAEN P44471 HYPOTHETICAL PROTEIN H0034. ;
3084	16121		0.87	6.0E-83	AF231919.1	NT	QV4-S10234-181198-037-405 ST0234 Homo sapiens cDNA
3093	16140	29051	1.03	6.0E-83	AA701457.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3575	16820	29541	2.54	6.0E-83	11430241	NT	256205.s1 Soares_fetal_liver_spleen_1NFL5_S1 Homo sapiens cDNA clone IMAGE:435080 3'
5167	18176	31054	1.2	6.0E-83	4827033	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
							Homo sapiens tumor necrosis factor (ligand) superfamily, member 18 (TNFSF18) mRNA
							Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,
							and translated products
5368	18471	31342	1.53	6.0E-83	4507568	NT	Homo sapiens hyaluron gene, exons 1-50
6139	18215	32444	1.32	6.0E-83	AJ010770.1	NT	Homo sapiens mat proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
7745	20999	34056	2.1	6.0E-83	11422024	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10035	22962	39430	2.6	6.0E-83	4503314	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA
10127	23053	36531	0.78	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prip18 (PRP18), mRNA
10127	23053	36532	0.78	6.0E-83	11430647	NT	ab14610.t1 Stratigene lung (4637210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains
							THR-42 THR repetitive element ;
11859	24741		2.01	6.0E-83	AA486105.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
							genes, complete cds
12179	25027		5.85	6.0E-83	AF240786.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
945	13698		1.42	5.0E-83	U17983.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
2086	15823		1	5.0E-83	AF006305.1	NT	Novel human gene mapping to chromosome X
3552	16095	28910	0.97	6.0E-83	AL133207.2	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
3826	16986	29579	1.02	5.0E-83	4885190	NT	Homo sapiens catalase (CAT) mRNA
5115	18125	31000	14.32	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5115	18125	31001	14.32	5.0E-83	4557013	NT	Homo sapiens phosphatidylinositol 3-kinase, catalytic, gamma polypeptide (PIK3CG) mRNA
5245	18253	31124	0.93	5.0E-83	4509602	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
641	13707	26828	2.26	4.0E-83	AF224659.1	NT	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913185 5'
3528	16371	29494	1	4.0E-83	BE888078.1	EST_HUMAN	EST76642 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
999	14050		8.39	3.0E-83	AA368311.1	EST_HUMAN	



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11272	24224	37749	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZ5547135_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ5547135 5'
11272	24224	37750	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZ5547135_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ5547135 5'
12802	25429		4.91	2.0E-83	AB011359.1	NT	Homo sapiens gene for AF-6, complete cds
1410	14443	27414	1.56	1.0E-83	4504328	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1410	14443	27415	1.56	1.0E-83	4504328	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1453	14486	27461	0.93	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1453	14486	27462	0.93	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2665	15592	29681	1.16	1.0E-83	BE883680.1	EST_HUMAN	601607376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5083754 5'
3188	16253	29173	0.95	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0866), mRNA
3882	16922	29630	3.33	1.0E-83	AF052768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4273	17502	30182	2.31	1.0E-83	Z55822.1	NT	H sapiens gene for mitochondrial dodecenoyl-CoA delta-iscemerase, exon 3
6854	16907	33203	1.53	1.0E-83	AI02761.1	EST_HUMAN	059808.XT Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM
3810	16950	29758	3.98	7.0E-84	BE907209.1	EST_HUMAN	PROTEIN (HUMAN);
1298	14333	27294	4.11	6.0E-84	BE638664.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1298	14333	27295	4.11	6.0E-84	BE638664.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2407	15414	28438	5.78	6.0E-84	AA776574.1	EST_HUMAN	aa6603.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5311	18326		1.9	6.0E-84	AL042863.2	EST_HUMAN	DKFZ544840322_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ544840322 5'
5596	18692	31692	1.89	6.0E-84	AA897338.1	EST_HUMAN	s47603.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
5743	18837	32018	1.09	6.0E-84	11428718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5743	18837	32019	1.09	6.0E-84	11428718	NT	Homo sapiens acetyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7714	20671	34038	3.35	6.0E-84	BE810371.1	EST_HUMAN	Homo sapiens acetyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7895	20686	34269	0.89	6.0E-84	AF038397.1	NT	PMOL-T0019-180600-004-F02 LT0019 Homo sapiens cDNA
8408	21377	34783	2.05	6.0E-84	BE770198.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
715	13777	28712	0.81	6.0E-84	AA352811.1	EST_HUMAN	PM4-F1004-160500-004-a10 F1004 Homo sapiens cDNA
3027	16084		1.54	6.0E-84	AF109718.1	NT	EST186094 Testis1 Homo sapiens cDNA 5' end
6227	19301	32634	0.49	6.0E-84	AA161678.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
							z49607.r1 Stragene hNT neuron (4637238) Homo sapiens cDNA clone IMAGE:632100 5' similar to
							TR:G483915 G483915 RETROTRANSCRIPTABLE L1 ELEMENT L'RE2 FROM CHROMOSOME 1Q.1;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11871	24763	38334	2.06	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (REF33), mRNA
11884	24843	38437	2.29	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11884	24843	38438	2.29	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1409	14442	27413	1.88	4.0E-84	AF085321.1	EST_HUMAN	SW/NRDC_HUMAN O43847 NARDLYSIN PRECURSOR ;
4987	18002	30891	0.99	4.0E-84	4605928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
4988	18003	30982	2.19	4.0E-84	AF089012	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5338	18440	31183	0.53	4.0E-84	AF022635.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5942	18738	31802	1.28	4.0E-84	11386188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5942	18738	31803	1.28	4.0E-84	11386188	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
6369	19497	32714	1.89	4.0E-84	AF058650.1	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7609	20852	34259	12.53	4.0E-84	11421328	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8282	22228	36658	0.9	4.0E-84	4657528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9282	22228	36659	0.9	4.0E-84	4657528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11283	24215	37739	5.34	4.0E-84	AB032958.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
316	13408	28334	1.92	3.0E-84	AF026200.1	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1157	14169	27146	5.95	3.0E-84	4758081	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1977	14988	28000	1.24	3.0E-84	5453855	NT	Novel human mRNA containing Zinc finger C2H2 type domains
2024	15044	28057	3.11	3.0E-84	AL086880.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3804	16649	29565	1.15	3.0E-84	AB026898.1	NT	Homo sapiens X-linked juvenile rheumatoid arthritis precursor protein (XLR31) mRNA, complete cds
3762	16803	29715	8.28	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile rheumatoid arthritis precursor protein (XLR31) mRNA, complete cds
11228	24176	28132	17.2	3.0E-84	AF083801.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
2115	15132	28193	5.68	2.0E-84	BE695397.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
2115	15132	28194	5.68	2.0E-84	BE695397.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
2964	16012	28839	7.98	2.0E-84	AF038943.1	NT	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
2973	16031	28854	1.35	2.0E-84	AF038943.1	NT	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
5604	18700	31671	0.88	2.0E-84	BF0511575.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
5604	18700	31672	0.88	2.0E-84	BF0511575.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
6793	19847	33132	0.88	2.0E-84	AF038943.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
8392	21381	35121	1.62	2.0E-84	AF038943.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
8728	21998	35121	0.86	2.0E-84	AF038943.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to
8728	21998	35122	0.86	2.0E-84	AF038943.1	EST_HUMAN	h200053.x1 Soares_Dickgrafe_colon_NHGD Homo sapiens cDNA clone IMAGE:2520565 3' similar to

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9701	22654	38108	0.99	2.0E-84	AI02080.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone IMAGE:100339 5'
10089	23015	38491	0.55	2.0E-84	H22841.1	EST_HUMAN	ym4911.1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOH_RAT P26844 BETA-2-GLYCOPROTEIN I:
12445	25206	31829	3.28	2.0E-84	BF448000.1	EST_HUMAN	nao30402.x1 Lupski_sympathetic trunk Homo sapiens cDNA clone IMAGE:409251 3' similar to TR:QBU053 QBU053 DJ756G23.1:
12445	25206	31830	3.28	2.0E-84	BF448000.1	EST_HUMAN	nao30402.x1 Lupski_sympathetic trunk Homo sapiens cDNA clone IMAGE:409251 3' similar to TR:QBU053 QBU053 DJ756G23.1:
312	13404	28330	1.44	1.0E-84	AF114488.1	EST_HUMAN	Homo sapiens intercrin short isoform (ITSN) mRNA, complete cds
551	13621	28541	15.78	1.0E-84	4607662	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
721	13783	27181	1.16	1.0E-84	11427831	NT	Homo sapiens complement component 5 (C5), mRNA
1296	14331	27282	3.31	1.0E-84	AA984379.1	EST_HUMAN	emb5011.1 Stratigene schizo brain S11 Homo sapiens cDNA clone IMAGE:162885 3'
2070	15087	28105	2.34	1.0E-84	BE592137.1	EST_HUMAN	60130006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3329237 5'
2232	16248	28268	1.27	1.0E-84	11427187	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3764	16806	29717	2.47	1.0E-84	AA720851.1	EST_HUMAN	hw12806.st NCI CGAP_SST Homo sapiens cDNA clone IMAGE:1238106 3'
4446	17472	30360	3.92	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4728	17748	30639	2.65	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_11 434 (synonym: hla3) Homo sapiens cDNA clone DKFZp434N0323 5'
4728	17748	30840	2.65	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_11 434 (synonym: hla3) Homo sapiens cDNA clone DKFZp434N0323 5'
4949	17472	30360	2.12	1.0E-84	AI028041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6029	19112	32314	0.95	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6314	19385	32827	1.38	1.0E-84	S73482.1	NT	Utaie water channel-28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
7054	20086	33394	1.44	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7054	20086	33395	1.44	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7314	20285	33628	2.65	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
7708	20665	34032	4.72	1.0E-84	8393594	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7814	20763	34139	0.63	1.0E-84	11430848	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7859	20763	34139	2.91	1.0E-84	11430848	NT	Homo sapiens NGF-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8963	22849	34139	2.91	1.0E-84	6031684	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15), mRNA
10128	23054	36533	0.82	1.0E-84	AF22451.1	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3) gene, exon 6 and partial cds
10160	18337	31285	2.65	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 13) (USP13) mRNA
10160	18337	31286	2.65	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 13) (USP13) mRNA
12224	20285	33926	2.67	1.0E-84	AL048784.1	NT	Novel human gene mapping to chromosome 13
12321	25126	33926	2.03	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X2-like 1, orphan receptor (P2RXL1), mRNA



Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12436	26201	31825	2.32	1.0E-84	11418185	NT	Homo sapiens acotinase 2, mitochondrial (ACQ2), mRNA
988	14020		1.9	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1074	14119	27059	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Slp mRNA, complete cds
1074	14119	27070	2.21	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Slp mRNA, complete cds
1581	14614	27596	1.31	9.0E-85	M63282.1	NT	Human plasminogen gene, exon 7
1581	14614	27587	1.31	9.0E-85	M63282.1	NT	Human plasminogen gene, exon 7
1684	14715	27655	2.95	9.0E-85	7657020	NT	Homo sapiens DKFZ434P211 protein (DKFZ434P211), mRNA
4280	17309	30188	1.11	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4913	17930	30821	1.05	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4850	17965	30855	1	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1138	14181	27132	13.33	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11958	24837		9.76	7.0E-85	AF13210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11745	24630	38209	2.51	6.0E-85	11438573	NT	Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11745	24630	38210	2.51	6.0E-85	11438573	NT	Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2340	15350	28371	1.67	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5528	18625	31580	1.37	5.0E-85	BF035874.1	EST_HUMAN	601458648FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3882402 5'
5528	18625	31581	1.37	5.0E-85	BF035874.1	EST_HUMAN	601458648FT NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3882402 5'
13030	18344		6.19	5.0E-85	AF21189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-1 isoform (CACNA1I) mRNA, complete cds
6271	19344	32576	1.42	4.0E-85	BF077910.1	EST_HUMAN	602084730FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
6271	19344	32577	1.42	4.0E-85	BF077910.1	EST_HUMAN	602084730FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
7013	20139	33456	0.58	4.0E-85	AI628119.1	EST_HUMAN	964g01.x1 NC1_CGAP K1811 Homo sapiens cDNA clone IMAGE:2265508 3'
10937	23857		1.35	4.0E-85	BE079283.1	EST_HUMAN	RC1-BT0623-120205-011-c07 BT0623 Homo sapiens cDNA
12375	25772		1.31	4.0E-85	Z18887.1	EST_HUMAN	HSDHEG03 Stradiolone cDNA library Human heart, cat8936208 Homo sapiens cDNA clone HEGC03
1302	14938	27301	1.02	3.0E-85	AF066157.1	NT	Homo sapiens protein phosphatase 2A B5 gamma subunit gene, exon 8
1765	14924	27803	3.19	3.0E-85	T87495.1	EST_HUMAN	ye83g05.r1 Soares fetal liver spleen cDNA clone IMAGE:121504 5'
4935	17951	30842	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4935	17951	30843	1.37	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5475	18576	31485	0.85	3.0E-85	11436001	NT	Homo sapiens leucine rich protein (LPRP), mRNA
6204	19278	32511	0.66	3.0E-85	11422024	NT	Homo sapiens mel proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6257	19330	32590	5.69	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6257	19330	32591	5.93	3.0E-85	7652309	NT	Homo sapiens KIAA0769 gene product (KIAA0769), mRNA
7140	20116		7.73	3.0E-85	AIJ40468.1	NT	Homo sapiens mRNA for dyx19 heavy chain (DYX19 gene)
7626	20598	33546	0.88	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK), KIAA0621 protein (KIAA0621), mRNA
8204	21174	34584	1.84	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8853	21820	35240	1.05	3.0E-85	11525823	NT	Homo sapiens CGI-87 protein (LOC511108), mRNA
9329	22294	35723	3.37	3.0E-85	11430899	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9651	22818	36272	1.03	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRPB2), mRNA
9651	22818	36273	1.03	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRPB2), mRNA
10949	23769	37268	1.16	3.0E-85	AF09842.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11834	24717	38303	1.72	3.0E-85	5031650	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
12819	25495		2.14	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
954	14016	26570	0.87	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein, Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1041	14087	27039	2.52	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D18), mRNA, complete cds
1418	14451	27424	8.49	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1478	14451	27425	8.49	2.0E-85	5174776	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2239	15253	28277	1.8	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2834	14375		14.60	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3035	16093	29011	1.16	2.0E-85	N30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4381	17388	30270	4.83	2.0E-85	4505580	NT	Homo sapiens plasminogen (PLG) mRNA
4948	17964	30854	0.93	2.0E-85	AI163284.2	NT	Homo sapiens chromosome 21, segment HS21C084
5178	18187	31064	1.37	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARG1) mRNA
8928	22572	36022	2.67	2.0E-85	AI760820.1	EST_HUMAN	MSR1 repetitive element;
10007	22934	36598	0.94	2.0E-85	AI014550.1	EST_HUMAN	wf448d03.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:23331467 3'
10526	23547	37048	1.31	2.0E-85	AI886394.1	EST_HUMAN	wf96d12.x1 NCL CGAP, U2 Homo sapiens cDNA clone IMAGE:24433607 3'
2295	15307		2.51	1.0E-85	BE764306.1	EST_HUMAN	601891416F1 NIH_MGC, 7 Homo sapiens cDNA clone IMAGE:3945518 5'
2403	15410	28434	6.6	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC, 67 Homo sapiens cDNA clone IMAGE:3869021 6'
2403	15410	28435	6.6	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC, 67 Homo sapiens cDNA clone IMAGE:3869021 5'
8091	21027	34428	0.52	1.0E-85	BE002951.1	EST_HUMAN	MR0-BT0264-221189-002-603 BT0264 Homo sapiens cDNA
10140	23066	36542	2.41	1.0E-85	BE287917.1	EST_HUMAN	601109738F1 NIH_MGC, 18 Homo sapiens cDNA clone IMAGE:3360553 5'
10571	23493	36985	0.53	1.0E-85	AW813525.1	EST_HUMAN	RC1-ST0186-081089-011-d05 ST0186 Homo sapiens cDNA
11269	24221	37145	2.01	1.0E-85	AA178785.1	EST_HUMAN	24503.at Soares, field_liver_spleen, TNFLS, S1 Homo sapiens cDNA clone IMAGE:493246 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11289	24221	37746	2.01	1.0E-85	AA718785.1	EST_HUMAN	244903.s1 Soares fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11342	24292	37816	2.46	1.0E-86	BF311552.1	EST_HUMAN	60180703FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
11342	24292	37817	2.46	1.0E-85	BF311552.1	EST_HUMAN	60180703FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
12064	24377	38533	2.37	1.0E-85	AI189420.1	EST_HUMAN	q16a07.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1160468 3'
12328	25289	31780	3.47	1.0E-85	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
12383	25289	31780	3.37	1.0E-85	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
1428	14458	32552	12.78	9.0E-86	BE274217.1	EST_HUMAN	60112078FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867680 5'
6249	18522	32552	1.27	8.0E-86	11424140	NT	Homo sapiens similar to GDC28 protein kinase 1 (H_sapiens) (LOC63041), mRNA
12004	24881	38477	1.57	8.0E-86	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
638	13589	26030	0.93	7.0E-86	AA860801.1	EST_HUMAN	q88f08.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403569 3'
638	13589	26040	0.93	7.0E-86	AA860801.1	EST_HUMAN	q88f08.s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403569 3'
6320	16591	32631	0.85	7.0E-86	9968838	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6320	16591	32632	0.85	7.0E-86	9968838	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7169	18400	31246	6.12	7.0E-86	11421737	NT	Homo sapiens Tact (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
6086	22062	35487	4.12	7.0E-86	138557.1	NT	Homo sapiens galealactoblasticase (GALC) gene, exon 15
10058	22885	36522	1.49	7.0E-86	5453967	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10116	23042	36522	1.67	7.0E-86	11523007	NT	Homo sapiens oocyte cytoplasmic dehydrogenase (lipoamide) (OGDH), mRNA
1287	14332	27293	3.29	6.0E-86	4505492	NT	Homo sapiens oocyte cytoplasmic dehydrogenase (lipoamide) (OGDH), mRNA
212	13312	26241	1.76	4.0E-86	BE547173.1	EST_HUMAN	601072594FT NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6151	19228	32456	10.99	4.0E-86	BE547173.1	EST_HUMAN	60117855FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
11572	13512	26241	2.44	4.0E-86	BE547173.1	EST_HUMAN	60117855FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
5877	18772	31944	8.64	3.0E-86	AW340946.1	EST_HUMAN	582h12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone HTB5D04 5'
8605	21573	34988	1.12	3.0E-86	AV72329.1	EST_HUMAN	AV72329 HTB Homo sapiens cDNA clone IMAGE:3911903 5'
10551	23503	36995	3.26	3.0E-86	BE886478.1	EST_HUMAN	60150989FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911903 5'
10551	23503	36996	3.26	3.0E-86	BE886479.1	EST_HUMAN	60150989FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911903 5'
11764	23619	37437	5.6	3.0E-86	AI85240.1	EST_HUMAN	bu1802.x1 NCI CGAP_F28 Homo sapiens cDNA clone IMAGE:2251371 3'
11842	24725	38512	1.95	3.0E-86	AV600469.1	EST_HUMAN	AV600468 GKG Homo sapiens cDNA clone GKGSE02 5'
12295	25784	38512	1.35	3.0E-86	BE410354.1	EST_HUMAN	AV600468 GKG Homo sapiens cDNA clone IMAGE:3638753 5'
268	13362	26286	1.83	2.0E-86	AA305284.1	EST_HUMAN	EST1177232 Jutek T-cells VI Homo sapiens cDNA clone IMAGE:3638753 5'
414	13487	27189	2.72	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1194	14234	27189	2.88	2.0E-86	NS5977.1	EST_HUMAN	3219a08.r1 Soares multiple sclerosis_2NblHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2201	15216	26238	2.54	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2277	15230	26315	1.14	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3428	16474	29393	1.47	2.0E-86	AW596142.1	EST_HUMAN	EST178215 IMAGE resequences, MAG1 Homo sapiens cDNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3759	16800	28711	2.55	2.0E-86	AF165778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3759	16800	28712	2.55	2.0E-86	AF165778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4070	17108		3.01	2.0E-86	AW516742.1	EST_HUMAN	h87g08.x1 NC1 CGAP GC6 Homo sapiens cDNA clone IMAGE2916542 3'
4828	17845	30745	3.3	2.0E-86	AF096400.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5872	18057	32257	1.53	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5872	18057	32258	1.53	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7277	25672	33314	0.81	2.0E-86	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8343	21312	34726	0.77	2.0E-86	U84744.1	NT	Human Chediak-Higuchi syndrome protein short isoform (LYST) mRNA, complete cds
8861	21828		0.53	2.0E-86	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8920	21866	35312	2.44	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8920	21866	35313	2.44	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9254	22220	35651	1.48	2.0E-86	10693876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9873	22628	36080	2.12	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog-like (CSE1L), mRNA
10814	23735	37237	2.88	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10814	23735	37238	2.88	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10859	23769	37289	1.63	2.0E-86	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
12732	25383	31750	2.92	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70KD (Ku antigen) (G22P1), mRNA
12501	26485		6.37	2.0E-86	AB011359.1	NT	Homo sapiens gene for AF-6, complete cds
1601	14633	27609	1.28	1.0E-86	4828895	NT	Homo sapiens NADH dehydrogenase (ubiquinone) F6-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1), mRNA
3176	16231	29147	1.52	1.0E-86	6453949	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3245	16304	29228	2.61	1.0E-86	20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3307	16390	29279	2.18	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3307	16390	29280	2.18	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3966	17006	29921	1.01	1.0E-86	7709161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3966	17006	29922	1.01	1.0E-86	7709161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4293	17322	30202	5.66	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4651	17672	30359	1.12	1.0E-86	4507334	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
5632	18728	31869	1.44	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5430	18533		1.78	9.0E-87	AH150703.1	EST_HUMAN	q677005.x1 Soares_Yeah_Hu21.NGH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7681	20639	34001	1.73	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7681	20639	34002	1.73	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7681	20639	34003	1.73	9.0E-87	4757721	NT	Oculin mRNA for elongation factor 1 alpha
2304	13552	28480	82.98	8.0E-87	X92245.1	NT	718502.x1 NCI CGAP C616 Homo sapiens cDNA clone IMAGE:3322779 3'
2304	13516	28336	3.11	7.0E-87	BF063211.1	EST_HUMAN	718502.x1 NCI CGAP C616 Homo sapiens cDNA clone IMAGE:3322779 3'
2304	13516	29337	3.11	7.0E-87	BF063211.1	EST_HUMAN	718502.x1 NCI CGAP C616 Homo sapiens cDNA clone IMAGE:3322779 3'
6540	15902	32884	1.01	7.0E-87	AW890339.1	EST_HUMAN	MRO-NT0039-020600-004-a11 NT0039 Homo sapiens cDNA
8531	21499	34015	2.59	7.0E-87	BF352776.1	EST_HUMAN	IL3-H10702-160600-103-d08 HT0702 Homo sapiens cDNA
8809	21132	34935	0.86	7.0E-87	BE712661.1	EST_HUMAN	IL3-H10702-160600-103-d08 HT0702 Homo sapiens cDNA
10431	23353	36837	3.41	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323.5'
10431	23353	36838	3.41	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323.5'
10834	25703	37708	0.48	7.0E-87	AL081555.1	EST_HUMAN	ox59101.st Soares_NHHPV_S1 Homo sapiens cDNA clone IMAGE:1660657 3'
11237	24180	37708	10.09	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
11237	24180	37709	10.09	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 Intron A
3538	16594	29507	0.76	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated nest tumor-associated kinase (HUNK), mRNA
6561	19821	32886	1.84	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
11078	24041		6.13	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1162	14204	27157	1.89	5.0E-87	AA382811.1	EST_HUMAN	EST186094 Testis 1 Homo sapiens cDNA 5' end
12585	14204	27157	2	5.0E-87	AA382811.1	EST_HUMAN	EST186094 Testis 1 Homo sapiens cDNA 5' end
667	14019	26972	0.98	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1176	14217	27172	15.32	4.0E-87	AB037635.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2045	15064	28084	1.49	4.0E-87	AB007825.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
3478	16524	29448	1.57	4.0E-87	6174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (withoxax (Drosophila) homolog); translocated to, 4 (MLL1), mRNA
5307	18310	31167	0.98	4.0E-87	4759073	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 16 (SCYA16) mRNA
5307	18310	31168	0.98	4.0E-87	4759073	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 16 (SCYA16) mRNA
5521	18920	31554	5.85	4.0E-87	O00321	SWISSPROT	E15-RELATED PROTEIN 71 (E15) TRANSLATION VARIANT 2
5844	18934	32118	0.55	4.0E-87	U65428.1	NT	Human transcription factor NFATX3 mRNA, complete cds
6163	19238	32469	4.54	4.0E-87	BE247284.1	EST_HUMAN	TCBPAP1E4051 Pcellular pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBPAP4051
7653	20876	34264	0.3	4.0E-87	11425281	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7653	20876	34265	0.5	4.0E-87	11425281	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8050	20987	34383	0.81	4.0E-87	L49524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
9593	22545	35995	0.47	4.0E-87	AF229470.1	NT	Homo sapiens KIAA0971-1 protein (KIAA0971-1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11500	24443	37594	5.12	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
12878	25539	31426	1.47	4.0E-87	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
12878	25539	31426	1.47	4.0E-87	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
12825	26444		3.11	4.0E-87	11417812	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RX1), mRNA
2787	15719	28796	4.73	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2959	16017		0.79	2.0E-87	BF327820.1	EST_HUMAN	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3768	16938	29745	0.9	2.0E-87	ALJ18935.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
4951	17696	30896	1.84	2.0E-87	ALJ18935.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
4968	18013	30900	0.88	2.0E-87	BE175478.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
5744	18839	32020	8.67	2.0E-87	BE734190.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
5744	18839	32021	8.67	2.0E-87	BE734190.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
6460	19525		3.73	2.0E-87	BE657193.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
6957	19910	33205	1.12	2.0E-87	N48128.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
6946	20172	33456	0.84	2.0E-87	AV654143.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7379	20349	33700	1.31	2.0E-87	BE284432.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7436	20403	33757	0.81	2.0E-87	11433046	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7698	20644	34008	37.21	2.0E-87	N48128.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7951	20892	34284	36.03	2.0E-87	N48128.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
8738	21706	35130	13.21	2.0E-87	X52851.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
10144	23070		5.58	2.0E-87	BE531136.1	EST_HUMAN	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
1186	15818		3.71	1.0E-87	7705683	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
3723	16768	26877	4.15	1.0E-87	Y00052.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
3746	16768	29700	2.03	1.0E-87	47598827	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
5132	18102	31042	1.98	1.0E-87	U50949.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
6352	19421	32862	1.94	1.0E-87	AF073371.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
6352	19421	32863	1.94	1.0E-87	AF073371.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7393	20353	33704	0.84	1.0E-87	AF039517.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7393	20353	33705	0.84	1.0E-87	AF039517.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7396	20358	33710	1.03	1.0E-87	4500760	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7328	20568	33951	1.17	1.0E-87	11431560	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
7783	20736	34108	0.85	1.0E-87	4500766	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
8098	21005	34403	0.64	1.0E-87	4505528	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'
8453	21422	34837	11.12	1.0E-87	AF214562.1	NT	QVQ-BN0148-050600-254-e03 BN0148 Homo sapiens cDNA clone HEMBA100307 5'

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9260	22226	35655	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2-3-sialyltransferase ST3Gal VI, complete cds
9260	22226	35656	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2-3-sialyltransferase ST3Gal VI, complete cds
9260	22226	35656	0.97	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2-3-sialyltransferase ST3Gal VI, complete cds
9891	22918	36394	6.68	1.0E-87	BE818183.1	EST_HUMAN	RCB-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9891	22918	36395	6.68	1.0E-87	BE818183.1	EST_HUMAN	RCB-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10739	23681	37155	3.11	1.0E-87	M84426.1	NT	Human L-plastin mRNA, 5' end
11084	24045	37567	1.78	1.0E-87	5729967	NT	Homo sapiens heet domain and RLD 2 (HERC2), mRNA
12375	25978		1.48	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULT3), mRNA
1108	14192	27102	6.48	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1351	14386	27356	2.56	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1369 protein, partial cds
1351	14386	27356	2.56	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1369 protein, partial cds
2130	15147	28162	1.14	9.0E-88	7661701	NT	Homo sapiens DKFZP566P1522 protein (DKFZP566P1522), mRNA
3042	16885	28601	0.99	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS210009
4268	17327	30207	3.27	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4268	17327	30208	9.27	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
5038	18051	30931	1	9.0E-88	AB026938.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 12 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6975	22340	35771	3.69	6.0E-88	AF036528.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1845	14871		1.13	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2647	15844	28689	5.45	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart; Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3013	16071	28991	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3023	16080	29002	0.77	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3023	16080	29003	0.77	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3400	18446		2.75	5.0E-88	AL693217.1	EST_HUMAN	w68b08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element; contains element MER22, MER22 repetitive element
6938	22160	33481	3.32	6.0E-88	H10632.1	EST_HUMAN	3m08b10.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
8261	22430	34638	2.44	5.0E-88	AF163284.2	NT	Homo sapiens chromosome 21 segment HS210084
6866	22819	36070	0.57	5.0E-88	BF680206.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4298775 5'
12435	14871		1.73	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1332	14387	27336	1.49	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-504-f10 TN0028 Homo sapiens cDNA
1332	14387	27337	1.49	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-504-f10 TN0028 Homo sapiens cDNA
5185	18194	31069	0.81	4.0E-88	BF670714.1	EST_HUMAN	802149762F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4260875 6'
7454	20420	33775	1.35	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 88kD (TGFB1), mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11818	24701	38282	3.12	4.0E-88	7661047	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11818	24701	38283	3.12	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
733	13794	28731	0.85	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1829	14658	28731	1.78	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2958	16016	28544	2.51	3.0E-88	N69951.1	EST_HUMAN	zad812.s1 Soares fetal liver spleen TNF-LS Homo sapiens cDNA clone IMAGE:295823 3'
4289	17298	30176	0.93	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4289	17298	30176	0.93	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4504	17529		3.84	3.0E-88	11428300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5372	18477	31350	2.45	3.0E-88	11429667	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5668	18761	31630	4.05	3.0E-88	6969883	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5789	18881	32083	3.82	3.0E-88	11420667	NT	Homo sapiens vral simian leukemia viral oncogene homolog A (res related) (RALA), mRNA
6285	19357	32553	0.95	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6553	25662	32877	0.77	3.0E-88	11416210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6553	25662	32878	0.77	3.0E-88	11416210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7287	20002	33502	15.04	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7788	20741	34114	6.35	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8253	21222	34632	10.96	3.0E-88	11421728	NT	Homo sapiens growth differentiation factor 5 (cardiopo-derived morphogenetic protein-1) (GDF5), mRNA
8538	21508	34623	1.28	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds
9789	21612	34512	2.14	3.0E-88	11526262	NT	Homo sapiens vial avian erythroblastosis virus E26 oncogene related (ER6), mRNA
10258	23213	36686	0.74	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-2, complete cds
10288	23213	36697	0.74	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-2, complete cds
10316	23240	36721	0.69	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12086	24958	38554	3.65	3.0E-88	4457502	NT	Homo sapiens cubilin (putative factor-cobalamin receptor) (CUBN) mRNA
12421	26191		7.12	3.0E-88	11417974	NT	Homo sapiens transferrin receptor 1; macrocytic anemia (TGN2), mRNA
1037	14083	27033	61.67	2.0E-88	7305168	NT	Homo sapiens Calsenilin, preprotein-binding protein, EEF hand transcription factor (CSEN), mRNA
1628	14681	27637	1.66	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
1765	14784	27719	4.07	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
4455	17481	30369	1.86	2.0E-88	5031686	NT	Homo sapiens dyx1in, axonemal, light polypeptide 4 (DNAL4), mRNA
8016	19096	32300	5.17	1.0E-88	AW139565.1	EST_HUMAN	U1-H-B11-acc-0-04-0-U1.1 NCL CGAP_Su33 Homo sapiens cDNA clone IMAGE:2718750 3'
8016	19096	32301	5.17	1.0E-88	AW139565.1	EST_HUMAN	U1-H-B11-acc-0-04-0-U1.1 NCL CGAP_Su33 Homo sapiens cDNA clone IMAGE:2718750 3'
6802	19858	33141	23.82	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6802	19858	33142	23.82	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds



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Table 4

### Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7329	20300	33644	1.29	1.0E-88	AI989034.1	EST_HUMAN	wg70at12x1 NCI_CGAP GC8 Homo sapiens cDNA clone IMAGE:247608 3'
7390	20359	39711	3.91	1.0E-88	AA489891.1	EST_HUMAN	as54t11.1 NCI_CGAP G0B1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP_00272.2
8478	21445	34892	0.47	1.0E-88	AF195163.1	NT	CE00831.1
9597	22601	39050	1.09	1.0E-88	AA190368.1	EST_HUMAN	Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
9938	22665	36327	2.73	1.0E-88	AL043314.2	EST_HUMAN	z987602.1 Stragene HeLa cell c8 637216 Homo sapiens cDNA clone IMAGE:827170 5' similar to SW_POL_1 Stragene P10268 RETROVIRUS-RELATED POL POLYPROTEIN ; DKFZp434N0323.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
11773	23928	37449	3.86	1.0E-88	AA991479.1	EST_HUMAN	g091g03.1 NCI_CGAP GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gbM16342
12640	25324	24248	1.91	1.0E-88	AL163246.2	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
11298	24248	37774	3.66	1.0E-89	11421238.NT	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
2745	15738	28765	1.74	8.0E-89	BE311557.1	EST_HUMAN	Homo sapiens similar to serine domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC632332), mRNA
7118	20052	33356	1.21	8.0E-88	11421514.NT	EST_HUMAN	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
433	13507	28440	1.21	7.0E-89	7657213.NT	EST_HUMAN	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
433	13507	28441	1.21	7.0E-89	7657213.NT	EST_HUMAN	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
4919	17836	30828	2.95	7.0E-89	4557390.NT	EST_HUMAN	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4987	17892	30872	4.02	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434E246 5'
5505	18005	31534	1.22	7.0E-89	X98832.1	NT	H. sapiens CLN3 gene, complete CDS
5505	18005	31535	1.22	7.0E-89	X98832.1	NT	H. sapiens CLN3 gene, complete CDS
6477	19542	32769	0.77	7.0E-89	75489038.NT	EST_HUMAN	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
6477	19542	32769	0.77	7.0E-89	75489038.NT	EST_HUMAN	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
7741	20885	34080	1.42	7.0E-88	11420754.NT	EST_HUMAN	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
8211	21180	34559	0.57	7.0E-89	11417118.NT	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8211	21180	34560	0.57	7.0E-89	11417118.NT	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8823	21760	35212	3.98	7.0E-89	1029223.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10897	23817	37524	1.25	7.0E-89	X62048.1	NT	H. sapiens Wcst1 hu gene
10897	23817	37525	1.25	7.0E-89	X62048.1	NT	H. sapiens Wcst1 hu gene
10973	23817	37325	1.11	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10973	23817	37347	1.11	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10973	23833	37348	1.23	7.0E-89	AB020630.1	NT	Homo sapiens inner membrane protein, mitochondrial (mtolfin) (MMT), mRNA
1029	14071	27022	1.13	6.0E-89	59031114	NT	Homo sapiens serine/threonine-protein kinase PRP4 (PRP4) mRNA
2223	15237	28281	1.17	6.0E-89	4508124	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2440	15447	28464	0.60	6.0E-89	4507798	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2440	15447	28465	0.86	6.0E-89	4507798	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4657	17988	30573	4.04	5.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4657	17988	30574	4.04	5.0E-89	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5111	18121	30995	3.41	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA-P0383
5111	18121	30996	3.41	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA-P0383
7842	20789	34104	0.84	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-090900-219-q03 NT0022 Homo sapiens cDNA
2888	15947	28853	1.1	3.0E-89	AW976161.1	EST_HUMAN	EST388290 IMAGE reassessances, MAGN Homo sapiens cDNA
7347	20317	33583	1.25	3.0E-89	AI217359.1	EST_HUMAN	qht17000.x1 Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915 3'
11151	24111	37636	1.79	3.0E-89	NS7357.1	EST_HUMAN	yw86a1.r1 Sources_pleanta_8to5weeks_ZN1bHP809W Homo sapiens cDNA clone IMAGE:256148 5' similar to SW_P14K_HUMAN P42355 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
127	13481	28416	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
127	13481	28417	0.89	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
408	13481	28418	0.84	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
408	13481	28417	0.84	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
531	13802	28520	0.83	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2892	15951	28987	1.71	2.0E-89	AI222085.1	EST_HUMAN	gg96-c06.x1 Sources_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSFERASE 1 PRECURSOR (HUMAN); contains Atr repetitive element;
3565	16811	29532	0.65	2.0E-89	AA759149.1	EST_HUMAN	dh70903.s1 Sources_testis_NHT Homo sapiens cDNA clone 1320988 3'
3565	16811	29533	0.65	2.0E-89	AA759149.1	EST_HUMAN	dh70903.s1 Sources_testis_NHT Homo sapiens cDNA clone 1320988 3'
4193	17200	30066	1.41	2.0E-89	AF089897.1	NT	Homo sapiens isopentenylase-related function protein (TRF4-2) mRNA, partial cds
4190	17211	30068	4.86	2.0E-89	X59742.1	NT	H sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4190	17211	30069	4.89	2.0E-89	X59742.1	NT	H sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4376	17404	30284	0.83	2.0E-89	AI163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4524	17549	30437	1.1	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5416	18519	31600	1.39	2.0E-89	BE541744.1	EST_HUMAN	601065998r1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5558	18555	31600	2.77	2.0E-89	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
5888	18975	32167	1.66	2.0E-89	UC3985.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6335	19404	32644	0.67	2.0E-89	AI103285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7931	20874	34263	4.07	2.0E-89	U81004.1	NT	Human GT24 (GT24) mRNA, partial cds
8286	21235	34646	2.9	2.0E-89	1142880.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8760	21727	35149	0.84	2.0E-89	AL245503.1	NT	Homo sapiens partial mRNA for PEX3 related protein
8808	22812	35095	0.97	2.0E-89	AB03754.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10169	23084	36572	1.11	2.0E-89	AF170814.1	NT	Homo sapiens CABP5 (CABP5) gene, exon 5
10169	23084	36573	1.11	2.0E-89	AF170814.1	NT	Homo sapiens CABP5 (CABP5) gene, exon 5
11701	24868	38243	2.63	2.0E-89	11434411	NT	Homo sapiens Integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11898	24777	38363	3.64	2.0E-89	11433073	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (class homologue of L1) (CHL1), mRNA
12028	24902	38497	1.63	2.0E-89	U10692.1	NT	Human IMAGE-7 antigen (IMAGE7) pseudogenes, complete cds
11803	24784	38372	5.95	1.0E-89	BF196052.1	EST_HUMAN	h81d09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 054778 SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN ;
11903	24784	38373	6.65	1.0E-89	BF196052.1	EST_HUMAN	h81d09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 054778 SOLUTE CARRIER FAMILY 22 - LIKE 2 PROTEIN ;
8509	21637	34957	1.77	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8509	21637	34958	1.77	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1084	14110	27059	1.93	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1085	14110	27059	2.43	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1333	15864	27338	4.85	8.0E-90	BE670561.1	EST_HUMAN	7636008.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1333	15864	27339	4.85	8.0E-90	BE670561.1	EST_HUMAN	7636008.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8806	21872	35293	0.78	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-508 HT0598 Homo sapiens cDNA
11374	24321	37848	1.68	8.0E-90	AA705222.1	EST_HUMAN	282310.st Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
11374	24321	37849	1.68	8.0E-90	AA705222.1	EST_HUMAN	282310.st Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
837	13894		3.74	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8767	21734		2.07	7.0E-90	AA762977.1	EST_HUMAN	af330083.st Soares_testis_NHT Homo sapiens cDNA clone 13759503 3'
9317	22282	35712	1.82	7.0E-90	BE92525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9317	22282	35713	1.82	7.0E-90	BE92525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10495	23417	36916	2.08	7.0E-90	H68849.1	EST_HUMAN	y8604.st Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-C1TC_HUMAN P11588 C-1-TE TRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10495	23417	36916	2.08	7.0E-90	H68849.1	EST_HUMAN	y8604.st Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-C1TC_HUMAN P11588 C-1-TE TRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10821	23742	37243	0.58	7.0E-90	BF526098.1	EST_HUMAN	SP-C1TC_HUMAN P11588 C-1-TE TRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
3081	16138	29049	0.98	6.0E-90	X61928.1	NT	H.sapiens ECE-1 gene (exon 6)
3081	16138	29050	0.98	6.0E-90	X61928.1	NT	H.sapiens ECE-1 gene (exon 6)

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	17293	30164	0.71	6.0E-90	8522398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4284	17283	30165	0.71	6.0E-90	8522398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6097	19178	32363	3.07	6.0E-90	U77700.1	NT	Homo sapiens HSCGN1 mRNA, partial cds
6097	19178	32364	3.07	6.0E-90	U77700.1	NT	Homo sapiens HSCGN1 mRNA, partial cds
8870	21638	35081	3.16	6.0E-90	4504794	NT	Homo sapiens insulin 1,4,6-triphosphate receptor, type 3 (TIPR3) mRNA
8870	21638	35082	3.16	6.0E-90	4504794	NT	Homo sapiens insulin 1,4,6-triphosphate receptor, type 3 (TIPR3) mRNA
198	13259		25.81	5.0E-90	AB035344.1	NT	Homo sapiens TGLB gene, exon 1-10b
1197	14237	27192	1.84	5.0E-90	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1836	14863	27860	1.33	5.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Scaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1849022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
1836	14863	27861	1.33	5.0E-90	AI222095.1	EST_HUMAN	qg96c08.x1 Scaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1849022 3' similar to gb:J04131 GAMMA-GLUTAMYL-TRANSEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
2502	15563	28582	2.8	5.0E-90	AF114487.1	NT	Homo sapiens interectin long isoform (ITSN) mRNA, complete cds
4571	17563	30487	1.32	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4593	17614	30508	0.7	6.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5872	18767	31839	2.86	5.0E-90	Z10411.1	NT	H. sapiens mRNA encoding phospholipase c
6690	18785		0.81	6.0E-90	AF008915.1	NT	Homo sapiens EVI8 homolog mRNA, complete cds
5777	18869	32052	1.34	5.0E-90	AB015817.1	NT	Homo sapiens ELKS mRNA, complete cds
5880	18767	31839	2.22	5.0E-90	Z10411.1	NT	H. sapiens mRNA encoding phospholipase c
6864	19946	33242	0.73	6.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56634), mRNA
6864	19946	33243	0.73	6.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56634), mRNA
7423	20390	33741	2.09	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7423	20390	33742	2.06	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7813	20762	34138	8.82	5.0E-90	4557258	NT	Homo sapiens edénylate cyclase 9 (ADCY9) mRNA
8636	21604	35028	4.98	5.0E-90	11346463	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10039	22666	36433	1.13	5.0E-90	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63714), mRNA
10844	23566	37063	0.74	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10771	23698	37196	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10771	23698	37197	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10813	23734	37236	5.86	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10871	23791	37291	0.87	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10871	23791	37292	0.87	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12872	25506		2.89	5.0E-90	AB011386.1	NT	Homo sapiens gene for AF-6, complete cds
12920	25499		4.66	5.0E-90	AB23366.1	EST_HUMAN	ar78H05.X1 Baristaed beta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
302	13396	26323	2.82	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
302	13396	26324	2.82	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1088	14132	27084	4.74	4.0E-90	4503316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1698	14728	27711	8.84	4.0E-90	X98033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
4858	17707	30600	6.15	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4858	17852	30761	2.4	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4858	17873	30761	1.89	4.0E-90	M95967.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 8
12134	26003	36810	1.75	4.0E-90	D31124.1	EST_HUMAN	HUM12582 Human fetal lung Homo sapiens cDNA 5'
8185	21155	34563	1.72	3.0E-90	BF516168.1	EST_HUMAN	UHH-BW1-any-B-04-Q-UI-61 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8185	21155	34564	1.72	3.0E-90	BF516168.1	EST_HUMAN	UHH-BW1-any-B-04-Q-UI-61 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11651	24690	38426	67.66	3.0E-90	BE569333.1	EST_HUMAN	601335244FT NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
215	13315	26243	5.41	2.0E-90	BE537913.1	EST_HUMAN	601087378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1177	14218	27173	46.4	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1177	14218	27174	46.4	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3859	16988	29801	2.03	2.0E-90	AI138213.1	EST_HUMAN	similar to SW-OLP3 MOUSE P23275 OLFACTORY RECEPTOR OR3. ;
4714	17734	30627	1.17	2.0E-90	AF006827.1	NT	Homo sapiens mRNA for KIAA0269 gene, partial cds
4947	17963	30853	9.22	2.0E-90	6729865	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5870	18959	32147	0.57	2.0E-90	11525601	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5870	18959	32148	0.57	2.0E-90	11525601	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5879	18988	32159	4.7	2.0E-90	AW672686.1	EST_HUMAN	ba49H05.X3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 6' similar to TR-075208 075208 HYPOTHETICAL 35.5 KD PROTEIN. ;
10149	23075	36550	8.23	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10149	23075	36551	8.23	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10316	23243	36722	1.27	2.0E-90	AU118985.1	EST_HUMAN	AU118988 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
10316	23243	36723	1.27	2.0E-90	AU118985.1	EST_HUMAN	AU118988 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
11798	23933	37475	5.5	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
276	13372	26300	3.99	1.0E-90	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nepril-in, Alzheimer disease) (APP), mRNA
374	15812	26389	1.13	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
375	15812	26389	2.04	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
376	15812	26389	2.04	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
658	13768	26659	2.55	1.0E-90	AJ237839.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
658	13768	26659	2.55	1.0E-90	AJ237839.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
658	13768	26659	2.55	1.0E-90	AJ237839.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
731	13792	26728	17.02	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
731	13792	26728	17.02	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
731	13792	26728	17.02	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1112	14156	26728	2.23	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1309	14345	27310	2.99	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1309	14345	27310	2.99	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1309	14345	27310	2.99	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1876	14706	27636	1.78	1.0E-90	BE379884.1	EST_HUMAN	60159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE3511118 5'
1918	14942	27636	2.77	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sea Drosophila)-like (LOC571687), mRNA
2663	15028	28846	7.85	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3865	16904	28810	0.72	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3865	16904	28810	0.72	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3865	16904	28810	0.72	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4453	17479	30367	1.17	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5270	18277	31140	1.7	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
5270	18277	31140	1.7	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
5270	18277	31140	1.7	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
5758	18881	32031	1.76	1.0E-90	AB074533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5758	18881	32031	1.76	1.0E-90	AB074533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5758	18881	32031	1.76	1.0E-90	AB074533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5935	18022	32216	0.99	1.0E-90	11426910	NT	Homo sapiens KIAA0923 gene product (KIAA0923), mRNA
7216	20011	33313	0.97	1.0E-90	U91634.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7625	20469	33551	0.6	1.0E-90	6009002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7625	20469	33551	0.6	1.0E-90	6009002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7625	20469	33551	0.6	1.0E-90	6009002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7834	20878	34266	2.63	1.0E-90	11428768	NT	Homo sapiens soluble carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9173	22139	35556	3.96	1.0E-90	11422058	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9648	22592	36075	1.08	1.0E-90	AF163884.1	NT	Homo sapiens SNCA (adorn) (SNCA) gene, complete cds, alternatively spliced
9670	22623	36075	1.38	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9670	22623	36075	1.38	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9670	22623	36075	1.38	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
10950	23910	37425	0.93	1.0E-90	X65545.1	NT	Homo sapiens cDNA for CREB protein
10950	23910	37425	0.93	1.0E-90	X65545.1	NT	Homo sapiens cDNA for CREB protein
10950	23910	37425	0.93	1.0E-90	X65545.1	NT	Homo sapiens cDNA for CREB protein
11021	23966	37513	2.13	1.0E-90	R25688.1	EST_HUMAN	y944d11.2 Scores Infant brain T1MB Homo sapiens cDNA clone IMAGE35477 5'
4224	17253	30140	6.09	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9649	21617	35039	4.36	7.0E-91	11419234	NT	Homo sapiens malikofin, ring finger protein, 1 (MKRFN1), mRNA
10083	23585	37083	0.87	7.0E-91	A1804151.1	EST_HUMAN	CH-1043-090269-075 BT043 Homo sapiens cDNA
3488	16534	28469	1.71	5.0E-91	AA702764.1	EST_HUMAN	26004.61 Scars, fetal liver, spleen, INFLS S1 Homo sapiens cDNA clone IMAGE:448015 3'
4544	17657	30454	1.05	5.0E-91	AU143339.1	EST_HUMAN	AU143339 Y9AA1 Homo sapiens cDNA clone Y9AA1002087 5'
4544	17657	30455	1.05	5.0E-91	AU143339.1	EST_HUMAN	AU143339 Y9AA1 Homo sapiens cDNA clone Y9AA1002087 5'
6770	18925	33108	1.19	5.0E-91	A1879995.1	EST_HUMAN	au4908.x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2618121 3' similar to SW-ASP, FLAME Q47898 N4-(BETA-N-ACETYLGLUCOSAMINYL)-ASPARAGINASE PRECURSOR ;
8547	21516	34533	1.65	5.0E-91	BF3 4682.1	EST_HUMAN	601801624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130833 5'
9113	22079	35505	1.28	5.0E-91	A17649878.1	EST_HUMAN	A17649878 GLO Homo sapiens cDNA clone GLOBYF08 3'
9113	22079	35507	1.28	5.0E-91	A17649878.1	EST_HUMAN	A17649878 GLO Homo sapiens cDNA clone GLOBYF08 3'
12892	25479		2.28	5.0E-91	A1635966.1	EST_HUMAN	ae70111.x1 Scars, fetal lung, NIH-L19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR_b2 MIR MIR repetitive element ;
3215	18270	29192	1.41	4.0E-91	AF116776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3215	18270	29193	1.41	4.0E-91	AF116776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11276	24228	37755	3.24	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12377	25169	31811	1.55	4.0E-91	M77894.1	EST_HUMAN	EST01678 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHC60 similar to Retrovirus-related gag polyprotein
12377	25169	31858	1.55	4.0E-91	M77894.1	EST_HUMAN	EST01678 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHC60 similar to Retrovirus-related gag polyprotein
1621	14854	27630	5.97	3.0E-91	11430163	NT	Retrovirus-related gag polyprotein
1621	14854	27631	5.97	3.0E-91	11430163	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3350	16401	28323	1.78	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3476	16522	29446	3.84	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3476	16522	29446	3.84	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3802	16842	29750	1.47	3.0E-91	AF094330.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4821	17642	30550	4.36	3.0E-91	M30338.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5018	18030	30915	1.3	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5018	18030	30916	1.3	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5770	18882	32041	1.43	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5KD) (HE1), mRNA
6437	19003		2.97	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6735	19791	33071	3.34	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6755	19791	33072	3.34	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7800	20843	34228	4.07	3.0E-91	U86559.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7900	20843	34228	4.07	3.0E-91	U86559.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8278	21247	34659	0.44	3.0E-91	6801589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8123	22089	35517	2.51	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
8943	22587	36036	0.8	3.0E-91	AB01166.1	NT	Homo sapiens ERM2 mRNA, complete cds
11235	24188	37707	2.53	3.0E-91	AB032179.2	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11536	24471	38026	2.3	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11536	24471	38027	2.3	3.0E-91	AB029003.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12620	28314	31784	1.48	3.0E-91	AF240786.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12650	18335	31174	3.88	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12650	18335	31175	3.88	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
60	13170	26078	2.39	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1250	14286	27252	7.11	1.0E-91	AW449746.1	EST_HUMAN	UHH-B13-alc-d-01-0J.a1 NCI_OGAP_Sub55 Homo sapiens cDNA clone IMAGE:2735280 3'
5487	18597	31498	0.73	1.0E-91	BF348182.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
7020	20146	33464	1.9	1.0E-91	BF348182.1	EST_HUMAN	60202208BF1 NCI_OGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
7020	20146	33465	1.9	1.0E-91	BF348182.1	EST_HUMAN	60202208BF1 NCI_OGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
8161	21089	34498	0.59	1.0E-91	M20463.1	NT	Human nucleus-encoded mitochondrial aldehyde dehydrogenase 2 (ALDH2) gene, exon 10
1248	14283	27246	6.04	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1248	14283	27247	6.04	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1248	14283	27247	6.04	9.0E-92	AJ001689.1	NT	Human Na <sup>+</sup> /K <sup>+</sup> ATPase alpha-subunit mRNA, partial cds
5538	18635	31576	2.94	9.0E-92	J03007.1	NT	Homo sapiens hypothetical protein FLJ20280 (FLJ20280), mRNA
5688	18781	31953	2.18	9.0E-92	11427149	NT	Homo sapiens NALP1 mRNA, complete cds
6595	19556	32928	3.88	8.0E-92	AF310105.1	NT	Homo sapiens partial TMAS2 gene for tetraspanin protein, exon 5
8190	21160	34509	0.47	9.0E-92	AJ250366.1	NT	Homo sapiens partial TMAS2 gene for tetraspanin protein, exon 5
8190	21160	34570	0.47	9.0E-92	AJ250366.1	NT	Homo sapiens partial TMAS2 gene for tetraspanin protein, exon 5
8717	21685	35112	1.73	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1912 protein, partial cds
8717	21685	35113	1.73	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1912 protein, partial cds
8929	22573	35023	1.69	9.0E-92	11422086	NT	Homo sapiens brain A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
92	13208	26132	3.78	8.0E-92	U26367.1	EST_HUMAN	2683 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
285	13390	26308	4.52	8.0E-92	BE386363.1	EST_HUMAN	2683 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1833	14865	27893	1.08	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) (DGKG), mRNA
1838	14865	27894	1.08	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) (DGKG), mRNA



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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5140	18146	31028	0.7	8.0E-92	AW157571.1	EST_HUMAN	aa83108.XT Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:278291 3' similar to
5469	18566	31478	0.84	8.0E-92	AB046820.1	NT	TR060302 Q60302 KIAA0555 PROTEIN, contains element MER22 repetitive element ;
5676	18672	31635	0.81	8.0E-92	AF284717.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
6897	19752	33031	1.19	8.0E-92	AJ000976.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6701	19756	33036	0.79	8.0E-92	AF179428.1	NT	Homo sapiens MCP-4 gene
8164	21092	34491	1.16	8.0E-92	AF251025.2	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8428	21397	35155	0.56	8.0E-92	11416961	NT	Homo sapiens double FYVE-containing protein 1 mRNA, complete cds
8768	21735	35155	3.52	8.0E-92	L04193.1	NT	Homo sapiens AIM-1 protein (LOC51161), mRNA
8768	21735	35156	3.52	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8869	21635	35258	0.56	8.0E-92	11426589	NT	Homo sapiens transmembrane protein (mp19) gene, exon 11
9417	22382	35820	2.48	8.0E-92	AB014511.1	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
10366	23308	36786	1.86	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
11155	24114	37640	3.54	8.0E-92	AF074393.1	NT	Homo sapiens mRNA for MENL protein
11688	24954	38233	1.72	8.0E-92	4503340	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
27	13147	26046	1.69	7.0E-92	AB031007.1	NT	Homo sapiens dihydrodipamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
238	15836	25262	0.99	7.0E-92	AB018301.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
238	15836	25263	0.99	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
593	13660	13660	1.22	7.0E-92	AF007822.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
1285	14320	27283	1.14	7.0E-92	4502384	NT	Homo sapiens cytoplasmic Sepsis truncated isoform mRNA, complete cds
2197	15212	28230	3.62	7.0E-92	5031570	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2197	15212	28231	3.62	7.0E-92	5031570	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2570	15571	28591	1.27	7.0E-92	AF067708.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2735	15729	28743	2.86	7.0E-92	6005738	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2735	15729	28743	2.86	7.0E-92	6005738	NT	Homo sapiens cytoskeleton-rich repeat-containing protein S52 precursor, mRNA, complete cds
2753	15755	28776	1.31	7.0E-92	AB031007.1	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
3336	18314	28627	0.97	7.0E-92	4507500	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3336	18314	28628	0.97	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4617	17638	30528	1.44	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule (human, small cell lung cancer cell line OS2-R, mRNA, 2890 nt)
4617	17638	30529	1.44	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule (human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt)

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5040	18063	30932	0.91	7.0E-92	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
5333	18439	31181	6.57	7.0E-92	AA446268.1	EST_HUMAN	z686412.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:781175 5'
1591	14623		1.08	5.0E-92	BE390882.1	EST_HUMAN	G01283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
9947	22783		0.42	5.0E-92	W27698.1	EST_HUMAN	3867 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2778	15768	28788	2.03	3.0E-92	BE908714.1	EST_HUMAN	G01501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3602939 5'
5976	18091	32862	4.55	3.0E-92	AA378336.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
11116	24076	37599	6.32	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11116	24076	37600	5.32	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
28	13148	26047	1.09	2.0E-92	4501808	NT	Homo sapiens actin A receptor, type IIB (ACVR2B) mRNA
180	13280	26205	3.9	2.0E-92	11422946	NT	Homo sapiens hypothetical protein cJ462023.2 (CJ462023.2), mRNA
180	13280	26206	3.9	2.0E-92	11422946	NT	Homo sapiens hypothetical protein cJ462023.2 (CJ462023.2), mRNA
750	13811	28753	1.25	2.0E-92	BE289180.1	EST_HUMAN	G01118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
750	13811	28754	1.25	2.0E-92	BE289180.1	EST_HUMAN	G01118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1727	14767		1.4	2.0E-92	S78633.1	NT	mg-mta-related [human, Genomic, 2478 nt]
1953	14976	27978	1.73	2.0E-92	AI818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1853	14976	27977	1.73	2.0E-92	AI818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2084	15082	28101	6.36	2.0E-92	4608880	NT	Wk27d07.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2688	16665	28984	21.32	2.0E-92	6912457	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
3627	16970	28952	1.17	2.0E-92	AF231918.1	NT	Homo sapiens syndecan 4 (emphiglycan, ryudocan) (SDC4) mRNA
3627	16970	28952	1.17	2.0E-92	AF231918.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3627	16970	28953	1.17	2.0E-92	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
3627	16970	28953	1.17	2.0E-92	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
3698	16741	28654	5.32	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP-1), mRNA
4318	17347	30231	1.4	2.0E-92	MT0876.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5028	18043		2.37	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414.1_1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434C0414 5'
5853	18944	32129	0.63	2.0E-92	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6434	19500		13.83	2.0E-92	4504766	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGA1) mRNA
6768	19822	33104	2.24	2.0E-92	AB028891.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7701	20059		0.81	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7730	20659		0.71	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
8207	22173	35604	1.91	2.0E-92	AW340174.1	EST_HUMAN	h002902.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2608371 3' similar to TR:002711
							O02711 PRO-POL-DUTPASE POLYPROTEIN ;

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11112	24072	37564	4.68	2.0E-02	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11389	24335	37964	4.54	2.0E-02	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
12716	25370	31773	3.75	2.0E-02	AB029918.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12893	16665	28984	2.95	2.0E-02	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1867	14692	27850	1.77	1.0E-02	R78078.1	EST_HUMAN	X80608.1 Soares placenta NZHP: Homo sapiens cDNA clone IMAGE:145574 5'
1867	14692	27851	1.77	1.0E-02	R78078.1	EST_HUMAN	X80608.1 Soares placenta NZHP: Homo sapiens cDNA clone IMAGE:145574 5'
2087	15104	28122	34.88	1.0E-02	4505698	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8590	21658	34974	0.77	1.0E-02	BE439825.1	EST_HUMAN	HTM1:288F HTM1 Homo sapiens cDNA
							Ig11002.x1 NCL CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW/PTNF_HUMAN
9519	22482	35927	3.43	1.0E-02	A380358.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element, contains element MER17 repetitive element;
9519	22482	36928	3.49	1.0E-02	A380358.1	EST_HUMAN	Ig11002.x1 NCL CGAP_QLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW/PTNF_HUMAN
2044	15083	28083	2.77	9.0E-03	AU121681.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element; contains element MER17 repetitive element;
2058	15077		11.43	9.0E-03	AA316723.1	EST_HUMAN	AU121681 MAMMAT Homo sapiens cDNA clone MAMMA1000738 5'
							EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2655	15652		1.44	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3628	16671	29584	1.44	9.0E-03	BE38571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
11959	24838		35.01	9.0E-03	11418528	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6585	19845	32913	0.52	8.0E-03	AW014042.1	EST_HUMAN	U14H-B10-aah-h-06-c-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
6585	19845	32914	0.52	8.0E-03	AW014042.1	EST_HUMAN	U14H-B10-aah-h-06-c-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709371 3'
8744	19799	33079	3.82	8.0E-03	BF036364.1	EST_HUMAN	601400821F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3663908 5'
246	13343	26268	9.15	7.0E-03	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3091	19149	29083	1.58	6.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6098	19175	32391	0.59	8.0E-03	11450204	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
6098	19175	32392	0.59	8.0E-03	11450204	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
6838	19891	33186	0.89	6.0E-03	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
7101	20035	33338	1.14	6.0E-03	AF06571.1	NT	Homo sapiens PTH-responsive osteocalcinoma B1 protein (B1) mRNA, complete cds
1381	14415	27385	3.77	5.0E-03	AB014651.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
1406	14439	27408	4.78	5.0E-03	A1674184.1	EST_HUMAN	wc08c08.x1 NCL CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2314670 3'
1406	14439	27409	4.78	5.0E-03	A1674184.1	EST_HUMAN	wc08c08.x1 NCL CGAP_Pz28 Homo sapiens cDNA clone IMAGE:2314670 3'
1471	14504		1.02	5.0E-03	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001

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Table 4  
Single Exon Probes Expressed in Bone Marrow.

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3247	16302	29226	3.91	5.0E-93	X04201.1	NT	Human skeletal muscle 1,3 kb mRNA for tropomyosin
5897	16994	32175	0.9	6.0E-93	M22878.1	NT	Human somatic cytochrome c (HCT) processed pseudogene, complete cds
6230	19304		1.22	5.0E-93	AF045555.1	NT	Human sapiens vblor1 (WBSGR1) and vblor5 (WBSGR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7682	20921	34312	3.32	5.0E-93	AF067136.1	NT	Human sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8932	21918	35343	0.56	5.0E-93	4557528	NT	Human sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8952	21918	35344	0.56	5.0E-93	4557528	NT	Human sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9881	22908	36373	2.06	5.0E-93	AF274883.1	NT	Human sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10186	23091	36569	1.33	5.0E-93	5032166	NT	Human sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10430	23352	36836	1.59	5.0E-93	AF068313.2	NT	Human sapiens nucleobindin 2 (NUCB2), mRNA
11174	24131	37651	2.48	5.0E-93	11439586	NT	Human sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
12627	25922	31677	2.95	5.0E-93	11417877	NT	Human sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
13036	25922	31677	1.32	5.0E-93	11417877	NT	Human sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
88	13204		7.08	4.0E-93	AA459833.1	EST_HUMAN	P97397 CALPONIN, ACIDIC ISOFORM
446	13518	28450	1.25	4.0E-93	4557879	NT	Human sapiens interferon gamma receptor 1 (IFNGR1) mRNA
446	13518	28451	1.25	4.0E-93	4557879	NT	Human sapiens interferon gamma receptor 1 (IFNGR1) mRNA
773	13832	28177	1.39	4.0E-93	7657454	NT	Human sapiens pectadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
773	13832	28178	1.38	4.0E-93	7657454	NT	Human sapiens pectadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1187	14227	27183	1.62	4.0E-93	8923658	NT	Human sapiens hypothelial protein FL20731 (FL20731), mRNA
1694	15015	28022	4.21	4.0E-93	AF047677.1	NT	Human sapiens cytochrome (DMD) gene, deletion breakpoints 1-3 in intron 5
2816	15513	28639	1.08	4.0E-93	7656972	NT	Human sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3350	16925	29546	0.84	4.0E-93	7705356	NT	Human sapiens tumor antigen SLP-8p (HCC9), mRNA
4078	17113	30009	2.01	4.0E-93	4504654	NT	Human sapiens tumor antigen SLP-8p (HCC9), mRNA
4568	16925	29546	0.93	4.0E-93	7705356	NT	Human sapiens tumor antigen SLP-8p (HCC9), mRNA
5727	19821	32001	4.28	4.0E-93	T46884.1	EST_HUMAN	y994c12.1 Stradiene liver (#937224) Homo sapiens cDNA clone IMAGE:78938 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
11468	24411	37660	13.22	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GK Homo sapiens cDNA clone IMAGE:4332038 5'
3655	16708	29822	9.21	3.0E-93	BF69030.1	EST_HUMAN	60224654F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
3655	16708	29823	9.21	3.0E-93	BF69030.1	EST_HUMAN	60224654F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
4283	17292		1.23	3.0E-93	AF226596.1	NT	Homo sapiens tensin mRNA, complete cds

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Table 4

## Single Exon Probes Expressed In Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5881	18870	32181	0.56	3.0E-03	AI553853.1	EST_HUMAN	tr280303.x1 NCL CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2169076 3'
5881	18870	32182	0.56	3.0E-03	AI553853.1	EST_HUMAN	tr280303.x1 NCL CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2169076 3'
6715	18771	33051	1.55	3.0E-03	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homodog-like 2 (GCN5L2), mRNA
11152	24112	37637	3.04	3.0E-03	AI824828.1	EST_HUMAN	wb02005.x1 NCL CGAP_GC08 Homo sapiens cDNA clone IMAGE:2304485 3'
192	13263	28219	8.05	2.0E-03	AB015810.1	NT	Chloroebus aethiops mRNA for ribosomal protein S4X, complete cds
192	13263	28220	8.05	2.0E-03	AB015810.1	NT	Chloroebus aethiops mRNA for ribosomal protein S4X, complete cds
323	13415	28340	12.88	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
324	13415	28340	8.81	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2140	15157	28173	1.15	2.0E-03	U40763.1	NT	Human Oik-associated RS cytoplasmic GARS-Cyp mRNA, complete cds
2494	15497	28523	2.03	2.0E-03	BE252882.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3558220 5'
5491	18591	31502	5.94	2.0E-03	AW084385.1	EST_HUMAN	EST376458 IMAGE resequences: MAGH Homo sapiens cDNA
5602	18602	31531	0.78	2.0E-03	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5720	18814	31863	1.08	2.0E-03	BF351466.1	EST_HUMAN	QV3-H10573-280300-120-H04 HT0513 Homo sapiens cDNA
5734	18828	32006	0.7	2.0E-03	U74313.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51318), mRNA
6841	19694	28251	1.98	2.0E-03	AW502002.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
12520	25251	27237	3.14	2.0E-03	AA128735.1	EST_HUMAN	UI-HF-BN0-aks-q-09-0-UI-HF NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
12501	25203	27237	2.69	2.0E-03	L41825.1	NT	22610.x1 Sacae, pregnant, uterus, NH-HPU Homo sapiens cDNA clone IMAGE:5033446 3'
12533	25451	27237	3.49	2.0E-03	BF035327.1	EST_HUMAN	Homo sapiens CYP17 gene, 5' end
103	13219	28143	1.82	1.0E-03	AF23597.1	NT	601455531F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3862086 5'
103	13219	28144	1.82	1.0E-03	AF23597.1	NT	Homo sapiens CTR1 pseudogene
518	13660	26510	16.8	1.0E-03	7657016	NT	Homo sapiens CTR1 pseudogene
602	13669	26583	5.09	1.0E-03	AI146755.1	EST_HUMAN	Homo sapiens hypothetical protein (D328E18.C1.1), mRNA
873	13829	26887	4.11	1.0E-03	D87675.1	NT	cy4408.x1 NCL CGAP_GLL1 Homo sapiens cDNA clone IMAGE:1672603 3' similar to TR:Q62384 Q62384
1241	14277	27238	8.85	1.0E-03	8623270	NT	ZINC FINGER PROTEIN, 1
1241	14277	27238	8.85	1.0E-03	8623270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2344	15354	28375	1.27	1.0E-03	AF231681.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2471	14175	28499	8.92	1.0E-03	AF055069.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2833	14334	27298	2.05	1.0E-03	BE297389.1	EST_HUMAN	Homo sapiens MHC class I region
2833	14334	27297	2.05	1.0E-03	BE297389.1	EST_HUMAN	60117686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3552665 5'
2846	16003	28628	2.18	1.0E-03	D87675.1	NT	60117686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3552665 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3229	16284		1.3	1.0E-03	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4460	17489	30373	1.99	1.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5646	18742	31687	1.68	1.0E-03	U78509.1	NT	Homo sapiens glucocorticoid receptor (GR) gene, intron D, exon 5, and intron E
5646	18742	31688	1.66	1.0E-03	U78509.1	NT	Homo sapiens glucocorticoid receptor (GR) gene, intron D, exon 5, and intron E
5859	18949	32195	1.02	1.0E-03	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6022	19105	32308	10.93	1.0E-03	4557792	NT	Homo sapiens neurofilament 1 (neurofilamentosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6321	19392	32633	0.91	1.0E-03	7692241	NT	Homo sapiens KIAA0672 gene product (KIAA0672) mRNA
6959	20184	33507	2.08	1.0E-03	11431500	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7462	20428	33785	3.07	1.0E-03	D42072.1	NT	Human mRNA for NFI N1-isoform-exon11, complete cds
8903	21571	34987	1.97	1.0E-03	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8998	21854	35274	1.12	1.0E-03	Y10183.1	NT	Hi sapiens mRNA for MEND protein
8998	21854	35387	1.29	1.0E-03	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
8379	22344	35776	0.47	1.0E-03	AB023228.1	NT	Homo sapiens mRNA for KIAA1011 protein, partial cds
9379	22344	35776	0.47	1.0E-03	AB023228.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9807	21730	34533	1.85	1.0E-03	AB040918.1	NT	Homo sapiens Thio isoform mRNA, complete cds
9811	21734	34537	1.04	1.0E-03	AF091395.1	NT	Human PrkA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9946	22873	36333	4.03	1.0E-03	X13474.1	NT	Human PrkA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9946	22873	36334	4.08	1.0E-03	X13474.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10083	23010	36482	0.71	1.0E-03	AL45801.1	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
10504	23426	36924	0.63	1.0E-03	11433646	NT	Homo sapiens GGT1 gene, exon 1
12763	25405		2.11	1.0E-03	AJ200125.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12847	25457		3.14	1.0E-03	11417856	NT	Homo sapiens chromosome 21 segment HS21C009
10950	23876		1.26	8.0E-04	AL163209.2	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
3986	17026	29937	2.15	6.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5441	18543	31454	3.23	6.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5441	18543	31456	3.23	5.0E-04	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6166	19241	32472	3.08	5.0E-04	AA722434.1	EST_HUMAN	226705.s1 Soares, fetal, NH-H1617 Homo sapiens cDNA clone IMAGE:409594.3
7205	20230	33562	1.34	5.0E-04	AF016900.1	EST_HUMAN	603305.s1 Soares, total, fetus, ND2HFS_3w Homo sapiens cDNA clone IMAGE:1623369.3
8995	21992	35376	0.82	5.0E-04	BF529115.1	EST_HUMAN	9020421.63F1 NCI CGAP Bm57 Homo sapiens cDNA clone IMAGE:4180023.5
11318	24268	37795	2.81	5.0E-04	11423682	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11318	24268	37798	2.81	5.0E-04	11423902	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12497	25895	31318	6.07	5.0E-04	789398.1	EST_HUMAN	Y088904.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone IMAGE:116239.3

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13048	25888		1.8	5.0E-04	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
1859	14886		0.09	4.0E-04	U05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2990	15663	28692	1	4.0E-04	4505008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
4748	17768	30564	2.95	4.0E-04	AE69132.1	EST_HUMAN	hw1110.ct NCI CGAP_Bmt02 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR-Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE :
8812	19870	32947	1.98	4.0E-04	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8812	19870	32948	1.98	4.0E-04	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7087	20031		0.99	4.0E-04	U27398.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11782	23937	37458	1.83	4.0E-04	11545782	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
613	13878	28504	2.23	3.0E-04	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
722	13784	28718	1.02	3.0E-04	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1754	14783	27767	1.12	3.0E-04	AF167705.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1754	14783	27768	1.12	3.0E-04	AF167705.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1787	14816	27801	4.2	3.0E-04	4557566	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6274	18347	32570	0.99	3.0E-04	11489268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
5764	18856	32037	3.32	3.0E-04	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6584	18654	32928	4.81	3.0E-04	11529228	NT	Homo sapiens chromosome 21 open reading frame 18 (O2ORF18), mRNA
8088	21024	34423	0.52	3.0E-04	4828883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8540	21508	34925	1.03	3.0E-04	AF162308.1	NT	Homo sapiens proteodherin alpha 13 (PCH-alpha13) mRNA, complete cds
8934	21900	35327	4.93	3.0E-04	AB014578.1	NT	Homo sapiens mRNA for KIAA0676 protein, partial cds
9850	22877	36340	4.37	3.0E-04	AF007942.1	NT	Homo sapiens glycogin-1L mRNA, complete cds
11438	24376	37919	3.78	3.0E-04	4757821	NT	Homo sapiens acetal transport of synaptic vesicles
11487	24864	39460	2.17	3.0E-04	U28711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
10110	23036	39514	0.69	2.0E-04	AI910393.1	EST_HUMAN	w30H11.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
10110	23036	39515	0.66	2.0E-04	AI910393.1	EST_HUMAN	w30H11.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:2391813 3'
150	13263	26182	2.81	1.0E-04	BE285714.1	EST_HUMAN	601117692F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3651038 5'
3108	16102	28073	2.24	1.0E-04	BE263433.1	EST_HUMAN	601111685F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362559 5'
3108	16102	28074	2.24	1.0E-04	BE263433.1	EST_HUMAN	601111686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362559 5'
4386	17414	30299	1.18	1.0E-04	9506892	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6191	19265	32501	0.65	1.0E-04	AIE000269.1	NT	Escherichia coli K-12 MG1685 section 159 of 400 of the complete genome
6397	19465	32711	0.81	1.0E-04	AL040518.1	EST_HUMAN	DKFZP434G00314.1 1334 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G00314 5'
6409	19474	32722	0.77	1.0E-04	H08270.1	EST_HUMAN	y8702.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6668	19725	33000	0.56	1.0E-94	AV725692.1	EST_HUMAN	AV725692 HTG Homo sapiens cDNA clone HTCBEF05 5'
8450	21416	34933	0.56	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8450	21416	34834	0.58	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9611	22615	36007	2.57	1.0E-94	11428710	NT	Homo sapiens palmed box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
10146	23072	36547	1.83	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38172099 5'
11405	24346	37881	2.77	1.0E-94	U65690.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11846	24683	38151	1.94	1.0E-94	AI272244.1	EST_HUMAN	ap226d2.x1 Schiller oligodendrocyoma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TRG62845
12050	24923	38520	3.39	1.0E-94	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR ;
12615	13283	20182	1.43	1.0E-94	BE235714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12687	13283	26182	1.31	1.0E-94	BE235714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1473	14506	27460	1.3	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3170	18226	29140	1.19	9.0E-95	7662027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABO56) mRNA, complete cds
3170	18226	29141	1.19	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5478	18578	31489	1.38	9.0E-95	X82569.1	NT	M.musculus gly71 gene (exons 1c and 2)
5478	18578	31490	1.38	9.0E-95	X82569.1	NT	M.musculus gly71 gene (exons 1c and 2)
8595	21563	34977	1.61	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4567	17590	30482	1.82	8.0E-95	AI700598.1	EST_HUMAN	w609604.x1 NCL CGAP_Luz24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
4567	17590	30483	1.82	8.0E-95	AI700598.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
7136	20112	33475	0.83	8.0E-95	11416376	NT	w609604.x1 NCL CGAP_Luz24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
7462	20418	33723	1.55	8.0E-95	11426328	NT	Homo sapiens KIAA0163 gene product (KIAA0163), mRNA
7462	20418	33774	1.55	8.0E-95	11426328	NT	Homo sapiens KIAA0163 gene product (KIAA0163), mRNA
8538	21507	34924	2.02	8.0E-95	AF02697.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
9720	22748	35189	1.97	8.0E-95	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
9720	22748	35200	1.97	8.0E-95	11420944	NT	Homo sapiens proteasome channel subunit (HERG-3) mRNA, complete cds
10207	23132	35619	2.67	8.0E-95	517484.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10238	23163	37008	3.08	8.0E-95	AB037816.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10595	23517	37008	0.8	8.0E-95	9845523	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
11813	24698	38278	2.21	8.0E-95	10884024	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
12520	25442		26.02	8.0E-95	AA625056.1	EST_HUMAN	Homo sapiens HCF-binding transcription factor Zhanfeng (ZF), mRNA
							zsf4b01.61 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains 1.1.1.1 repetitive element;



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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
275	13371	26298	6.59	7.0E-95	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
275	13371	26299	6.59	7.0E-95	D87676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4394	17422	30307	4.55	7.0E-95	M95708.1	NT	Homo sapiens Lv-6-like protein (CD59) mRNA, complete cds
4443	17469		1.26	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5090	18100	30976	1	7.0E-95	M95929.1	EST	Human homeobox protein (PHOX1) mRNA, 3' end
9572	22534	35695	0.82	4.0E-95	BE439825.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
12013	24890	38487	1.93	4.0E-95	AW950634.1	EST_HUMAN	EST1362704 MAGE sequences, MAGE Homo sapiens cDNA
12013	24890	38488	34.08	4.0E-95	AW950634.1	EST_HUMAN	EST1362704 MAGE sequences, MAGE Homo sapiens cDNA
12065	24938	39534	1.78	4.0E-95	BF371302.1	EST_HUMAN	RC6-PNU0114-650600-011-507 FN0114 Homo sapiens cDNA
5517	18817	31550	0.91	3.0E-95	BF520401.1	EST_HUMAN	602071146F1 NCI CGAP BRM4 Homo sapiens cDNA clone IMAGE:4214147.5
5757	25644	32030	0.64	3.0E-95	4503354	NT	Homo sapiens dedicator of cytokinesis 1 (DOCK1) mRNA
7563	20554	33973	1	3.0E-95	AW958121.1	EST_HUMAN	EST1370181 MAGE sequences, MAGE Homo sapiens cDNA
7663	20554	33914	1	3.0E-95	AW958121.1	EST_HUMAN	EST1370181 MAGE sequences, MAGE Homo sapiens cDNA
9710	22693	38119	1.75	3.0E-95	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9710	22693	38120	0.79	3.0E-95	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
10104	23030	36508	0.60	3.0E-95	BF213444.1	EST_HUMAN	G0184921F1 NIH MGC_55 Homo sapiens cDNA clone IMAGE:4070461.5
1651	14683	27656	2.18	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1651	14683	27657	2.18	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
							Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1958	14980	27882	2.13	2.0E-95	4907512	NT	60132181F1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3658692.5
1981	14983	27865	1.36	2.0E-95	BE96387.1	EST_HUMAN	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2433	15440	28457	1.43	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2433	15440	28458	28.59	2.0E-95	5453665	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2473	15477	28500	3.35	2.0E-95	AF240786.1	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2620	15523	28545	1.2	2.0E-95	4759423	NT	Homo sapiens Usuarip-gamma mRNA, complete cds
3171	16226	29142	2.48	2.0E-95	AF015462.1	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3577	16622	29542	2.93	2.0E-95	7709900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3577	16622	29543	2.93	2.0E-95	7709900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3631	16674	29587	0.83	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds gim01c02.x1 Scores_NHMPU_51 Homo sapiens cDNA clone IMAGE:1800546.3 similar to WP:12937.4 CE03705
3763	16805	29716	1.08	2.0E-95	AI020284.1	EST_HUMAN	Homo sapiens hypochelical protein (HS322B7A), mRNA
4398	17416	30300	1.69	2.0E-95	7657185	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5077	18067	30967	2.92	2.0E-95	7661879	NT	

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5557	18654	31598	4.36	2.0E-95	7705764	NT	Homo sapiens GGI-48 protein (LOC31099), mRNA
5557	18654	31599	4.36	2.0E-95	7705764	NT	Homo sapiens GGI-48 protein (LOC31099), mRNA
5782	18874	32055	1.22	2.0E-95	112256038	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5782	18874	32056	1.22	2.0E-95	112256038	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5827	18917	32101	0.87	2.0E-95	115235893	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6255	19358	32571	3.71	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-A1) gene, exon 7
6592	19652	32923	1.01	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-53; variant hepatic nuclear factor (TCF2), mRNA
6592	19652	32924	1.01	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-53; variant hepatic nuclear factor (TCF2), mRNA
6722	19776	33057	2.39	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6828	20152	33471	1.37	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9496	22462	35803	2.51	2.0E-95	11421768	NT	Homo sapiens ribophorin II (RPN2), mRNA
10747	23609	37166	0.54	2.0E-95	11494330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
11078	24040	37564	1.72	2.0E-95	4757653	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
12011	24888	38484	2.35	2.0E-95	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12011	24888	38485	2.35	2.0E-95	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12687	25291	31782	2.69	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12684	25546	31718	5.81	2.0E-95	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
6696	18791	31962	7.21	1.0E-95	AA284851.1	EST_HUMAN	TR:G1067084 G1067084 F55H2.6; z23h04.1 Scores ovary tumor NHTOT Homo sapiens cDNA clone IMAGE:714007 5' similar to z23h04.1 Scores ovary tumor NHTOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
5696	18791	31963	7.21	1.0E-95	AA284851.1	EST_HUMAN	z23h04.1 Scores ovary tumor NHTOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
7757	20710	34079	4.21	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-200600-011-G11 FN0019 Homo sapiens cDNA
7757	20710	34080	4.21	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-200600-011-G11 FN0019 Homo sapiens cDNA
8536	21504	34822	1.58	9.0E-96	BE897259.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3822423 5'
442	15540	28447	1.36	8.0E-96	BE807607.1	EST_HUMAN	601497698F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
442	15540	28448	1.36	8.0E-96	BE807607.1	EST_HUMAN	601497698F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
5569	18685	32882	2.28	8.0E-96	AW835047.1	EST_HUMAN	PMO1-L70019-060300-002-489 L70019 Homo sapiens cDNA
3929	18698	28882	1.96	7.0E-96	AF131920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3329	16390	28301	0.94	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3494	16541	28465	15.12	6.0E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3 end
5722	18916	31905	0.82	6.0E-95	11422842	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11872	24754	38335	2.59	6.0E-98	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11872	24754	38338	2.59	6.0E-98	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11818	24759	34390	2.78	6.0E-98	8923639	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
320	13412	28336	3.08	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
843	13899	28855	3.47	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
843	13899	28858	3.47	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2626	16625	29013	1.23	5.0E-98	11416707	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
3039	16097	29013	0.71	5.0E-98	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4940	17956	31113	0.93	5.0E-98	XG0812.1	NT	H sapiens DNA for monomamine oxidase type A (7) (partial)
6233	18241	31113	0.93	5.0E-98	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
6807	19951	33148	1.15	5.0E-98	AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6870	19923	33219	0.5	5.0E-98	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleoside (dNT-2 gene), exons 1-5
6949	20173	33498	4.02	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6949	20173	33497	4.02	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7219	20241	33576	0.78	5.0E-98	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7168	20711	34081	0.7	5.0E-98	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8443	21412	34825	6.11	5.0E-98	M86347.1	NT	Human type IV collagenase (CLO4B) gene, exon 5
8443	21412	34826	6.11	5.0E-98	M86347.1	NT	Human type IV collagenase (CLO4B) gene, exon 5
12078	24948	38543	1.51	5.0E-98	7681973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4219	17248	4219	7.1	3.0E-98	H68958.1	EST_HUMAN	ye7h12.1 Sources field liver spleen INFLS Homo sapiens cDNA clone IMAGE:212327 5'
415	13488	4219	4.65	2.0E-98	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (matrilin-associated) (CSPG4), mRNA
748	13809	26750	1.12	2.0E-98	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4790	17808	30700	1.39	2.0E-98	BE148074.1	EST_HUMAN	RG3-H10230-040500-110-502 H10230 Homo sapiens cDNA
7896	20654	34017	0.98	2.0E-98	BF399731.1	EST_HUMAN	QVLA-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
7698	20654	34018	0.98	2.0E-98	BF399731.1	EST_HUMAN	QVLA-GN0120-250900-427-b12 GN0120 Homo sapiens cDNA
9332	22297	26854	6.83	2.0E-98	AV689461.1	EST_HUMAN	AV689461 GRG Homo sapiens cDNA clone GKCFM007 5'
12285	25102	26853	3.08	2.0E-98	AW249440.1	EST_HUMAN	2818381 Sprieme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818351 6'
672	13736	27863	2.47	1.0E-98	Y18880.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1769	14825	27809	2.35	1.0E-98	AW650504.1	EST_HUMAN	EST1387124 MAGC resequences, MAGC Homo sapiens cDNA
1769	14825	27810	2.35	1.0E-98	AW650504.1	EST_HUMAN	EST1387124 MAGC resequences, MAGC Homo sapiens cDNA
2237	15251	28274	1.04	1.0E-98	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
2237	15251	28275	1.04	1.0E-98	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
7158	18390	31234	1.15	1.0E-98	6812735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7290	18985	33293	0.65	1.0E-98	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8656	21523	34941	1.35	1.0E-98	7081803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8955	21523	34942	1.35	1.0E-98	7081803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
9086	22032	35455	24.51	1.0E-68	11419428	NT	Homo sapiens similar to ecdonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9202	22168	35998	2.21	1.0E-68	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10520	23442	36939	0.91	1.0E-98	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10520	23442	36940	0.91	1.0E-98	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
12272	18332	31169	1.59	1.0E-98	4828893	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12272	18332	31170	1.59	1.0E-98	4828893	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3338	16389	28310	0.65	1.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7605	20756		3.82	6.0E-97	BE141849.1	EST_HUMAN	IL34-HT0117-011089-004-D07 HT0117 Homo sapiens cDNA
9286	22252	35682	0.85	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3928133 5'
9286	22252	35683	0.85	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3928133 5'
10959	23878	37391	0.71	6.0E-97	AA320332.1	EST_HUMAN	EST122672 Adipose tissue, white II Homo sapiens cDNA 5' end
10959	23878	37392	0.71	6.0E-97	AA320332.1	EST_HUMAN	EST122672 Adipose tissue, white II Homo sapiens cDNA 5' end
11734	24620	38168	3.43	6.0E-97	X15804.1	NT	Human mRNA for alpha-tubulin
8348	21317	34732	2.27	6.0E-97	AL043314.2	EST_HUMAN	DKFZP434N0323_11 434 (synonym: hhes) Homo sapiens cDNA clone DKFZp434N0323 5'
8462	21450	34688	13.95	5.0E-97	AA418028.1	EST_HUMAN	z07e12.61 Soares_NH-MP1_S1 Homo sapiens cDNA clone IMAGE:767788 3' similar to TRG1304125
10034	22581	36429	2.61	6.0E-97	BF154912.1	EST_HUMAN	GI304125 PM54 MRNA :
11873	24765	38337	1.75	5.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-256500-032-009 BT0812 Homo sapiens cDNA
11873	24765	38338	1.75	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
11873	24765	38339	1.75	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
938	13961	28943	2.4	4.0E-97	BE004438.1	EST_HUMAN	OMC-BN0108-170300-293-s03 BN0108 Homo sapiens cDNA
948	14001	28953	1.87	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
948	14001	28954	1.87	4.0E-97	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
1825	14849	27945	0.69	4.0E-97	5453572	NT	Homo sapiens Brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5045	18741	31906	0.66	4.0E-97	4557238	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I)(APOH) mRNA
5956	19041	32259	0.62	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNR2A) mRNA, complete cds
5956	19041	32240	0.62	4.0E-97	U09002.1	NT	Human N-methyl-D-aspartate receptor modulatory subunit 2A (hNR2A) mRNA, complete cds
6997	20123	33437	5.9	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6997	20123	33438	5.9	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
7217	20239	35973	1.35	4.0E-97	7710126	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20005	33905	0.94	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8771	21443	34860	0.68	4.0E-97	4657708	NT	Homo sapiens laminin, alpha 2 (matrin, congenital muscular dystrophy) (LAMA2), mRNA
8770	21659	35052	1.92	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8826	21822	35320	0.49	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
8907	21933	35358	0.78	4.0E-97	11423233	NT	Homo sapiens cyclochrome P450, subfamily Vb, polypeptide 1 (CYP4B1), mRNA
8903	22007	35056	1.36	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9603	22607	36057	1.36	4.0E-97	AB011166.1	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
10903	23724	37226	0.79	4.0E-97	11431060	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11498	24441	37691	2.15	4.0E-97	11893122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11498	24441	37692	2.15	4.0E-97	11893122	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12487	25216		7.99	4.0E-97	11416378	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
243	13341	26268	1.01	3.0E-97	AB932698.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
875	13931	26869	2.71	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
875	13931	26890	2.71	3.0E-97	4502166	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
1435	15808	27446	1.72	3.0E-97	4759813	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
2445	15925	28470	1.57	3.0E-97	U36255.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3185	16240	29158	2.22	3.0E-97	K02212.1	NT	Homo sapiens perlecanin (PCNT), mRNA
3274	16328	29249	1.01	3.0E-97	5174476	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA
4815	17652	30730	18.16	1.0E-97	4503470	NT	8013395201 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
6587	19827	32892	2.5	1.0E-97	BE596486.1	EST_HUMAN	RCO-HT0268-211169-011-p05 HT0268 Homo sapiens cDNA
6709	21122	34525	0.51	1.0E-97	AW379976.1	EST_HUMAN	RCO-HT0268-211169-011-p05 HT0268 Homo sapiens cDNA
9769	21122	34526	0.51	1.0E-97	AW379976.1	EST_HUMAN	RCO-HT0268-211169-011-p05 HT0268 Homo sapiens cDNA
10122	23048	36527	1.46	1.0E-97	RT0887.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129134 3'
11062	24025	37549	3.07	1.0E-97	11427767	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11062	24025	37650	3.07	1.0E-97	11427767	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11639	24576	38142	1.67	1.0E-97	AA53761.1	EST_HUMAN	nk28g02.s1 NC1 CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014962 3'
11796	25951	37472	35.59	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11796	25951	37473	35.59	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
902	13957	26914	1.43	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-s12 BT0724 Homo sapiens cDNA
1281	14316	27278	2.02	9.0E-98	6393092	NT	Homo sapiens cell eye syndrome critical region gene 1 (CECR1), mRNA
6435	19501		0.63	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7507	20472	33832	0.55	9.0E-08	7681871	NT	Homo sapiens leucy-RNA synthetase, mitochondrial (KIAA0028), mRNA
7617	20377	33940	0.56	9.0E-08	11419408	NT	Homo sapiens A kinase (PRKA) anchor protein (ytloa) 9 (AKAP9), mRNA
8257	21226	34636	5.5	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8257	21226	34637	5.5	9.0E-08	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8471	22438	35873	2.01	9.0E-08	X05889.1	NT	Human mRNA for amyloid A4(751) protein
9579	22541	35991	1.44	9.0E-08	11321580	NT	Homo sapiens succinate-CoA ligase, GTP-forming, alpha subunit (SUCLG1), mRNA
9847	22591	36040	1.49	9.0E-08	AB037788.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9894	22647		0.83	9.0E-08	AJ057728.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9722	22750	36202	1.16	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9722	22750	36203	1.16	9.0E-08	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10623	23545	37045	0.5	9.0E-08	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
11346	24286	37823	2.08	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11346	24286	37824	2.08	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11407	24351	37883	1.75	9.0E-08	11418982	NT	Homo sapiens mitogen-activated protein kinase kinase 7 (MAP3K7), mRNA
26	13146		2.24	8.0E-08	AJ251158.1	NT	Homo sapiens partial MICE gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1562	14594	27588	1.49	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1562	14594	27589	1.49	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1739	14769	27784	2.73	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1739	14769	27755	2.73	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3007	16582	28569	0.97	8.0E-08	AJ225041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
3007	16582	28570	0.97	8.0E-08	AJ225041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
3809	16849	29757	8.45	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
6201	19276	32509	2.74	6.0E-08	BE885973.1	EST HUMAN	601507503F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3905097 5'
2188	15203	28223	1.23	3.0E-08	AJ403124.1	EST HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2316	15814	28539	1.19	3.0E-08	AA014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2769	16751		3.63	3.0E-08	AA077498.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
7131	20107	33418	0.7	3.0E-08	9698846	NT	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7134	20110	33422	1.83	3.0E-08	11419210	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7134	20110	33423	1.83	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
9104	22070	35496	3.59	3.0E-08	H46588.1	EST HUMAN	Y07903.1 Scores adult brain N265HB55 Homo sapiens cDNA clone IMAGE:178240 5'
9952	22595	36043	0.65	3.0E-08	8622086	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10243	23168	38866	1.61	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10243	23168	38866	1.51	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124.3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10839	23759	37259	0.99	3.0E-08	BE900454.1	EST_HUMAN	601673886FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3966517 5'
11299	24249	37775	2.09	3.0E-08	U59309.1	NT	Human farnesyl transferase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
12951	25935		1.4	3.0E-08	BE382519.1	EST_HUMAN	601287955FT NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3628213 5'
13039	25581		2.4	3.0E-08	111418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
737	13768	29737	0.94	2.0E-08	BE261654.1	EST_HUMAN	601149488FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2092	15109	28128	3.36	2.0E-08	BE284281.1	EST_HUMAN	601172658FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2247	15281	28288	1.49	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4325	17354	30274	0.75	2.0E-08	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4358	17395	30274	2.9	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4854	17881	30767	1.22	2.0E-08	AF218602.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4854	17881	30768	1.22	2.0E-08	AF218602.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5430	18552	31464	4.28	2.0E-08	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6811	19865	33153	1.09	2.0E-08	4505798	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7885	20329	34206	1.08	2.0E-08	11431271	NT	Homo sapiens hypohelical protein FLJ10489 (FLJ10489), mRNA
7885	20329	34207	1.08	2.0E-08	11431271	NT	Homo sapiens hypohelical protein FLJ10489 (FLJ10489), mRNA
8955	21821	35347	3.8	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8955	21821	35348	3.8	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
9039	22005	35425	0.97	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9039	22005	35426	0.97	2.0E-08	L76666.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8995	22848	36305	2.7	2.0E-08	X12564.1	NT	H sapiens agmatase gene exon 3 (EC 3.5.3.1)
10778	23699		1.25	2.0E-08	7709868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11942	24522	38418	1.58	2.0E-08	AF273048.1	NT	Homo sapiens CTCL tumor antigen sea20-9 mRNA, complete cds
405	13478	29413	23.04	1.0E-08	AI842007.1	EST_HUMAN	tw36504.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2281743 3' similar to SW:RL2B_HUMAN
455	13528	28458	2.12	1.0E-08	AV998611.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A. ;
1813	14940	27831	13.68	1.0E-08	N49818.1	EST_HUMAN	PACB-BN0065-10030C-001-c08 BN0065 Homo sapiens cDNA
5390	18403	31370	3.54	1.0E-08	AA196854.1	EST_HUMAN	Y62305.1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:243585 5' similar to
5849	18745	31912	1.07	1.0E-08	BE390627.1	EST_HUMAN	PIR-S54204 S54204 ribosomal protein L29 - human ;
5849	18745	31913	1.07	1.0E-08	BE390627.1	EST_HUMAN	2p98C09.1 Stragena muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G808562
5849	18745	31913	1.07	1.0E-08	BE390627.1	EST_HUMAN	G808562 NEBLIN. ;
5849	18745	31913	1.07	1.0E-08	BE390627.1	EST_HUMAN	601284986FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606892 5'
5849	18745	31913	1.07	1.0E-08	BE390627.1	EST_HUMAN	601284986FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606892 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9350	22315	35740	5.28	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
9350	22315	35741	5.26	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5917	19003	32165	0.84	9.0E-99	AI005004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
5917	19003	32166	0.84	9.0E-99	AI005004.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
6153	19233	32465	3.77	9.0E-99	AW968035.1	EST_HUMAN	EST380711 MAGE rescues, MAGU Homo sapiens cDNA
11456	24399	37848	3.71	9.0E-99	AI479829.1	EST_HUMAN	trf99407.x1 NCL CGAP Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW-BID_HUMAN
11456	24399	37947	3.71	9.0E-99	AI479829.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11480	24403	37951	2.19	9.0E-99	BF395878.1	EST_HUMAN	P55947 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11743	24628	39207	1.84	9.0E-99	AA134604.1	EST_HUMAN	PM2-MT0037-250700-003-G04 MT0037 Homo sapiens cDNA
9078	22044	35467	1.18	8.0E-99	9635487	NT	zr60042.1 Straglene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
5933	19019	32214	9.72	7.0E-99	AF035808.1	NT	Human endogenous retrovirus, complete genome
11933	24814	38410	1.99	7.0E-99	AF001886.1	NT	Homo sapiens occlatin (HLN) gene, exon 5
472	13544	29473	0.84	6.0E-99	U10591.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
4779	17799	30690	0.97	6.0E-99	4502660	NT	Human G2 protein mRNA, partial cds
6752	19808	33087	0.86	6.0E-99	7705136	NT	Homo sapiens CD34 antigen (CD34) mRNA
6835	19888	33162	0.87	6.0E-99	U43910.1	NT	Homo sapiens GAP-like protein (LOC51306) mRNA
6835	19888	33163	0.81	6.0E-99	U43910.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8441	21410	34823	1.05	6.0E-99	X69101.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8460	21429	34846	0.62	6.0E-99	6601589	NT	H sapiens mRNA for estrogen receptor
9117	22083	35511	2.24	6.0E-99	AB036429.1	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
9215	22181	35612	3.79	6.0E-99	AF080255.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
9215	22181	35613	3.78	6.0E-99	AF080255.1	NT	Homo sapiens iodostat protein mRNA, complete cds
9215	22241	35669	0.84	6.0E-99	11431894	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9275	22241	35670	0.84	6.0E-99	11431894	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
11763	24936	37460	3.32	6.0E-99	11502289	NT	Homo sapiens BR3 interacting domain death agonist (BID), mRNA
11763	24936	37461	1.98	6.0E-99	9910278	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11763	24936	37460	1.98	6.0E-99	9910278	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
1982	15003	28006	1.37	5.0E-99	Y11365.1	NT	H sapiens MPA gene, exon 8
4556	17617	30511	1.46	5.0E-99	AF003650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV/SSA2 to TCRBV/252 region
12496	25238		5.2	5.0E-99	BE980177.1	EST_HUMAN	30151315/FL11H_MGC_71 Homo sapiens cDNA clone IMAGE:5914691 5'
8694	21632		5.74	3.0E-99	M65598.1	NT	Human E2AFHL1 fusion protein (E2AFHLF) mRNA, complete cds



Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1244	14281		16.34	2.0E-99	AW27492.1	EST_HUMAN	xp09608.x1 NCL CGAP HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gbM31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3272	16326	29248	1.19	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4874	17598	30460	1.95	2.0E-99	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7838	20878	34268	0.97	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8955	22021	35440	12.17	2.0E-99	W23507.1	EST_HUMAN	23-6d06.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gbM15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
9507	22470	35914	0.65	2.0E-99	R78254.1	EST_HUMAN	y81b09.r1 Soares_pleural_Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11440	24993	37923	2.98	2.0E-99	AF247467.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
315	13407	26333	1.51	1.0E-99	AF114487.1	NT	Homo sapiens interechin long isoform (ITSN) mRNA, complete cds
379	13463	26393	1.98	1.0E-99	11528150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABP) (GABPA), mRNA
1419	14452	27426	1.04	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1559	14591	27593	1.32	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1546	14591	27593	1.32	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1944	14668	27664	1.52	1.0E-99	AF192523.1	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1944	14668	27664	1.52	1.0E-99	AF192523.1	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3101	16168	28070	1.16	1.0E-99	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-R) mRNA, complete cds
4407	17435	30320	2.28	1.0E-99	AF068018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4407	17435	30321	2.28	1.0E-99	AF068018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5836	18826	32110	0.59	1.0E-99	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0669), mRNA
6978	20199	33528	1.77	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6978	20199	33529	1.77	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7346	20980	33662	0.91	1.0E-99	X68022.1	NT	H sapiens EG-AP gene exon 2
9554	22516		0.86	1.0E-99	11419721	NT	H sapiens ALEX1 protein (LOC91309), mRNA
9878	22831	39285	1.99	1.0E-99	AW340174.1	EST_HUMAN	h020402.x1 Soares_NFL_T_GBC_S4 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR-002711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
11473	24416	37965	1.89	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11473	24416	37966	1.89	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11705	24670	38247	2.17	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12253	25078		9.09	1.0E-99	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	13123	28021	1.83	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	13123	28021	1.18	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
68	13187	26105	1.3	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
69	13187	26106	1.3	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
87	13203	26128	0.67	1.0E-100	AW279327.1	EST_HUMAN	xy78871.1 X1 NCI CGAP Brn53 Homo sapiens cDNA clone IMAGE2824605 3'
170	13272	26197	2.52	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
317	13409	26335	0.98	1.0E-100	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
343	13432	26334	2.53	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#535205) Homo sapiens cDNA clone HBCR32
437	13511		2.36	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
480	13543		4.8	1.0E-100	X69631.1	NT	G.gorilla DNA for ZNF80 gene homolog
510	13581	26502	1.4	1.0E-100	BE180609.1	EST_HUMAN	RC3-H10625-040500-022-kb9 HT0625 Homo sapiens cDNA
1021	14067	27017	4.33	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1021	14067	27018	4.33	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1549	14592		1.23	1.0E-100	AW207555.1	EST_HUMAN	UI-H-B11-afk-c07-dJL.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE2722164 3'
1554	14586	27558	1.49	1.0E-100	AI200857.1	EST_HUMAN	qf62009.x1 Sovera, testis_NHT Homo sapiens cDNA clone IMAGE1754633 3' similar to SW:CYT_COTUA
1881	14906	27806	0.98	1.0E-100	AB032664.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2254	15268		1.25	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2717	15711	28728	1.98	1.0E-100	11418976	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
3031	16089		3.1	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4238	17287	30154	1.46	1.0E-100	AF057954.1	NT	Homo sapiens myoblastin-related protein 1a mRNA, partial cds
4284	17293	30172	1.94	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR), mRNA
5127	18136	31012	3.58	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOL) mRNA
5127	18136	31013	3.58	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOL) mRNA
5362	18467	31336	1.71	1.0E-100	BF244218.1	EST_HUMAN	601883164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080960 5'
5586	18682	31650	0.66	1.0E-100	AW075983.1	EST_HUMAN	xa6201.x1 NCI CGAP GML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:Y12433
5785	18877	32059	1.5	1.0E-100	AU118182.1	EST_HUMAN	PROTEIN PHPS1-2 (HUMAN).
5839	18928	32113	1.29	1.0E-100	AF135116.1	NT	AUT118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5837	19023	32217	0.9	1.0E-100	X14690.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6287	18356	32595	0.89	1.0E-100	4557668	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6287	18356	32596	0.89	1.0E-100	4557668	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6287	18359	32596	0.89	1.0E-100	4557668	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6576	18636		1.1	1.0E-100	5728867	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
6845	19703	32979	4.85	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6704	19760	33038	0.61	1.0E-100	AU138800.1	EST_HUMAN	AUT138800 PLACE1 Homo sapiens cDNA clone PLACE1003069 5'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

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Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12127	24968	38600	3.03	1.0E-100	AJ131034.1	NT	Homo sapiens class gene, exon 12
12128	24997	38601	1.65	1.0E-100	BE791491.1	EST_HUMAN	G0158031F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3940423 5'
12177	25025	38622	15.03	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12307	25851		2.32	1.0E-100	BF446549.1	EST_HUMAN	748803.X1 NCI_CGAP Lu24 Homo sapiens cDNA clone IMAGE: 3 similar to TR:Q21897 Q21897
12488	25233	31799	2.58	1.0E-100	11545732.NT	NT	COSMID R151, [2] TR:Q6UA08 ;
13084	25815	31691	8.6	1.0E-100	11417974.NT	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
78	13105	28118	1.19	1.0E-101	7110714.NT	NT	Homo sapiens transcobalamin II macrocytic anemia (TCN2), mRNA
78	13105	28119	1.18	1.0E-101	7110714.NT	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
887	13750	28676	2.83	1.0E-101	AB007815.2	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
705	13767	28702	6.85	1.0E-101	7110734.NT	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
705	13767	28703	8.85	1.0E-101	7110734.NT	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
772	13831	28703	1.48	1.0E-101	7857454.NT	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
854	13910	28688	2.88	1.0E-101	4503814.NT	NT	Homo sapiens psecadillo (zebrafish) homolog 1, containing BRCT domain (PEST), mRNA
824	13977	28628	1.22	1.0E-101	Z20659.1	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase (GART) mRNA
887	14038	28694	7.23	1.0E-101	BF681218.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1085	14101	27051	0.78	1.0E-101	AJ221878.1	EST_HUMAN	G0215647F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4287281 5'
1588	14619	27594	1.34	1.0E-101	5921450.NT	NT	g999409.X1 Soares_NFL_T_GBO_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1588	14619	27595	1.34	1.0E-101	5921450.NT	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1761	14780	27776	1.12	1.0E-101	7862183.NT	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1761	14780	27777	1.12	1.0E-101	7862183.NT	NT	Homo sapiens KIAA0559 gene product (KIAA0559), mRNA
1962	14984	27987	1.58	1.0E-101	4502698.NT	NT	Homo sapiens KIAA0559 gene product (KIAA0559), mRNA
2072	15089	28107	1.07	1.0E-101	BE943070.1	EST_HUMAN	Homo sapiens carboxypeptidase A1 (pancreatic) (CPAT) mRNA
2367	15591	28387	1.17	1.0E-101	5728692.NT	NT	RC3-S10281-160500-016-H09 ST0281 Homo sapiens cDNA
2822	15921	28646	5.3	1.0E-101	X72993.1	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2763	15745	28763	2.07	1.0E-101	AJ237744.1	NT	Homo sapiens EUS gene, exon 5
2753	15745	28764	2.07	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2987	16025		13.42	1.0E-101	AJ252312.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3216	16271	29194	1.88	1.0E-101	4868270.NT	NT	Homo sapiens genomic downstream Rhesus box
3255	16309		2.48	1.0E-101	BF038327.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3392	16441	29397	1.73	1.0E-101	AW965556.1	EST_HUMAN	G0149803F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862089 5'
3411	15745	28763	2.03	1.0E-101	AJ237744.1	NT	EST377629 MAGI8 resequences, MAGI8 Homo sapiens cDNA
							Homo sapiens RIBIIR gene (partial), exon 12

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3411	15745	28784	2.03	1.0E-101	AIJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3390	16330	29839	4.58	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5072	18092	30983	1.54	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5072	18092	30984	1.54	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5391	18494	31371	2.08	1.0E-101	AW965139.1	EST_HUMAN	EST137212 IMAGE ressequencing, MAGI Homo sapiens cDNA
6118	19196	32420	3.59	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6118	19196	32421	3.59	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6853	19800	33202	1.16	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7488	20453	33883	4.82	1.0E-101	AF208970.1	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7542	20505	33883	4.82	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEGS) mRNA, alternative splice form 4, partial cds
7642	20505	33884	4.82	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEGS) mRNA, alternative splice form 4, partial cds
7111	20674	34040	7.39	1.0E-101	AW008475.1	EST_HUMAN	w535012.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2833487 3'
7828	20774	34327	1.76	1.0E-101	BE257384.1	EST_HUMAN	601109217FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3348901 5'
7933	20932	34327	6.3	1.0E-101	BF530759.1	EST_HUMAN	RG1-BT0313-22070-018-412 BT0313 Homo sapiens cDNA
8245	21214	34621	1.07	1.0E-101	BE275821.1	EST_HUMAN	601121621FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8245	21214	34622	1.07	1.0E-101	BE275821.1	EST_HUMAN	601121621FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
8350	21359	34766	5.11	1.0E-101	BF029174.1	EST_HUMAN	601764886FT NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3996837 5'
8665	21633	35053	0.83	1.0E-101	AW630070.1	EST_HUMAN	h74510.v1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2688578 5' similar to gb:J03143
8665	21633	35064	0.83	1.0E-101	AW630070.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); h74910.v1 NCI CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2688578 5' similar to gb:J03143
9364	22529	35758	0.93	1.0E-101	AA036800.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); P19-S5640 S5640 YD835.03c protein - yeast;
9885	22838	36094	0.82	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9885	22838	36095	0.82	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9817	21139	34544	19.42	1.0E-101	X60059.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9817	21139	34546	19.42	1.0E-101	X60059.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9830	22879	35135	18.13	1.0E-101	8845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
10115	23041	36520	13.91	1.0E-101	BE616687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10115	23041	36521	13.91	1.0E-101	BE616687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10254	23179	36966	0.81	1.0E-101	10653900	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10773	23594	37162	1.08	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10807	23728	37229	0.56	1.0E-101	AI970263.1	EST_HUMAN	h77d11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2164309 3' similar to gb:M6328 KERATIN, TYPE I (CYTOSKELETAL, 18 (HUMAN);

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10807	23728	37230	0.66	1.0E-101	AB970283.1	EST_HUMAN	167d11.x1 NCI CGAP_G44 Homo sapiens cDNA clone IMAGE:2164309 3' similar to gb:M26325 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10914	23834	37249	0.64	1.0E-101	BE973848.1	EST_HUMAN	80169032FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3890887 5'
10914	23834	37350	0.64	1.0E-101	BE973948.1	EST_HUMAN	80169032FT NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950887 5'
11225	24178	37705	2.38	1.0E-101	S58327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
12083	24955	38550	102.1	1.0E-101	AA321316.1	EST_HUMAN	EST_237183 Bone marrow Homo sapiens cDNA 5' end similar to defensin 1
12735	25387	38701	7.64	1.0E-101	AW593051.1	EST_HUMAN	QV1-DT0065-240200-095-a01 DT0068 Homo sapiens cDNA
41	13161	28064	0.73	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
341	13430	28351	5.2	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
778	13835	28781	1.07	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (ORA) mRNA
1119	14163	27114	1.8	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1273	14308	27268	2.27	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1273	14308	27269	2.27	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1417	14450	27423	200.41	1.0E-102	BE408447.1	EST_HUMAN	801266982FT NIH_MGC_Z1 Homo sapiens cDNA clone IMAGE:3628901 5'
2318	15329	28352	1.36	1.0E-102	AU124669.1	EST_HUMAN	arr60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:G095_HUMAN Q08379 GOLGIN-95 ;
2318	15329	28353	1.36	1.0E-102	AU124669.1	EST_HUMAN	arr60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:G095_HUMAN Q08379 GOLGIN-95 ;
3037	16095	28047	0.73	1.0E-102	Y13932.1	NT	Homo sapiens PRK7 exon 7
3078	16135	28047	1.46	1.0E-102	7961979	NT	Homo sapiens KIAA0187 gene product (KAA0187), mRNA
3150	16207	29120	3.24	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens PLAGE4 Homo sapiens cDNA clone FLAGE4000650 5'
3150	16207	29121	3.24	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLAGE4 Homo sapiens cDNA clone FLAGE4000650 5'
4290	17289	30170	1.63	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4441	17467	30366	1.95	1.0E-102	BE251310.1	EST_HUMAN	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5157	18197	31045	1	1.0E-102	R66488.1	EST_HUMAN	Y52C04.1f Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:140834 5'
5445	18547	31460	1.52	1.0E-102	AF007133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
8842	18932	32163	3.3	1.0E-102	AB034951.1	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5982	18971	32163	3.45	1.0E-102	7703398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5982	18971	32164	3.45	1.0E-102	7703398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5980	18977	32169	0.88	1.0E-102	11433046	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
6425	19492	32744	2.74	1.0E-102	AA59825.1	EST_HUMAN	arr2009.x1 Bardstead cotton HPLR87 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR-Q13137 Q13137 NDP52 ;
7283	20016	33319	0.5	1.0E-102	AW451643.1	EST_HUMAN	UHH-B3-aj-d-70-0-J1-st NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20314	33658	0.76	1.0E-102	BE728323.1	EST_HUMAN	601561505F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3831241 5'
7371	20341	33683	0.77	1.0E-102	BE386106.1	EST_HUMAN	601272155F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3818243 5'
7494	20459	33818	0.64	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7578	20540	33889	8.85	1.0E-102	AL238594.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7888	20530	34208	2.84	1.0E-102	AV170738.1	EST_HUMAN	AV170738 Cu Homo sapiens cDNA clone CUA-K003 5'
8168	21106	34505	0.58	1.0E-102	10847053	NT	Homo sapiens ankrym 2, neuronal (ANK2), transcript variant 2, mRNA
8455	21533	34853	3.61	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210800-238-H08 NT0025 Homo sapiens cDNA
8845	21613	35035	0.91	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3603145 5'
8839	21806	35223	1.22	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GK Homo sapiens cDNA clone GKGE11 5'
8839	21806	35224	1.22	1.0E-102	AV694817.1	EST_HUMAN	Homo sapiens mRNA for KIAA0484 protein, partial cds
8950	21916	35340	0.74	1.0E-102	AB007823.1	NT	601283770F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3605536 5'
8283	22249	35678	0.73	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3605536 5'
8283	22249	35680	0.73	1.0E-102	BE388063.1	EST_HUMAN	w63b06.x1 NCL_OGAP_Kid12 Homo sapiens cDNA clone IMAGE:2397971 3' similar to contains MERA.11
8806	22810	36062	0.56	1.0E-102	AI762859.1	EST_HUMAN	MERA4 MERA4 repetitive element
8936	22990	36030	0.89	1.0E-102	AV765842.1	EST_HUMAN	AV759842 BM Homo sapiens cDNA clone BMFALD08 5'
8976	22929	36082	2.15	1.0E-102	170353.1	EST_HUMAN	yt13c07.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:67021 5'
8976	22929	36083	2.15	1.0E-102	170353.1	EST_HUMAN	yt13c07.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:67021 5'
8766	22707	36163	3.86	1.0E-102	AU724620.1	EST_HUMAN	AU724620 NT28M4 Homo sapiens cDNA clone NT28M400309 5'
10748	23670	37221	0.71	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10768	23719	37222	0.43	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (16SKD) (MYOM2), mRNA
40798	23719	37254	3	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-280469-014 BT074 Homo sapiens cDNA
10835	23755	37254	3	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-280469-014 BT074 Homo sapiens cDNA
10835	23755	37255	3	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-280469-014 BT074 Homo sapiens cDNA
10896	23816	37323	1.15	1.0E-102	AA970786.1	EST_HUMAN	SW:GAV2_HUMAN P61636 CAVEOLIN-2 [1]:
11410	24354	37887	2.38	1.0E-102	4507822	NT	on57h04.s1 Scores_NF_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1909823 3' similar to
11410	24354	37887	2.38	1.0E-102	4507822	NT	on57h04.s1 Scores_NF_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1909823 3' similar to
11410	24354	37888	2.38	1.0E-102	4507822	NT	on57h04.s1 Scores_NF_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1909823 3' similar to
11732	24618	38195	2.7	1.0E-102	BF359243.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
12019	24898	38494	4.74	1.0E-102	U41302.1	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
12079	24951	38548	5.67	1.0E-102	U57053.1	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
12182	25030	38548	2.49	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C086
12727	25380	31748	4.15	1.0E-102	AW300862.1	EST_HUMAN	K07c12.x1 NCL_OGAP_O620 Homo sapiens cDNA clone IMAGE:2666038 3'

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Probe Seq ID Seq NO:	Exon Seq ID Seq NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13028	25576		1.59	1.0E-102	J05235.1	NT	Human gamma-gliutamyl transpeptidase mRNA, complete cds
70	13188	26107	1.14	1.0E-103	BE908158.1	EST_HUMAN	601500403F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3902305 5'
70	13188	26108	1.14	1.0E-103	BE908158.1	EST_HUMAN	601500403F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3902305 5'
100	13216	26140	9.95	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
989	13310	26237	4.18	1.0E-103	5453763	NT	Homo sapiens nuclear protein (KRCO repeat) (NOP56) mRNA
982	14033	26985	1.02	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE) gene
1248	14284	27250	18.75	1.0E-103	BE875941.1	EST_HUMAN	601495930F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3887876 5'
1600	14682	27608	2.39	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1892	15013	28018	1.4	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1892	15013	28019	1.4	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2313	15325	28348	0.83	1.0E-103	AU134691.1	EST_HUMAN	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2457	15461	28484	1.66	1.0E-103	AF030568.1	NT	Homo sapiens PLCE1 Homo sapiens cDNA clone PLCE1000985 5'
2601	15601	28622	1.07	1.0E-103	BF52379.1	EST_HUMAN	602041882F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4179429 5'
2601	15601	28623	1.07	1.0E-103	BF52379.1	EST_HUMAN	602041882F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4179429 5'
2627	15926	28650	1.01	1.0E-103	N82770.1	EST_HUMAN	wt01408.s1 Soares, placenta_800weeks_2N81P8109W Homo sapiens cDNA clone IMAGE:2565989 3'
3082	16139		2.5	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3834315 5'
3391	16440	28686	4.42	1.0E-103	AW288245.1	EST_HUMAN	U1-H-BWO-8t-b-11-4-U1.s1 NCL CGAP_Suj05 Homo sapiens cDNA clone IMAGE:2733165 3'
3453	16499	28416	1.29	1.0E-103	ABC00892.1	NT	Homo sapiens mRNA for KIAA1469 protein, partial cds
3767	16509		5.31	1.0E-103	AF023861.1	NT	Musca domestica cyclophilin A mRNA, complete cds
3808	16846	29766	1.28	1.0E-103	AA485663.1	EST_HUMAN	ab10df12.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3841	16881	29785	3.16	1.0E-103	11430878	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4028	17087	29868	2.6	1.0E-103	T23683.1	EST_HUMAN	seq340 b4H83MA-Cor108+10-816 Homo sapiens cDNA clone b4H83MA-Cor108+10-816 7 3'
4858	17875	30763	0.83	1.0E-103	BE900203.1	EST_HUMAN	601673135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955983 5'
6044	19126	32332	0.66	1.0E-103	BF569527.1	EST_HUMAN	602106023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4810573 5'
6052	19133	32342	1.87	1.0E-103	AF176095.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6398	19466	32712	0.73	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6398	19466	32712	0.73	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6902	19651	32934	0.79	1.0E-103	AW854568.1	EST_HUMAN	EST368636 MAGC sequences, MAGC Homo sapiens cDNA
6902	19651	32934	0.79	1.0E-103	AW854568.1	EST_HUMAN	EST368636 MAGC sequences, MAGC Homo sapiens cDNA
6947	19705	32981	0.53	1.0E-103	10847051	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 1, mRNA
6745	29687	33081	1.28	1.0E-103	AA781442.1	EST_HUMAN	Homo sapiens testis_NHT Homo sapiens cDNA clone 1391452 3'
6787	19842	33125	0.98	1.0E-103	AF053460.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6879	19331	33229	1.47	1.0E-103	AI590071.1	EST_HUMAN	trn58b05.xt NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6879	19331	33230	1.47	1.0E-103	AI590071.1	EST_HUMAN	trn58b05.xt NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
7024	18356	31276	1.73	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7024	18356	31276	1.73	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7161	18393	31237	1.92	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7234	20255	33569	1.05	1.0E-103	AJ268880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7437	20404	33768	2.68	1.0E-103	AJ1665776.1	EST_HUMAN	EST:37849 IMAGE sequences, MAGI Homo sapiens cDNA
7550	20519	33874	3.47	1.0E-103	EE748188.1	EST_HUMAN	601571637.F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3338545 5'
8051	20988	34384	3.69	1.0E-103	AI590071.1	EST_HUMAN	trn58b05.xt NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
8051	20988	34385	3.69	1.0E-103	AI590071.1	EST_HUMAN	trn58b05.xt NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
8832	21600	35022	0.45	1.0E-103	T31080.1	EST_HUMAN	EST:27183 Human Brain Homo sapiens cDNA 5' and similar to None
8868	21934	35359	0.92	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8968	21934	35360	0.92	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9051	22017	35441	1.06	1.0E-103	BF105244.1	EST_HUMAN	716e03.xt Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525684 3' similar to SW:P7NF_HUMAN Q16826 PROTEIN-TYROSINE PHOSPHATASE D1:
9463	22427	35865	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9463	22427	35866	2.86	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8503	22467	35808	1.13	1.0E-103	AA551088.1	EST_HUMAN	nd13402.xt NCL CGAP_OV1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
8544	22507	35856	0.48	1.0E-103	AA774680.1	EST_HUMAN	ae4412.xt Stragelino schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb:X03747.cds1 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
10418	23340	36826	1.28	1.0E-103	Z37976.1	NT	Hi sapiens mRNA for latent transforming growth factor-beta binding protein (LTBR-2)
10459	23361	36874	1.81	1.0E-103	AW563676.1	EST_HUMAN	EST:376749 IMAGE sequences, MAGH Homo sapiens cDNA
10508	23620	37012	10.03	1.0E-103	AI878956.1	EST_HUMAN	au51504.yt Schneider field brain 00004 Homo sapiens cDNA clone IMAGE:2518328 5' similar to TR:O15046 KIAA0338 ;

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11004	23970	37494	1.64	1.0E-103	BE646706.1	EST_HUMAN	7b4103.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:320813 3' similar to gb:168043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
11085	24046	37568	3.98	1.0E-103	AI792759.1	EST_HUMAN	902406.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
11183	24139	37672	1.89	1.0E-103	11424061	NT	Homo sapiens AXI receptor tyrosine kinase (AXI), mRNA
11183	24139	37673	1.89	1.0E-103	11424061	NT	Homo sapiens AXI receptor tyrosine kinase (AXI), mRNA
11341	24281		1.48	1.0E-103	BE671418.1	EST_HUMAN	7e5008.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3286927 3' similar to gb:J05272 INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE 1 (HUMAN);
11570	24509	38056	6	1.0E-103	BE885278.1	EST_HUMAN	801505347F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3908147 5'
11702	24657	38244	2.58	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLAC81 Homo sapiens cDNA clone PLACE1003823 5'
11774	23929	37450	7.57	1.0E-103	L43610.1	NT	Homo sapiens polydystrophic kidney disease (PKD1) gene, exons 27-30
11980	24657		1.47	1.0E-103	AB024759.1	NT	Homo sapiens TSA305 gene, exon 16
12047	24020	38516	2.25	1.0E-103	BE644611.1	EST_HUMAN	7e68a10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER28.13 MER29 repetitive element ;
12178	28028		1.88	1.0E-103	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12208	25040		1.95	1.0E-103	11526291	NT	(UBE2D)3 genes, complete cds
12410	25183	31820	4.32	1.0E-103	AB011399.1	NT	Homo sapiens hydrophobic protein FLJ20454 (FLJ20454), mRNA
236	13336	26260	1.65	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
236	13336	26261	1.65	1.0E-104	AL037549.3	EST_HUMAN	DKFZ2554H1072_r1 584 (synonym: hbr2) Homo sapiens cDNA clone DKFZ2554H1072 5'
1805	14929	27825	1.86	1.0E-104	4502428	NT	DKFZ2554H1072_r1 584 (synonym: hbr2) Homo sapiens cDNA clone DKFZ2554H1072 5'
2203	15218	28238	2.52	1.0E-104	AA132075.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteoinductive protein 2) (BMP8) mRNA
2214	15228	28251	2.87	1.0E-104	BE744628.1	EST_HUMAN	z02206.s1 Stragene cdnt (#837284) Homo sapiens cDNA clone IMAGE:3926438 5'
2377	13395	28408	1.02	1.0E-104	BF334221.1	EST_HUMAN	gb:Z14118.mai CD58 GLYCOPROTEIN PRECURSOR (HUMAN);
2377	13395	28409	1.02	1.0E-104	BF334221.1	EST_HUMAN	601577460F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3926438 5'
2444	15450	28469	2.43	1.0E-104	5031670	NT	RC1-CT0249-110800-214-F12 CT0249 Homo sapiens cDNA
2882	15941	28858	7.18	1.0E-104	NS44671.1	NT	RC1-CT0249-110800-214-F12 CT0249 Homo sapiens cDNA
2927	15935		2.84	1.0E-104	Y1151.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
3277	16331	29262	0.94	1.0E-104	AU139826.1	EST_HUMAN	Human lymphocyte antigen CD59/MEIM43 mRNA, complete cds
3402	16451		1.86	1.0E-104	AA319436.1	EST_HUMAN	H sapiens gene encoding phenylpyruvate tautomerase II
3615	16559	29577	0.8	1.0E-104	AB033102.1	NT	AU133328 OVARC1 Homo sapiens cDNA clone OVARC1000636 5'
3615	16559	29578	0.8	1.0E-104	AB033102.1	NT	EST121668 Adrenal gland tumor Homo sapiens cDNA 5' end
3663	17003	29917	0.94	1.0E-104	AB033298.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
							Homo sapiens mRNA for KIAA1172 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4166	17187	30076	0.88	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4404	17432	30317	4.11	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4839	17680	30547	1.44	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4839	17680	30548	1.44	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5255	18293	31152	1.02	1.0E-104	4685570	NT	Homo sapiens novel centromeric protein RanBP1 (RANBP1), mRNA
5292	18297	31158	0.63	1.0E-104	AF202314.1	NT	Homo sapiens erythropoietin (EPO) gene, exons 4 and 5 and complete cds
5292	18297	31159	0.63	1.0E-104	AF202314.1	NT	Homo sapiens erythropoietin (EPO) gene, exons 4 and 5 and complete cds
6050	19131	32338	1.44	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6050	19131	32339	1.44	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6100	19179	32398	0.89	1.0E-104	A6017332.1	NT	Homo sapiens alk3 mRNA for Aurora/Plt-related kinase 3, complete cds
6611	19669	32945	24.48	1.0E-104	A1768797.1	EST_HUMAN	w03b12.x1 NCL CGAP_K1612 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element ;
6811	19689	32946	24.48	1.0E-104	A1768797.1	EST_HUMAN	w03b12.x1 NCL CGAP_K1612 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN, contains element LTR7 repetitive element ;
6855	19699	33146	0.92	1.0E-104	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6973	20166	33523	1.53	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6973	20166	33524	1.53	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7435	20402	33746	2.14	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8844	21910	35335	0.74	1.0E-104	BF502244.1	EST_HUMAN	U4H-B14-2006-b-09-0-L11x1 NCL CGAP_S1028 Homo sapiens cDNA clone IMAGE:3086176 3'
9522	22465	35652	3.98	1.0E-104	BF448200.1	EST_HUMAN	rad16g11.x1 NCL CGAP_L1024 Homo sapiens cDNA clone IMAGE:3365948 3'
9618	22562	36010	0.63	1.0E-104	AA682308.1	EST_HUMAN	Z98805.s1 Soares_fetal_liver_spleen_INFILS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9639	22583		1.21	1.0E-104	174219.1	EST_HUMAN	w03b102.71 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22440 5'
9669	22622	38073	4.58	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9669	22622	38074	4.58	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9768	21119	34520	4.97	1.0E-104	BF352841.1	EST_HUMAN	IL3-IT06109-080600-249-F07 HT0619 Homo sapiens cDNA
9798	21119	34621	4.97	1.0E-104	BF352841.1	EST_HUMAN	IL3-IT06109-080600-249-F07 HT0619 Homo sapiens cDNA
10111	23037	36516	0.68	1.0E-104	AW103848.1	EST_HUMAN	Q24116 HYPO-THETICAL 29.4 KD PROTEIN ;
10111	23037	36517	0.68	1.0E-104	AW103848.1	EST_HUMAN	Q24116 HYPO-THETICAL 29.4 KD PROTEIN ;
10307	23231	38714	0.62	1.0E-104	AF113514.1	NT	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10463	23375	39887	3.35	1.0E-104	BE791713.1	EST_HUMAN	6011581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10463	23375	39888	3.35	1.0E-104	BE791713.1	EST_HUMAN	6011581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10765	23886	37182	1.35	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBA07 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10808	23729	37231	5.11	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398.5'
10917	23937	37353	4.5	1.0E-104	U66535.1	NT	Human beta4-integrin (ITGB4) gene, exon 10/20, 21, 22, 23, 24 and 25
10931	23951		0.82	1.0E-104	11427757	NT	Human beta4-integrin (ITGB4) gene product (KIAA0849), mRNA
11629	24657	38120	3.09	1.0E-104	BE720191.1	EST_HUMAN	RQO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11629	24657	38120	3.09	1.0E-104	BE720191.1	EST_HUMAN	RQO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11656	24592	38165	3.48	1.0E-104	BF684288.1	EST_HUMAN	30241218FT NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507.5'
12988	25548		1.43	1.0E-104	BE93892.1	EST_HUMAN	80131218FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689878.5'
278	15810	26302	1.61	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
425	13120	26018	9.28	1.0E-105	4505160	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
566	13663	26576	3.89	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
596	13663	26577	3.89	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1689	14720		2.33	1.0E-105	AB020591.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1837	14654	27582	1.47	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C089
1943	14697	27964	2.09	1.0E-105	D80918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2199	15214	28234	1.07	1.0E-105	AA318366.1	EST_HUMAN	EST20809 Spleen1 Homo sapiens cDNA 5' end similar to autoimmunity antigen Ku, p70/p80 subunit
2731	15725		3.14	1.0E-105	AA564608.1	EST_HUMAN	no10605.s1 NC1_OGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265.3'
3018	16076		3.14	1.0E-105	AI229041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3382	16412	28336	1.11	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3382	16412	28337	1.11	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4125	17158	30046	3.14	1.0E-105	AW991688.1	EST_HUMAN	EST73761 IMAGE resequencing, MAGB Homo sapiens cDNA
4773	17793	30584	0.69	1.0E-105	BE868881.1	EST_HUMAN	801445823FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3880156.5'
4773	17793	30585	0.69	1.0E-105	BE868881.1	EST_HUMAN	801445823FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3880156.5'
4793	17810	30702	1.05	1.0E-105	AA099355.1	EST_HUMAN	24492.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:433682.3'
4976	17991		4.04	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5147	18156	31036	1.21	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0766 protein, partial cds
5403	18506	31983	1.02	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5471	18572		1.02	1.0E-105	11420134	NT	Homo sapiens Ralme-derived POU-domain factor-1 (RPF-1), mRNA
7089	20023	33524	1.57	1.0E-105	BF314302.1	EST_HUMAN	801901028FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334.5'
7089	20023	33525	1.57	1.0E-105	BF314302.1	EST_HUMAN	801901028FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334.5'
7174	18405	31203	3.49	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7174	18405	31204	3.49	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7223	20245	33579	0.96	1.0E-105	AW951634.1	EST_HUMAN	EST7355659 IMAGE resequencing, MAGB Homo sapiens cDNA
7501	20466	33527	0.86	1.0E-105	BE902616.1	EST_HUMAN	801977278FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8192	21162	34572	1.09	1.0E-105	X12556.1	NT	Human mRNA for dbl proto-oncogene
8362	21331	34743	0.09	1.0E-105	T05087.1	EST_HUMAN	EST02075 Fetal brain, Stradiene (ca#933206) Homo sapiens cDNA clone IMAGE:2500626 3' similar to
8741	21709	35132	1.82	1.0E-105	AW007194.1	EST_HUMAN	SW-ACCSA_PENCH P38333 ACETYL-COENZYME A SYNTHETASE ;
9280	22246	35676	0.76	1.0E-105	AW840317.1	EST_HUMAN	RC1-CHN05-070100-011-e05 CHN008 Homo sapiens cDNA
9405	22370	35805	3.19	1.0E-105	AW016876.1	EST_HUMAN	UHH-B10p-abk-12-q-U11.s1 NCL_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9558	22520	35868	0.91	1.0E-105	AW852372.1	EST_HUMAN	QV2-070062-140300-083-008 OT0062 Homo sapiens cDNA
9558	22520	35868	0.91	1.0E-105	AW852372.1	EST_HUMAN	QV2-070062-140300-083-008 OT0062 Homo sapiens cDNA
9928	22810	36262	0.76	1.0E-105	BE867793.1	EST_HUMAN	801443755FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
9928	22810	36263	0.76	1.0E-105	BE867793.1	EST_HUMAN	801443755FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11278	24229	37756	4.59	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11584	24504	38081	1.61	1.0E-105	D63548.1	NT	Homo sapiens COL4A3 gene for $\alpha 5(V)$ collagen, exon 31
11811	24549	38109	2.93	1.0E-105	7705306	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11914	24795	38386	2.81	1.0E-105	AW027554.1	EST_HUMAN	w7407.x1 Soares_lymnu5_NH15th Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87862
11984	24861	38457	2.59	1.0E-105	BF430921.1	EST_HUMAN	P87862 PROTEASE ;
12104	24975	38672	1.5	1.0E-105	AB004924.1	NT	7018c10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574281 3' similar to TR:P97680 P97680
12104	24975	38673	1.5	1.0E-105	AB004924.1	NT	RIN1.1 ;
152	13265	26235	1.76	1.0E-108	AW503208.1	EST_HUMAN	Homo sapiens gene for Smad3, exon 2 and 3
206	13307	26235	1.59	1.0E-108	AW503208.1	EST_HUMAN	Homo sapiens gene for Smad3, exon 2 and 3
543	13614	26534	2.23	1.0E-108	AW655555.1	EST_HUMAN	UHH-BND-actg-07-Q-U111 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
607	13674	26589	3.07	1.0E-108	J00146.1	NT	UHH-BND-actg-07-Q-U111 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:2215088 3'
608	13674	26589	1.71	1.0E-108	J00146.1	NT	UHH-BND-actg-07-Q-U111 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:2215088 3'
1712	14742	27726	4.6	1.0E-108	U48724.1	NT	EST137659 MAGC resequences, MAG1 Homo sapiens cDNA
1732	14762	27746	1.01	1.0E-108	U04510.1	NT	Human dihydrofolate reductase pseudogene (psl-hd1)
1820	14847	27639	4.27	1.0E-108	AA527446.1	EST_HUMAN	Human dihydrofolate reductase pseudogene (psl-hd1)
1820	14847	27640	4.27	1.0E-108	AA527446.1	EST_HUMAN	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
2132	15149	28164	1.52	1.0E-106	BE144285.1	EST_HUMAN	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
2325	15336	28359	3.89	1.0E-106	4504184	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
2612	15515	28539	1.07	1.0E-106	AF003528.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
							LTR3 repetitive element ;
							LTR3 repetitive element ;
							pg41cd5.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
							LTR3 repetitive element ;
							MR0-HT0765-140200-008-d10 HT0765 Homo sapiens cDNA
							Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
							Homo sapiens X-linked anhrilotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2610	15609	26633	1.79	1.0E-108	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2768	15760	28782	4.05	1.0E-108	AI276526.1	EST_HUMAN	q76h10.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1978307 3'
2836	14461	27437	1.13	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2836	14461	27438	1.13	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2886	15545	28660	0.99	1.0E-108	BE384288.1	EST_HUMAN	601227257F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613819 5'
2952	16009	28634	4.42	1.0E-108	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2952	16009	29535	4.42	1.0E-108	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3165	15250	29168	1.72	1.0E-108	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3185	16250	29168	1.72	1.0E-108	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3454	16500	29417	1	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3454	16500	29418	1	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4068	17104	29986	7.68	1.0E-108	AW974650.1	EST_HUMAN	EST3368375 IMAGE ressequences, MAGN Homo sapiens cDNA
4068	17104	29987	7.68	1.0E-108	AW974650.1	EST_HUMAN	EST3368375 IMAGE ressequences, MAGN Homo sapiens cDNA
4631	17652	30539	0.73	1.0E-108	BE144288.1	EST_HUMAN	MRO-HT0165-10200-008-c10 HT0165 Homo sapiens cDNA
4834	17950	30841	0.82	1.0E-108	U31520.1	NT	Human alpha mannosidase II mRNA, complete cds
5289	18294		0.96	1.0E-108	L41644.1	NT	Homo sapiens cytochrome gene, exon 41
5443	18545	31457	2.82	1.0E-108	AA781155.1	EST_HUMAN	PHPS1-2 (HUMAN);
5954	19039	32238	0.82	1.0E-108	AU130113.1	EST_HUMAN	AU130113.NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5954	19039	32237	0.82	1.0E-108	AU130113.1	EST_HUMAN	AU130113.NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6009	19092	32292	0.93	1.0E-108	AA434168.1	EST_HUMAN	2w28612.s1 Scores ovary tumor NHR-OT Homo sapiens cDNA clone IMAGE:770615 3'
6108	19187	32405	0.78	1.0E-108	AU143428.1	EST_HUMAN	AU143428.Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6108	19187	32407	0.78	1.0E-108	AU143428.1	EST_HUMAN	AU143428.Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6221	19295	32528	18	1.0E-108	BF678574.1	EST_HUMAN	002154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285087 5'
6332	19402	32643	0.68	1.0E-108	BE897112.1	EST_HUMAN	801439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6538	19402	32643	0.82	1.0E-108	BE897112.1	EST_HUMAN	801439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6559	19819	32884	17.32	1.0E-108	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
6559	19819	32885	17.32	1.0E-108	11545913	NT	Homo sapiens xylotransferase II (XT2), mRNA
7369	20557	33917	5.25	1.0E-108	AA693779.1	EST_HUMAN	ae72807.s1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7655	20615	33979	5.04	1.0E-108	11429617	NT	KINESIN HEAVY CHAIN (HUMAN);
7746	20700	34066	1.17	1.0E-108	BE292722.1	EST_HUMAN	801105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7869	20813	34190	8.49	1.0E-108	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7869	20813	34191	8.48	1.0E-108	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8119	21058	34463	0.83	1.0E-108	AU116850.1	EST_HUMAN	AU116850 HEMBA1 Homo sapiens cDNA clone HEMBA100129 5'
8317	21288	34689	5.05	1.0E-108	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948463 5'
8317	21288	34700	5.05	1.0E-108	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3948463 5'
8515	21483	34697	108.87	1.0E-108	A1523088.1	EST_HUMAN	606807.x1 Breast/cervix HPLRB6 Homo sapiens cDNA clone IMAGE:2127782 3' similar to gb-X06233
8976	21942	35358	0.78	1.0E-108	BE387850.1	EST_HUMAN	CALCRANULIN B (HUMAN);
8976	21942	35387	0.78	1.0E-108	BE387850.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9054	22020	35445	3.3	1.0E-108	A1654123.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9060	22026	35449	0.53	1.0E-108	A1691108.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9407	22372	35807	0.87	1.0E-108	AW838831.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9502	22466	35806	2.47	1.0E-108	AA823307.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9502	22468	35907	2.47	1.0E-108	AA823307.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9841	22585	36034	1.55	1.0E-108	A1750447.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9784	22725	36181	1.81	1.0E-108	A1479569.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
9784	22725	36182	1.81	1.0E-108	A1479569.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
10361	23284	36781	1.22	1.0E-108	BE388284.1	EST_HUMAN	60128271F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604483 5'
10444	23366	36856	0.92	1.0E-108	BF027310.1	EST_HUMAN	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10444	23366	36857	0.92	1.0E-108	BF027310.1	EST_HUMAN	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10501	23523	37017	5.48	1.0E-108	AA604417.1	EST_HUMAN	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10801	23523	37018	5.48	1.0E-108	AA604417.1	EST_HUMAN	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10848	23570	37068	1.58	1.0E-108	A1363296.1	EST_HUMAN	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10653	23575	37071	0.5	1.0E-108	11459432	NT	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10653	23575	37072	0.5	1.0E-108	11459432	NT	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10827	23748	37249	0.49	1.0E-108	AL038886.1	EST_HUMAN	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
10944	23864	37379	3.52	1.0E-108	AL163202.2	NT	601071674F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3954403 5'
11242	24195	37713	4.84	1.0E-108	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC 60 Homo sapiens cDNA clone IMAGE:3857366 5'
11242	24195	37714	4.84	1.0E-108	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC 60 Homo sapiens cDNA clone IMAGE:3857366 5'
11402	24346	37878	2.78	1.0E-108	J05200.1	NT	Human tyrosine kinase receptor mRNA, complete cds
11402	24346	37880	2.78	1.0E-108	J05200.1	NT	Human tyrosine kinase receptor mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11736	24822	38200	3.21	1.0E-108	BE257395.1	EST_HUMAN	601108219FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE3349697 5'
12280	25763		8.02	1.0E-108	AW470405.1	EST_HUMAN	fl056111.xt NIH_MGC_17 Homo sapiens cDNA clone IMAGE2981844 5'
12481	25229	31768	3.58	1.0E-106	BE864483.1	EST_HUMAN	601433087FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE3918524 5'
12481	25229	31797	3.58	1.0E-106	BE864483.1	EST_HUMAN	601433087FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE3918524 5'
12697	25354		4.46	1.0E-108	BE865945.1	EST_HUMAN	RC1-CT0248-06060-024-005 CT0248 Homo sapiens cDNA
237	13337		4.26	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
284	13360		1.85	1.0E-107	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
631	13698	26616	3.39	1.0E-107	AF165103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
814	13872	26820	2.77	1.0E-107	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
887	13942	26900	1.31	1.0E-107	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
970	14022	26975	12.86	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity deoxyribose transporter (NADC3) mRNA, complete cds
1283	14318	27281	1.8	1.0E-107	AB032263.1	NT	Homo sapiens SAZ18 mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1573	14608	27579	3.93	1.0E-107	BF087405.1	EST_HUMAN	OY2-HT0540-120800-358-e05 HT0540 Homo sapiens cDNA
1767	14706	27781	2.54	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (C15Z) gene, exon 3
1857	14883	27879	0.96	1.0E-107	AB007692.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1857	14883	27880	0.96	1.0E-107	AB007692.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2218	15232	28256	1.11	1.0E-107	U13728.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2370	15378	28401	1.02	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-003 CN0031 Homo sapiens cDNA
2370	15378	28402	1.02	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-003 CN0031 Homo sapiens cDNA
2540	15342	28556	1.12	1.0E-107	BE732460.1	EST_HUMAN	601567619FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE3842309 5'
2540	15342	28567	1.12	1.0E-107	BE732460.1	EST_HUMAN	601567619FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE3842309 5'
3019	16077	28697	3.8	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-003 CN0031 Homo sapiens cDNA
3019	16077	28698	3.8	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-003 CN0031 Homo sapiens cDNA
3116	16173	29083	3.16	1.0E-107	5902097	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
3839	16379	29782	4.78	1.0E-107	AF02671.1	NT	Homo sapiens SM13 (suppressor of mlf two 3, yeast) homolog 2 (SM13H2), mRNA
5706	18801	31978	0.56	1.0E-107	AW690338.1	EST_HUMAN	EST1381115 IMAGE sequences, MAGK Homo sapiens cDNA
5965	19050	32251	3.4	1.0E-107	BE867460.1	EST_HUMAN	601442559FT NIH_MGC_65 Homo sapiens cDNA clone IMAGE3646494 5'
6976	20188	33527	0.56	1.0E-107	6005706	NT	Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA
7107	20041	33343	0.63	1.0E-107	11431468	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220KD ) (GTF3C1), mRNA
7107	20041	33344	0.63	1.0E-107	11431468	NT	Homo sapiens general transcription factor IIIC, polypeptide 1 (alpha subunit, 220KD ) (GTF3C1), mRNA
7688	20549	33609	1.16	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BNO-sil-c-08-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE3078310 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7588	20549	33910	1.16	1.0E-107	AW503913.1	EST_HUMAN	U-HF-BNO-af-c8-CLJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7703	20728	34098	1.54	1.0E-107	AI765078.1	EST_HUMAN	WH5604.X1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
8004	20943	34336	0.81	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
8024	20943	34337	0.81	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
8028	21015	34415	0.59	1.0E-107	AW410361.1	EST_HUMAN	h50911.x2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2864624 5'
8078	22770	36225	1	1.0E-107	AI122469.1	EST_HUMAN	AU122469 MAMMAT Homo sapiens cDNA clone MAMMA1002433 5'
							IG1006.X1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW-AACT_DICDI
11061	24024	37648	2.92	1.0E-107	AI392850.1	EST_HUMAN	P05096 ALPHA-ACTININ 3, NON MUSCULAR;
11293	24243	37770	1.82	1.0E-107	A61411.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11308	24258	37784	2.08	1.0E-107	BF68551.1	EST_HUMAN	602123635F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11651	24588	38158	4.76	1.0E-107	BE840590.1	EST_HUMAN	60106681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:346282D 5'
11721	23918	37435	2.44	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11721	23918	37436	2.44	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12321	25602		5.18	1.0E-107	AA001415.1	EST_HUMAN	2d4501.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361844 3' similar to contains THR b1
12345	25769		1.48	1.0E-107	11418318	NT	THR repetitive element;
956	14009	26962	1.66	1.0E-108	BE266042.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSET), mRNA
1270	14305	27265	4.89	1.0E-108	Y18000.1	NT	801177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2091	15108	28127	1.24	1.0E-108	BF028728.1	EST_HUMAN	Homo sapiens NF2 gene
							601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954639 5'
2435	15442	28460	9.44	1.0E-108	BE206594.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2865389 3' similar to gbX53777 80S
3360	18410	29332	0.79	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN); gbJ05277 Mouse hexokinase mRNA, complete cds
3360	18410	29333	0.79	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4184	17215	30102	1.13	1.0E-108	AW684438.1	EST_HUMAN	h172411.X1 NC1_CGAP_GUT Homo sapiens cDNA clone IMAGE:2872090 3' similar to SW:3BP1_MOUSE
4555	17578	30469	1.73	1.0E-108	U72861.1	NT	P51564 SH3-BINDING PROTEIN 3BP-1;
4565	17578	30469	1.73	1.0E-108	U72861.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4842	17859	30754	1.39	1.0E-108	7651978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4966	17971	30862	0.89	1.0E-108	AW504769.1	EST_HUMAN	U-HF-BNO-af-c8-CLJ1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
4860	18001	30860	2.59	1.0E-108	AJ008005.1	NT	Homo sapiens PSNT gene, alternative transcript
5184	18193	31058	0.71	1.0E-108	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5556	18653	31697	1.1	1.0E-108	AW384094.1	EST_HUMAN	RC0-H10372-241190-031-003 HT0372 Homo sapiens cDNA
5605	18701	31673	2.27	1.0E-108	BE860161.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	18701	31674	2.27	1.0E-108	BE869018.1	EST_HUMAN	601444922F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3848680 5'
6038	19719		0.8	1.0E-108	AF012823.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6117	19195	32419	0.92	1.0E-108	BF334851.1	EST_HUMAN	PfM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6262	19395	32567	8.27	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6262	19395	32568	6.27	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6392	19460	32708	1.22	1.0E-108	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6494	19165	32419	0.99	1.0E-108	BF334851.1	EST_HUMAN	PfM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6773	19828	33110	0.67	1.0E-108	AF016708.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6773	19828	33111	0.67	1.0E-108	AF016708.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7395	20335	33685	5.42	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family G, group 5, member B (GPRC3B), mRNA
7673	20631	33965	1.68	1.0E-108	4798333	NT	Homo sapiens delta-8 fatty acid desaturase (FADS6) mRNA
7718	20675	34041	1.13	1.0E-108	BE252907.1	EST_HUMAN	60113471F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3354064 5'
7749	20702	34069	0.68	1.0E-108	BF526912.1	EST_HUMAN	602043384F1 NC_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
7749	20702	34070	0.68	1.0E-108	BF526912.1	EST_HUMAN	602043384F1 NC_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181037 5'
8149	21069	34485	0.57	1.0E-108	11422155	NT	Homo sapiens cyclic fibroblast transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8399	21368		1.8	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8452	21421	34855	5.44	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMG-ade-e-12-0-UL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8452	21421	34836	5.44	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMG-ade-e-12-0-UL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
9402	22367	35800	0.53	1.0E-108	AF203077.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
9441	22405	35842	0.48	1.0E-108	N44674.1	EST_HUMAN	Y95910.1 Soares melanocyte 2N44HM Homo sapiens cDNA clone IMAGE:273263 5' similar to PIR-A45773
10693	23803	37417	2.67	1.0E-108	11422155	NT	A45773 kelch protein, long form - fruit fly
11027	21040	34439	2.14	1.0E-108	BE595227.1	EST_HUMAN	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC84446), mRNA
11177	18363	31268	1.64	1.0E-108	Y12490.1	NT	601058759F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446361 5'
11602	24540	38099	3.33	1.0E-108	AW965186.1	EST_HUMAN	Homo sapiens mRNA for Gdgi-associated microtubule-binding protein (GMAP-210)
11653	24590	38160	1.76	1.0E-108	AW708760.1	EST_HUMAN	EST138258 MAGE sequences, MAGE Homo sapiens cDNA
11653	24590	38161	1.75	1.0E-108	AW708760.1	EST_HUMAN	AV708760 ADC Homo sapiens cDNA clone AOC4EE03 5'
11653	24590	38161	1.75	1.0E-108	AW708760.1	EST_HUMAN	AV708760 ADC Homo sapiens cDNA clone AOC4EE03 5'
11696	24663		2.05	1.0E-108	11441468	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11757	24695	36295	1.6	1.0E-108	D63339.1	NT	Homo sapiens COL4A5 gene for $\alpha 5(V)$ collagen, exon 23

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12483	25236	31800	5.14	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12854	25467		11.97	1.0E-108	BF346356.1	EST_HUMAN	602018571 F1 N1 CGAP_Binf67 Homo sapiens cDNA clone IMAGE:4154297 5'
44	13164	26067	2.17	1.0E-109	AW803116.1	EST_HUMAN	IL2JUM0077-260400-070-008 UM0077 Homo sapiens cDNA
67	13185	26104	6.98	1.0E-109	D86974.1	NT	Homo sapiens mRNA for KIAA0220 gene, partial cds
220	13320	26245	1.51	1.0E-109	11422465	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
229	13328	26251	1.97	1.0E-109	11438351	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
467	13540	26465	2.2	1.0E-109	4507712	NT	Homo sapiens tetrahydrocyclopeptide repeat domain 2 (TTCD2), mRNA
600	13667	26581	13.45	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
600	13667	26582	13.45	1.0E-109	AB023218.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1014	14082	27013	0.98	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1207	14246	27204	23.68	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1), complete cds
1208	14246	27204	21.33	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1), complete cds
1644	14577	27546	1.2	1.0E-109	BE263673.1	EST_HUMAN	607186922 F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959638 5'
1944	14577	27550	1.2	1.0E-109	BE263673.1	EST_HUMAN	607186922 F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959638 5'
1891	14916	27911	1.93	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2253	15267	28294	2.68	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2262	15276	28300	2.59	1.0E-109	Y1123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2630	15629	28654	3.42	1.0E-109	A022328.1	EST_HUMAN	aw95401.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1954536 3' similar to TR-002197 C02197 CIRCULATING CATHODIC ANTIGEN ;
2630	15629	28655	3.42	1.0E-109	A022328.1	EST_HUMAN	aw95401.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1954536 3' similar to TR-002197 C02197 CIRCULATING CATHODIC ANTIGEN ;
2631	15630	28656	1.84	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A), mRNA
3071	16128	29040	1.81	1.0E-109	N86190.1	EST_HUMAN	J2818F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2818 5' similar to ZINC FINGER PROTEIN ZNF43
3399	18448	29374	1.33	1.0E-109	AW863192.1	EST_HUMAN	CNA3-NN0006-190400-150-010 NN0009 Homo sapiens cDNA
3399	18448	29375	1.33	1.0E-109	AW863192.1	EST_HUMAN	CNA3-NN0006-190400-150-010 NN0009 Homo sapiens cDNA
3330	19376	29469	1.66	1.0E-109	AF240598.1	NT	Homo sapiens retinol dehydrogenase homolog, isoform-1 (RDH), complete cds
3572	19517	29538	0.92	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3572	19517	29539	0.92	1.0E-109	M37928.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3556	16986		2.3	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0206-110400-108-604 HT0206 Homo sapiens cDNA
4171	17202	30089	4.97	1.0E-109	AI655417.1	EST_HUMAN	ts9a606.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP-F53A2.8 CE16100 ;
4189	17220	30107	1.33	1.0E-109	AA662274.1	EST_HUMAN	nu68a12.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTATHIONE S-TRANSFERASE THETA 2 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4189	17220	30108	1.33	1.0E-109	AA602274.1	EST_HUMAN	nu80412.s1 NCL_GGAP_P22 Homo sapiens cDNA clone IMAGE:1218282 3' similar to SW:GTT2_HUMAN
4432	17450	30350	2.38	1.0E-109	4504208	NT	P30712 GLUTATHIONE S-TRANSFERASE THETA 2;
4530	17651	30538	1.42	1.0E-109	7682083	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCAT1A) mRNA
4558	17973	30884	0.94	1.0E-109	R15400.1	EST_HUMAN	Y46806.t1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE:53057 5'
5318	18424	31227	0.5	1.0E-109	AF137282.1	EST_HUMAN	AUT37282 PLACE1 Homo sapiens cDNA clone PLACE1008189 5'
5332	18438	31190	0.86	1.0E-109	BF673718.1	EST_HUMAN	602139446FT NIH_MGC 33 Homo sapiens cDNA clone IMAGE:4272922 5'
5380	18489	31394	2.28	1.0E-109	5174822	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5688	18783		1.49	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-004 HT0615 Homo sapiens cDNA
6037	25551	32323	0.83	1.0E-109	BF379688.1	EST_HUMAN	GM1-UT0038-060900-366-H07 UT0038 Homo sapiens cDNA
6111	18783		1.28	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-004 HT0615 Homo sapiens cDNA
6485	19550	32708	0.57	1.0E-109	N23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6485	19550	32800	0.57	1.0E-109	N23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6742	19787	33077	8.08	1.0E-109	A1221585.1	EST_HUMAN	g56108.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
6933	20167	33476	0.52	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6933	20167	33477	0.52	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7145	18377	31295	0.49	1.0E-109	BE074888.1	EST_HUMAN	RG5-BT0580-170300-021-F08 BT0580 Homo sapiens cDNA
7451	20417	33772	0.93	1.0E-109	AB046831.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7815	20784	34140	3.31	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7817	20766	34142	5.45	1.0E-109	BF182707.1	EST_HUMAN	601809495FT NIH_MGC 18 Homo sapiens cDNA clone IMAGE:4040279 5'
7817	20766	34143	5.45	1.0E-109	BF182707.1	EST_HUMAN	601809495FT NIH_MGC 18 Homo sapiens cDNA clone IMAGE:4040279 5'
8513	21481	34895	1.37	1.0E-109	AL046784.1	NT	Novel human gene mapping to chromosome 13
8628	21580	35017	1.08	1.0E-109	AW749130.1	EST_HUMAN	PM0-BT0340-001295-002-c05 BT0340 Homo sapiens cDNA
9004	21870		3.59	1.0E-109	AA077498.1	EST_HUMAN	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone IMAGE:7818H01
9086	22052	35474	17.25	1.0E-109	BE787540.1	EST_HUMAN	601479417FT NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3882124 5'
9086	22052	35475	17.25	1.0E-109	BE787540.1	EST_HUMAN	601479417FT NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3882124 5'
9593	22555	36005	1.78	1.0E-109	H64860.1	EST_HUMAN	Y65009.t1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP-A53491
9705	22558	36113	0.65	1.0E-109	BE397088.1	EST_HUMAN	A53491 BUMETA1NIDE-SENSITIVE NAK-C1 CO-TRANSPORTER - SPINY;
9705	22558	36114	0.65	1.0E-109	BE397088.1	EST_HUMAN	Y67289760FT NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3620030 5'
9839	22715	36230	2.5	1.0E-109	F06604.1	EST_HUMAN	601289760FT NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3620030 5'
11128	24088	37518	2.42	1.0E-109	BE540309.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
11128	24088	37518	2.42	1.0E-109	BE540309.1	EST_HUMAN	601063030FT NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3449599 5'
11128	24088	37517	2.42	1.0E-109	BE540309.1	EST_HUMAN	601063030FT NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3449599 5'
11158	24116	37542	31.85	1.0E-109	BF594831.1	EST_HUMAN	60208072F2 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4245341 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11459	24402	37650	1.65	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002590 5'
11697	24692	38240	2.82	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11735	24621	38199	5.45	1.0E-109	W16510.1	EST_HUMAN	2b08012.r Soares, field, lung, NIH-L19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:543969 S43969 p54-beta stress-activated protein kinases - rat.
11810	24781	38380	1.59	1.0E-109	BE045590.1	EST_HUMAN	ih2305.x1 NCL CGAP_Luz24 Homo sapiens cDNA clone IMAGE:2655969 3' similar to TR:Q82124 Q82124
12125	24694	38597	2.03	1.0E-109	BF339540.1	EST_HUMAN	YGR163W MRNA HOMOLOGUE, COMPLETE CDS.
12125	24694	38598	2.03	1.0E-109	BF339540.1	EST_HUMAN	602036003.F1 NCL CGAP_Bm54 Homo sapiens cDNA clone IMAGE:4188753 5'
12132	25001	38607	1.65	1.0E-109	AA490558.1	EST_HUMAN	602036003.F1 NCL CGAP_Bm54 Homo sapiens cDNA clone IMAGE:4188753 5'
12395	15276	28300	2.1	1.0E-109	Y17123.1	NT	ea2807.r1 Soares, NIH-HMP_S1 Homo sapiens cDNA clone IMAGE:823821 5'
12613	15278	28300	2.24	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12720	25374	31774	1.85	1.0E-109	AB011399.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	13124	26022	0.89	1.0E-110	7549804	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
39	13159	26051	4.69	1.0E-110	5803073	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
39	13159	26052	4.68	1.0E-110	5803073	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
109	13124	26022	1.73	1.0E-110	7549804	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
284	13388	26316	1.5	1.0E-110	D87291.1	NT	Homo sapiens diiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
528	13589	26517	13.41	1.0E-110	U84550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1184	14235	27181	1	1.0E-110	5031620	NT	Human dyalatroxin (DTN) gene, exon 20
1284	14319	27282	0.72	1.0E-110	AB032253.1	NT	Homo sapiens calcitonin receptor-like (CALRL) mRNA
1637	14991	27658	1.35	1.0E-110	BE378477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2073	15090		1.85	1.0E-110	BF508896.1	EST_HUMAN	601287546.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2853	15913		1.05	1.0E-110	4503098	NT	UHH-B14-acsc-b-05-c-U1s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
3043	14319	27282	0.89	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3103	16190		1.01	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
3209	16294	29165	1.55	1.0E-110	11438041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3209	16294	29166	1.55	1.0E-110	11438041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4231	17280	30145	0.83	1.0E-110	M15918.1	NT	Human subcutaneous antigen small nuclear ribonucleoprotein E pseudogene
4665	17696	30570	2.11	1.0E-110	A017213.1	EST_HUMAN	ou03201X1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827963 3' similar to SW:NI21_RAT_P82891 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4884	17705	30597	4.29	1.0E-110	AU117612.1	EST_HUMAN	AU117612 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5009	18023		1.94	1.0E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5307	18472	31343	2.23	1.0E-110	BE289403.1	EST_HUMAN	601118710.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5814	18804	32087	0.78	1.0E-110	BE621069.1	EST_HUMAN	601436877F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895795 5'
5834	18924	32108	7.66	1.0E-110	11418323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5834	18924	32108	7.66	1.0E-110	11418323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6878	25570	33228	3.64	1.0E-110	ME5112.1	NT	Human cyclic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7255	20256	33550	0.59	1.0E-110	BE251466.1	EST_HUMAN	601103389F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3360277 5'
7309	20260	33619	0.71	1.0E-110	U06888.1	NT	Human G52 gene, exon 2
7309	20260	33620	0.71	1.0E-110	U06888.1	NT	Human G52 gene, exon 2
7545	20508	33867	0.69	1.0E-110	AI590289.1	EST_HUMAN	U12008.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7656	20516	33980	10.79	1.0E-110	AV714278.1	EST_HUMAN	P90549.ETS TRANSLOCATION VARIANT 1;
7656	20516	33981	10.79	1.0E-110	AV714278.1	EST_HUMAN	AV714278 DGB Homo sapiens cDNA clone DCBCGE01 5'
7693	20846	34010	2.84	1.0E-110	AB020075.1	NT	Homo sapiens mRNA for KIAA0689 protein, partial cds
7820	20769	34145	1.01	1.0E-110	AI137623.1	EST_HUMAN	AI137623 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9660	22843	38101	0.76	1.0E-110	BE302594.1	EST_HUMAN	bc68801.Y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905661 5' similar to TR:O77268 O77258
9936	22843	38324	3.25	1.0E-110	AW838394.1	EST_HUMAN	EC:14.D02 PROTEIN.1;
10686	23608	37102	3.4	1.0E-110	11432732	NT	QV2.LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
11099	24059	37583	2.76	1.0E-110	Y12337.1	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
11314	24284	37791	3.18	1.0E-110	BE734357.1	EST_HUMAN	H.sapiens mRNA for myofibrin dystrophy protein kinase like protein
11314	24284	37791	3.18	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11314	24284	37792	3.18	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11770	23925	37445	2.49	1.0E-110	AA446528.1	EST_HUMAN	zw67g02.1 Scores, tests, NHT Homo sapiens cDNA clone IMAGE:781286 5' similar to TR:G1145816
12210	25051	38072	5.81	1.0E-110	BE807218.1	EST_HUMAN	G1145816 FKBP4;
12359	25137	38324	9.66	1.0E-110	AV082268.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12579	25288	38324	1.72	1.0E-110	AB011399.1	NT	LC-BT0163-040559-094-g10 BT0163 Homo sapiens cDNA
12706	25913	38324	2.05	1.0E-110	BF364546.1	EST_HUMAN	Homo sapiens gene for A1-6, complete cds
12987	15090	38324	1.34	1.0E-110	BF508995.1	EST_HUMAN	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
176	13277	38324	12.39	1.0E-111	U43701.1	NT	U1-H-B14-bos-5-05-0-U1a1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
736	13797	38324	3.39	1.0E-111	BF035327.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
745	13808	26746	5.69	1.0E-111	8393092	NT	601468551F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862085 5'
927	13860	26934	3.63	1.0E-111	M25142.1	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECRT), mRNA
2250	13264	26230	1.53	1.0E-111	AF036126.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4357	17384	30266	4.66	1.0E-111	K02268.1	NT	Homo sapiens collagen type IX alpha 1 chain (COL9A1) gene, exons 29, 30, 31, and 32
5293	18298	31760	0.72	1.0E-111	AB035356.1	NT	Homo entkephalin 5 (enkb) gene, exon 4 and 3' flank and complete cds
							Homo sapiens mRNA for neuron alpha protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5553	18650	31593	0.66	1.0E-111	AA151017.1	EST_HUMAN	247607.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23375 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5553	18650	31594	0.66	1.0E-111	AA151017.1	EST_HUMAN	gb:M23375 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5714	18608	31686	0.69	1.0E-111	BE987909.1	EST_HUMAN	gb:M23375 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5937	18927	32111	0.49	1.0E-111	U19669.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6148	19223	32453	1.5	1.0E-111	AK344679.1	EST_HUMAN	RELATED PROTEIN RAL-A (HUMAN);
6937	18690	33165	0.95	1.0E-111	ALC40762.1	EST_HUMAN	DKEF2p34C1815_r1_434 (synonym: hla33) Homo sapiens cDNA clone DKEF2p34C1815 5'
6978	20201	33531	1.3	1.0E-111	AW294948.1	EST_HUMAN	UHH-BW10-ail-3-03-DU1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729526 3'
7405	20373	33724	0.52	1.0E-111	AW683165.1	EST_HUMAN	RC2-BN0033-160200-013-b05 BN0033 Homo sapiens cDNA
7690	20638	34000	2.67	1.0E-111	BF368228.1	EST_HUMAN	IL2-NT101-280700-114-E03 NT101 Homo sapiens cDNA
7772	20725	34097	0.51	1.0E-111	6961253	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant A, mRNA
7779	20732	34104	0.69	1.0E-111	AT761228.1	EST_HUMAN	wf8601.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2388465 3' similar to gb:J04813
7873	20817	34195	0.8	1.0E-111	U80017.1	NT	CYTOTOCHROME P450 IIA5 (HUMAN);
8097	21004	34402	1.52	1.0E-111	AA133614.1	EST_HUMAN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8431	21400	34812	0.82	1.0E-111	AA278658.1	EST_HUMAN	zfr2c12.r1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:562774 5' similar to gb:X03740
8431	21400	34813	0.82	1.0E-111	AA278658.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8530	21498	34914	0.55	1.0E-111	11420516	NT	zsf7903.r1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8593	21551	34969	3.24	1.0E-111	U66533.1	NT	G1259410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
9027	21603	35413	0.77	1.0E-111	11420516	NT	G1259410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
9128	22094	35522	0.83	1.0E-111	AK024453.1	NT	G1259410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
9160	22126	35632	23.95	1.0E-111	BF214602.1	EST_HUMAN	G1259410 11-ZINC-FINGER TRANSCRIPTION FACTOR.1
9236	22202	35633	15.22	1.0E-111	X17033.1	NT	Homo sapiens protein x0001 (LOC31185), mRNA
9443	22407	35844	2.88	1.0E-111	AF091395.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9572	22625	36079	0.46	1.0E-111	BF333210.1	EST_HUMAN	Homo sapiens mRNA for EL00045 protein, partial cds
							Human mRNA for Integrin alpha-2 subunit
							Human mRNA for Integrin alpha-2 subunit
							Homo sapiens T10 isoform mRNA, complete cds
							QV2-B70817-270000-308-e05 B70817 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10512	23434	36632	1.96	1.0E-111	AA504180.1	EST_HUMAN	aa50402.s1 NCL_CGAP_CCB1 Homo sapiens cDNA clone IMAGE:826170 3' similar to gb.L09235
10540	23462		1.69	1.0E-111	U10083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10635	23557	37057	6.39	1.0E-111	AA131248.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
11110	24070	37892	3.4	1.0E-111	AW296467.1	EST_HUMAN	281601.r1 Soares prepatant virus, NBRPU Homo sapiens cDNA clone IMAGE:503545 5'
11288	24238		2.84	1.0E-111	AW374340.1	EST_HUMAN	U1H-BV10-act-407-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730276 3'
11383	24330	37859	2.08	1.0E-111	U681650.1	NT	LOC70031-221089-113-408 C10031 Homo sapiens cDNA
12168	25018	38518	4.71	1.0E-111	11417801	NT	Homo sapiens meningeal receptor (MPL) gene, exons 1,2,3,4,5 and 6
12355	18298	31180	1.75	1.0E-111	AB035556.1	NT	Homo sapiens mRNA for neurodin-1 alpha protein, complete cds
810	13875	26590	0.9	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
812	13877	26592	5.51	1.0E-112	U29103.1	NT	Homo sapiens sterologenic acute regulatory protein (SAR) gene, exon 5
812	13877	26593	5.51	1.0E-112	U29103.1	NT	Homo sapiens sterologenic acute regulatory protein (SAR) gene, exon 5
833	13698	26618	1.01	1.0E-112	BF500039.1	EST_HUMAN	U1H-B14-act-9-04-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
833	13698	26619	1.91	1.0E-112	BF500039.1	EST_HUMAN	U1H-B14-act-9-04-Q-UJ.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1003	14054	27008	1.21	1.0E-112	AF157823.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1063	14109	27058	1.85	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1692	14722	27703	3.1	1.0E-112	7652125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1692	14722	27704	3.1	1.0E-112	7652125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2207	16222	28242	1.08	1.0E-112	AF166925.1	EST_HUMAN	w50908.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400611 3'
2516	16518	28541	1.34	1.0E-112	BE686850.1	EST_HUMAN	501442674.F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848988 5'
3094	16152		3.53	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3371	16421	28346	1.07	1.0E-112	AB28551.1	EST_HUMAN	w44512.x1 NCL_CGAP_P222 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb.M81650_rna1
3688	16938	28649	0.69	1.0E-112	BE076073.1	EST_HUMAN	SEMOCELIN 1, PROTEIN PRECURSOR (HUMAN);
4634	17655	30542	0.76	1.0E-112	4504116	NT	W2-210360-060300-113-409 BT0580 Homo sapiens cDNA
4784	17803	30694	5.01	1.0E-112	AB037632.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4784	17803	30695	5.01	1.0E-112	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5750	18844	32027	38.43	1.0E-112	U48046.1	EST_HUMAN	y95507.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273229 5'
6195	18269	32504	1.28	1.0E-112	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6298	18341	32573	0.89	1.0E-112	AW502437.1	EST_HUMAN	U1HF-BR0P-els-9-06-Q-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075659 5'
6378	19446	32587	0.9	1.0E-112	BE741686.1	EST_HUMAN	U1HF-BR0P-els-9-06-Q-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075659 5'
6603	19932	32935	0.83	1.0E-112	BF972815.1	EST_HUMAN	801594717.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6792	16848	33130	0.74	1.0E-112	BE273103.1	EST_HUMAN	802162540.F1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:4293420 5'
							801142755.F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:306908 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6762	18646	33131	0.74	1.0E-112	BE273103.1	EST_HUMAN	501142755F1 NIH_MGC.14 Homo sapiens cDNA clone IMAGE:3506508 5'
7018	20144	33461	1.23	1.0E-112	BF574235.1	EST_HUMAN	502131405F1 NIH_MGC.81 Homo sapiens cDNA clone IMAGE:4270921 5'
7382	20332	33682	0.66	1.0E-112	AL043269.1	EST_HUMAN	DKFZP434M0523.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434M0523 5'
7559	20522	33879	1.62	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7659	20522	33880	1.62	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8535	21503	34921	1.93	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEIMBA1002773 5'
9509	22274	35705	2.56	1.0E-112	BE867635.1	EST_HUMAN	501443151F1 NIH_MGC.95 Homo sapiens cDNA clone IMAGE:3847285 5'
9509	22274	35705	2.56	1.0E-112	BE867635.1	EST_HUMAN	501443151F1 NIH_MGC.95 Homo sapiens cDNA clone IMAGE:3847285 5'
10293	23176	36065	2.18	1.0E-112	BF111413.1	EST_HUMAN	730g07.x1 Scora_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
11132	24092	37621	2.93	1.0E-112	AW953327.1	EST_HUMAN	TR:Q9VW35 Q9VW35 CB8743 PROTEIN. ;
11265	24245	37772	2.35	1.0E-112	AJ246001.1	NT	MR3-SN0009-100400-103-572 SN0009 Homo sapiens cDNA
11433	24371	37917	1.7	1.0E-112	BE280478.1	EST_HUMAN	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11518	24459	38009	3.38	1.0E-112	AW377870.1	EST_HUMAN	PMO-CT0237-141059-001-402 CT0237 Homo sapiens cDNA
12095	24966	39593	0.59	1.0E-112	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa I)
744	13505	26744	5.37	1.0E-113	AI365586.1	EST_HUMAN	aa56101.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
744	13505	26745	5.37	1.0E-113	AI365586.1	EST_HUMAN	aa56101.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
941	13384	26946	5.76	1.0E-113	M11985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1543	1476	27648	3.01	1.0E-113	AI365586.1	EST_HUMAN	aa56101.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953825 3'
1953	15821	27980	1.26	1.0E-113	AF240775.1	NT	Homo sapiens cDNA clone IMAGE:3872636 3'
2103	15123	28143	0.99	1.0E-113	BF515218.1	EST_HUMAN	U1-H.BW1-antF-03-0-U1 s1 NCI CGAP_Su57 Homo sapiens cDNA clone IMAGE:3882878 3'
3147	18204	28118	1.16	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5316	25748		1.54	1.0E-113	BE780858.1	EST_HUMAN	501469465F1 NIH_MGC.87 Homo sapiens cDNA clone IMAGE:3872636 5'
5570	18687	31628	6.68	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5918	19002	32103	0.54	1.0E-113	BE789172.1	EST_HUMAN	501476266F1 NIH_MGC.98 Homo sapiens cDNA clone IMAGE:3879406 5'
5916	19002	32104	0.54	1.0E-113	BE789172.1	EST_HUMAN	501476266F1 NIH_MGC.98 Homo sapiens cDNA clone IMAGE:3879406 5'
6031	19114	32317	4.18	1.0E-113	AU140261.1	EST_HUMAN	AU140261 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6081	19142	32354	0.97	1.0E-113	AF016635.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6188	19293	32499	2.42	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polysaccharide N-acetylglucosaminyltransferase 8 (GALNT8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6280	19352	32557	0.62	1.0E-113	6961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6280	19352	32558	0.62	1.0E-113	6961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6449	19514	32764	0.89	1.0E-113	6005002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6449	19514	32765	0.89	1.0E-113	6005002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7543	20506	33865	0.72	1.0E-113	BE262161.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7543	20506	33866	0.72	1.0E-113	BE262161.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
9450	22414	35580	2.83	1.0E-113	BE382842.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3627554 5'
9450	22414	35581	2.83	1.0E-113	BE382842.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3627554 5'
9756	22697	37556	0.67	1.0E-113	BE772597.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3627554 5'
10190	23115	36559	1.3	1.0E-113	11429367	NT	RC1-F10134-280600-021-002 F10134 Homo sapiens cDNA
10280	23215	36559	0.73	1.0E-113	M21535.1	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10410	23332	36817	0.77	1.0E-113	5453907	NT	Homo sapiens protein (est-related gene) mRNA, complete cds
10410	23332	36818	0.77	1.0E-113	5453907	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11457	24400	37948	1.61	1.0E-113	AW500319.1	EST_HUMAN	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11468	24409	37956	3	1.0E-113	AW500281.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3077328 5'
11468	24409	37957	3	1.0E-113	AW500281.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3077328 5'
11592	24530	38087	2.84	1.0E-113	BE292688.1	EST_HUMAN	h81608.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR-O60327 O60327 KIAA0564 PROTEIN;
11826	24709	38292	3.1	1.0E-113	AA580720.1	EST_HUMAN	h81608.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR-O60327 O60327 KIAA0564 PROTEIN;
11826	24709	38293	3.1	1.0E-113	AA580720.1	EST_HUMAN	h81608.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR-O60327 O60327 KIAA0564 PROTEIN;
60	13179	26092	0.65	1.0E-114	Y17151.2	NT	801105529FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988366 5'
60	13179	26093	0.65	1.0E-114	Y17151.2	NT	801105529FT NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988366 5'
60	13179	26094	0.65	1.0E-114	Y17151.2	NT	P93748 FLAP ENDONUCLEASE-1;
60	13179	26094	0.65	1.0E-114	Y17151.2	NT	P93748 FLAP ENDONUCLEASE-1;
646	13712	26634	5.97	1.0E-114	T07551.1	EST_HUMAN	nc000033.1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:297069 5' similar to SW-FEN1_HUMAN
1072	14117	27069	1.78	1.0E-114	8923037	NT	P93748 FLAP ENDONUCLEASE-1;
1376	14351	27319	1.79	1.0E-114	7657526	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
1348	14680	27653	1.79	1.0E-114	6931094	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
646	13712	26634	5.97	1.0E-114	T07551.1	EST_HUMAN	y415601.s1 Scores fetal liver spleen N1FSL Homo sapiens cDNA clone IMAGE:108288 3' similar to gbA21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN) contains A1u repetitive element;
1072	14117	27069	1.78	1.0E-114	8923037	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1 (HGPRT), mRNA
1376	14351	27319	1.79	1.0E-114	7657526	NT	Homo sapiens fibroblast tumor deletion region protein 1 (RTDR1), mRNA
1348	14680	27653	1.79	1.0E-114	6931094	NT	Homo sapiens mitochondriome maintenance deficient (S. cerevisiae) 3 (MOM3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1681	14713	27691	5.92	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
3148	16205	29119	2.81	1.0E-114	XO4088.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3187	16242	29160	1.28	1.0E-114	BF206374.1	EST_HUMAN	601865932F NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4100214 5'
4044	17082	29890	1.26	1.0E-114	AF149773.1	NT	Homo sapiens NOP1 protein (NOP1) gene, exons 1, 2, and 3
4417	17444	30335	0.78	1.0E-114	J03171.1	NT	Human Interferon-alpha receptor (hIFN-alpha-R) mRNA, complete cds
5228	18236	31110	0.99	1.0E-114	AA194468.1	EST_HUMAN	z0505r11 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:628832 5' similar to contains MER22 3' MER22 repetitive element
5474	18875	31483	1.47	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5474	18875	31484	1.47	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5976	18771	31843	1	1.0E-114	8257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
6354	19423	32686	0.51	1.0E-114	Z26283.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 20
7191	18422	31224	0.54	1.0E-114	4759163	NT	Homo sapiens speractinectin, cwc9 and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
7280	20014		1.01	1.0E-114	AB041533.1	NT	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds
7460	20416	33770	1.08	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARG1 Homo sapiens cDNA clone OVARC1001444 5'
7460	20416	33771	1.08	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARG1 Homo sapiens cDNA clone OVARC1001444 5'
7489	20464	33824	5.65	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7489	20464	33825	5.65	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8223	21192	34600	1.87	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8507	21475	34888	1.95	1.0E-114	AJ363139.1	EST_HUMAN	qy68005.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8607	21475	34889	1.95	1.0E-114	AJ363139.1	EST_HUMAN	qy68005.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
9048	22015	35499	3.38	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD58 mRNA, complete cds
9119	22085	35514	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9119	22085	35515	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9353	22318	35744	0.42	1.0E-114	AB046784.1	NT	Homo sapiens mRNA for KIAA1564 protein, partial cds
9537	22500	35948	0.61	1.0E-114	BF106832.1	EST_HUMAN	X69412.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:352847 3' similar to
9769	22710		14.09	1.0E-114	AW327455.1	EST_HUMAN	TRQ8UH6 Q8UH6 TRANSMEMBRANE PROTEIN 2 ;
9818	21140	34546	3.34	1.0E-114	AF077754.1	NT	q03050.x1 NIH_MGC 2 Homo sapiens cDNA clone IMAGE:2848744 5'
9906	22858		1.15	1.0E-114	M13536.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
10498	23420	36919	0.95	1.0E-114	BE370004.1	EST_HUMAN	Human caruloplasmin mRNA
10522	23444	36942	1.42	1.0E-114	AB169227.2	NT	801449752F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3853500 5'
							Homo sapiens chromosome 21 segment HS21C027

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10607	23827	37340	0.87	1.0E-114	BE171984.1	EST_HUMAN	MRO-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
11140	24100						baf3g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906088 5' similar to gb-X17208 40S
11524	24465	38018	15.04	1.0E-114	BE302668.1	EST_HUMAN	RIBOSOMAL_PROTEIN_S4 (HUMAN); gp-M20832 Mouse LLRcp3 protein mRNA from a repetitive element, complete (MOUSE).
11524	24465	38019	3.01	1.0E-114	AU733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cDABA08 5'
12819	25674		2.9	1.0E-114	11418041.NT	EST_HUMAN	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12859	25464	31725	3.55	1.0E-114	11034950.NT	NT	Homo sapiens hypothetical protein QJ1042K10.2), mRNA
12859	25464	31726	3.55	1.0E-114	11034950.NT	NT	Homo sapiens hypothetical protein QJ1042K10.2), mRNA
24	13144	28044	2.83	1.0E-115	4795811.NT	NT	Homo sapiens HLA-B associated transcript1 (DG581E) mRNA
130	13235	29165	2.37	1.0E-115	4505938.NT	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
134	13236		3.36	1.0E-115	4557887.NT	NT	Homo sapiens keratin 18 (KT18) mRNA
292	13366	28313	5.22	1.0E-115	AW804759.1	EST_HUMAN	OVA-LIM0094-300300-156-308 UM0094 Homo sapiens cDNA
537	13608	26526	1.12	1.0E-115	AI339206.1	EST_HUMAN	q0601.x1 NC1_GCAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR-O00536 O00536 TF1-INTERACTING PEPTIDE 5;
537	13608	26527	1.12	1.0E-115	AI339206.1	EST_HUMAN	q0601.x1 NC1_GCAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR-O00536 O00536 TF1-INTERACTING PEPTIDE 6;
787	13846	26762	0.78	1.0E-115	5174702.NT	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
787	13846	26763	0.78	1.0E-115	5174702.NT	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
789	13848	26765	66.69	1.0E-115	4503764.NT	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1561	14593	27566	1.46	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoacidate semialdehyde synthase mRNA, complete cds
1561	14593	27567	1.46	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoacidate semialdehyde synthase mRNA, complete cds
1559	14894	27691	1.24	1.0E-115	U76027.1	NT	Homo sapiens Bruten's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTF3 (FTF3) genes, complete cds
2693	15923		1.7	1.0E-115	AW804759.1	EST_HUMAN	OVA-LIM0094-300300-156-308 UM0094 Homo sapiens cDNA
3132	16189	28009	2.74	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3132	16189	28100	2.74	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3468	16532	29457	2.07	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4072	17108	30002	4.75	1.0E-115	AB020348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4255	17324	30294	0.86	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4429	17466	30347	3.89	1.0E-115	6912669.NT	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4465	17491	30378	3.73	1.0E-115	4758279.NT	NT	Homo sapiens EphA4 (EPHA4) mRNA
4702	17723	30816	2.63	1.0E-115	AL068957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4702	17723	30817	2.63	1.0E-115	AL068957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4943	17859	30949	2.57	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C098
4943	17859	30950	2.57	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C098
5420	18523	31401	0.81	1.0E-115	AW070335.1	EST_HUMAN	EST382416 IMAGE resequencing, MAGK Homo sapiens cDNA
5498	18598	31610	1.06	1.0E-115	BF665397.1	EST_HUMAN	602119346F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276738 5'
5920	18716	31875	1.68	1.0E-115	11425728	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) [LOC83433], mRNA
5920	18716	31876	1.68	1.0E-115	11425728	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) [LOC83433], mRNA
5775	18887	32049	1.1	1.0E-115	AI928769.1	EST_HUMAN	au84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519598 3' similar to gbl.07807
5775	18887	32050	1.1	1.0E-115	AI928769.1	EST_HUMAN	au84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519598 3' similar to gbl.07807
5391	19459	32704	0.68	1.0E-115	11428786	NT	DYNAMIN-1 (HUMAN); Homo sapiens sperm surface protein (HSS), mRNA
6391	19459	32705	0.68	1.0E-115	11428786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6335	19598	32891	18.47	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) [LOC63436], mRNA
6678	19735	33010	1.82	1.0E-115	7681883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
6678	19735	33011	1.82	1.0E-115	7681883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
7120	20054	33358	0.57	1.0E-115	T89774.1	EST_HUMAN	y88b08.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP-DPOG_YEAST P15601 DNA POLYMERASE GAMMA;
7493	20456	33816	1.22	1.0E-115	AI076598.1	EST_HUMAN	0231a03.x1 Scores total fetus N62HF8, 9w Homo sapiens cDNA clone IMAGE:1676914 3'
7493	20456	33817	1.22	1.0E-115	AI076598.1	EST_HUMAN	0231a03.x1 Scores total fetus N62HF8, 9w Homo sapiens cDNA clone IMAGE:1676914 3'
7638	20566	33962	7.12	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0695 protein, partial cds
8500	21466	34984	11.55	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8500	21468	34885	11.55	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8164	22130	35567	4.68	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
10133	23059	36536	0.64	1.0E-115	BF392029.1	EST_HUMAN	018181652F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050108 5'
10358	23282	36768	1.74	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10358	23282	36769	1.74	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10887	23807	37312	1.02	1.0E-115	AI221878.1	EST_HUMAN	q989w09.x1 Scores NFE1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10887	23807	37313	1.02	1.0E-115	AI221878.1	EST_HUMAN	q989w09.x1 Scores NFE1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10887	23807	37313	1.02	1.0E-115	AI221878.1	EST_HUMAN	q989w09.x1 Scores NFE1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10894	23814	37321	0.7	1.0E-115	AI524687.1	EST_HUMAN	ht12a07.x1 NCI_CGAP_GLLT Homo sapiens cDNA clone IMAGE:2118036 3' similar to TR-O18129 016129 PHENYLALANIN TRNA SYNTHETASE;
10520	23840	37356	0.73	1.0E-115	BE886295.1	EST_HUMAN	601509879F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3611610 5'
11072	24034	37558	3.4	1.0E-115	AW571644.1	EST_HUMAN	x932a03.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW-CAYP_CANFA P10463 CALYPTOSINE;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11589	24527	38083	2.1	1.0E-115	BE045890.1	EST_HUMAN	h944c10.x1 NCI_CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O68378 O68378
11589	24527	38084	2.1	1.0E-115	BE045890.1	EST_HUMAN	h944c10.x1 NCI_CGAP_Par3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O68378 O68378
11728	24512	38188	2.06	1.0E-115	4502528	NT	PRP4 PROTEIN KINASE HOMOLOG ; Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
12191	25036		1.52	1.0E-115	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
574	13943	26557	1.02	1.0E-116	BE275502.1	EST_HUMAN	601121347.F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2988975 5'
801	13960	26807	2.44	1.0E-116	4507334	NT	Homo sapiens synaptophysin 1 (SYNJ1) mRNA
860	13918		0.86	1.0E-116	4507334	NT	Homo sapiens synaptophysin 1 (SYNJ1) mRNA
2013	15034	28044	2.89	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2013	15034	28045	2.89	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2316	15327	28350	1.88	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2348	15357		1.88	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-401 (OR17-401) pseudogenes, complete cds
2482	15466	28489	2.99	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0760 protein, partial cds
2744	15629	28754	3.32	1.0E-116	BE889256.1	EST_HUMAN	601513337.F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3914900 5'
3180	16235		0.95	1.0E-116	T07515.1	EST_HUMAN	EST04005 Fetal brain, Stratagene (cell636206) Homo sapiens cDNA clone HFBK28 similar to EST containing L1 repeat
3189	16244	29161	5.44	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3189	16244	29162	5.44	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4405	17433	30318	2.36	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4892	17009	30798	2.03	1.0E-116	A1907088.1	EST_HUMAN	PM-BT135-07068-016 BT135 Homo sapiens cDNA
5230	18238	31111	0.92	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5351	18466	31328	0.92	1.0E-116	A1302062.1	EST_HUMAN	q118004.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1898595 3' similar to contains element MER25 repetitive element ;
6080	19169	32384	2.18	1.0E-116	W42822.1	EST_HUMAN	zc3d407.r1 Soares, senescent, fibroblasts, NB-HSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6336	19405	32845	1.8	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6336	19405	32846	1.8	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6408	19476	32723	0.95	1.0E-116	BE408037.1	EST_HUMAN	601302281.F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3636764 5'
6849	19707	32882	0.73	1.0E-116	5729867	NT	Homo sapiens head domain and RLD 2 (HERC2), mRNA
6849	19707	32883	0.73	1.0E-116	5729867	NT	Homo sapiens head domain and RLD 2 (HERC2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6863	19720		2.08	1.0E-116	BE168133.1	EST_HUMAN	MR2-HT0376-210200-102-604 HT0379 Homo sapiens cDNA
7130	20106	33417	1.59	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NH00567
7410	20377	33728	7.19	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCE Homo sapiens cDNA clone DCBBG306 5'
8712	21680	35106	1.32	1.0E-116	AA354256.1	EST_HUMAN	EST162685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8712	21680	35107	1.32	1.0E-116	AA354256.1	EST_HUMAN	EST162685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
8824	21781	35213	1.04	1.0E-116	AI004151.1	EST_HUMAN	CM-BT043-060298-075 BT043 Homo sapiens cDNA
9290	22256	35688	1.39	1.0E-116	BE665507.1	EST_HUMAN	q00392368F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
9455	22419	35857	2.8	1.0E-116	AJ216352.1	EST_HUMAN	q00605.X1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to p0X53741_mnet FIBULIN-1, ISOFORM A, PRECURSOR (HUMAN);
10033	22960	36428	1.48	1.0E-116	11418948	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
10633	23555	37055	0.71	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10633	23555	37056	0.71	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10713	23635	37128	0.91	1.0E-116	BE168873.1	EST_HUMAN	QV4-HT0401-281268-063-c09 HT0401 Homo sapiens cDNA
11046	24010	37536	2.44	1.0E-116	BF33849.1	EST_HUMAN	CM2-CT0482-300600-349-c06 CT0482 Homo sapiens cDNA
11470	24413	37692	2.63	1.0E-116	AI387140.1	EST_HUMAN	qq41604.X1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1835102 3' similar to WP180495.7
12804	25940		1.95	1.0E-116	AL134889.1	EST_HUMAN	CE01765 ;
550	13530	26547	1.04	1.0E-117	48268326	NT	DKFZp782L1110_11 762 (synonym: hma2) Homo sapiens cDNA clone DKFZp782L1110 5'
1078	15858	27078	0.88	1.0E-117	AF124393.1	NT	Homo sapiens acyl-CoA:Coenzyme A carboxylase alpha (ACACA), mRNA
1229	14267	27224	2.2	1.0E-117	AF264750.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1) gene, exons 13a through 15
1848	14874	27670	2.04	1.0E-117	M19816.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2221	15235	28250	1.38	1.0E-117	AW057699.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
3281	16335	29255	1.51	1.0E-117	AA978114.1	EST_HUMAN	EST1389769 IMAGE resequences, IMAGE Homo sapiens cDNA
4016	17055	29598	5.88	1.0E-117	AA316723.1	EST_HUMAN	cp32611.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4371	17368	30278	2.1	1.0E-117	85509564	NT	EST108414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4808	17929	30521	1.95	1.0E-117	AL042120.1	EST_HUMAN	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4755	17775	30670	1.18	1.0E-117	X88670.1	NT	DKFZp434G1120_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G1120 5'
4765	17775	30671	1.18	1.0E-117	X88670.1	NT	H sapiens mRNA for TPCR16 protein
4847	17864	30757	10.31	1.0E-117	AF134304.2	NT	H sapiens mRNA for TPCR16 protein
4847	17864	30758	10.31	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4977	17592	30881	4.01	1.0E-117	AB020673.1	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5421	18524	31402	3.29	1.0E-117	BE730508.1	EST_HUMAN	Homo sapiens mRNA for KIAA0868 protein, complete cds
7148	18380	31269	0.93	1.0E-117	AA323348.1	EST_HUMAN	601626557F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3632214 5'
							EST126111 Cerebellum II Homo sapiens cDNA 5' end similar to zinc finger domain

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7683	20841	34004	4.55	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7683	20841	34005	4.55	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7785	20747	34121	3.71	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DGB Homo sapiens cDNA clone DCBBAE01 5'
7785	20747	34122	3.71	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DGB Homo sapiens cDNA clone DCBBAE01 5'
8311	21280	34691	3.78	1.0E-117	AI805415.1	EST_HUMAN	wp8607.1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468829 3' similar to TR:075065
8954	21622	35042	1.01	1.0E-117	10834689	NT	Q75065 KIAA0477 PROTEIN ;
8954	21622	35043	1.01	1.0E-117	10834689	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8754	21722	35144	0.63	1.0E-117	AI804151.1	EST_HUMAN	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8754	21722	35145	0.63	1.0E-117	AI804151.1	EST_HUMAN	CU-B7043-060288-075 BT043 Homo sapiens cDNA
8654	22597	35046	1.61	1.0E-117	D16524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
10145	23071	36546	1.71	1.0E-117	BE733922.1	EST_HUMAN	CU-B7043-060288-075 BT043 Homo sapiens cDNA
10306	25701	36713	0.64	1.0E-117	AF090333.1	EST_HUMAN	601569317FT NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843749 5'
10324	23854	37370	1.98	1.0E-117	11420222	NT	Homo sapiens Drosophila Katch like protein (DKELGHL), mRNA
11207	24161	37691	2.17	1.0E-117	D63778.1	NT	Human mRNA for KIAA0191 gene, partial cds
11375	24322	37850	1.96	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11375	24322	37851	1.96	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11804	24542	38101	2.72	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11804	24542	38102	2.72	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11722	24608	38393	34.45	1.0E-117	BE269855.1	EST_HUMAN	601168035FT NIH_MGC 3 Homo sapiens cDNA clone IMAGE:3544298 5'
11921	24802	38394	1.76	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCT), member 3 (ABCA3), mRNA
11921	24802	38394	1.76	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCT), member 3 (ABCA3), mRNA
12429	25911		1.39	1.0E-117	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
71	13189	26109	2.9	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
65	13211	26136	1.27	1.0E-118	AL049854.1	EST_HUMAN	DKFZp334J056 J1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp334J056 5'
518	13569	26509	4.46	1.0E-118	7657016	NT	Homo sapiens hypophthalmic protein (DJ328E19 C1.1), mRNA
915	15854	25923	1.66	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2242	16258	26280	1.93	1.0E-118	BE369705.1	EST_HUMAN	801281947FT NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5'
2242	16258	26281	1.93	1.0E-118	BE369705.1	EST_HUMAN	801281947FT NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5'
2242	15256	26282	1.93	1.0E-118	BE369705.1	EST_HUMAN	801281947FT NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3604019 5'
2337	15348		1.55	1.0E-118	AW951729.1	EST_HUMAN	EST1363769 IMAGE resequences, MAGB Homo sapiens cDNA
2750	15743	28760	2.48	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2750	15743	28761	2.48	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3121	16178		3.87	1.0E-118	Y19322.1	NT	Homo sapiens PRKY exon 7
3210	16285	28187	4.81	1.0E-118	A1347694.1	EST_HUMAN	gq0105.x1 NCI CGAP K65 Homo sapiens cDNA clone IMAGE:1916789 3'
3210	16285	28188	4.81	1.0E-118	A1347694.1	EST_HUMAN	gq0105.x1 NCI CGAP K65 Homo sapiens cDNA clone IMAGE:1916789 3'
3970	17010	25924	0.98	1.0E-118	AB024489.1	NT	Pango pyruvate DNA, similar to pol gene of HERSV-W and MSRV, isolate:ORW3-3
4116	17149	30041	5.07	1.0E-118	D233650.1	NT	Human mRNA for ribosomal protein, complete cds
5497	18597	31908	1.86	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5497	18597	31909	1.86	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5713	18607	31584	0.60	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5713	18607	31585	0.66	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5900	18692	32074	0.58	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5900	18692	32075	0.58	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5965	18954	32141	1.44	1.0E-118	M35102.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5965	18954	32141	1.44	1.0E-118	M35102.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
5962	19047	32247	0.95	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
5962	19047	32248	0.95	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6053	19134	32343	1.81	1.0E-118	11420784	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6849	19802	33166	1.79	1.0E-118	4657732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6849	19802	33167	1.79	1.0E-118	4657732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7304	20276	33611	1.07	1.0E-118	AL043781.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O0127 5'
7304	20276	33612	1.07	1.0E-118	AL043781.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O0127 5'
7658	20903	34179	6.13	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7872	20816	34184	0.72	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
8305	21274	34685	2.41	1.0E-118	BE781223.1	EST_HUMAN	801489159F1 NIH_MGC 87 Homo sapiens cDNA clone IMAGE:3872247 5'
8726	21694	35119	7.01	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-H03 BT0263 Homo sapiens cDNA
8726	21694	35120	7.01	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-H03 BT0263 Homo sapiens cDNA
8732	21700	35125	1.39	1.0E-118	AA443024.1	EST_HUMAN	2x98007.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8732	21700	35126	1.39	1.0E-118	AA443024.1	EST_HUMAN	2x98007.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811789 5'
9021	21987	35408	1.02	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
9021	21987	35409	1.02	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
9071	22037	35460	1.32	1.0E-118	4657732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9071	22037	35461	1.32	1.0E-118	4657732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9390	22355	35786	5.12	1.0E-118	BE263134.1	EST_HUMAN	80114493F2 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3160502 5'
9421	22396	35825	0.53	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586K1824
9931	23878	36541	2.29	1.0E-118	7657018	NT	Homo sapiens hypothetical protein (D3528E19.G1.1), mRNA
10598	23620	37115	0.46	1.0E-118	BE736213.1	EST_HUMAN	801307146F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3641603 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10598	23620	37116	0.48	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10741	23663	37158	2.31	1.0E-118	BF195407.1	EST_HUMAN	7n17609.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW_ZP3A_HUMAN
10599	23819	37328	0.54	1.0E-118	AW286351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ; UHR-BW0-alc-a-07-Q.U1st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2729772 3'
11807	24545	38108	8.48	1.0E-118	AA315007.1	EST_HUMAN	EST118614 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to cymeth, light chain 1, cytoplasmic
11884	24766	38331	1.9	1.0E-118	BE006676.1	EST_HUMAN	601489514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11884	24765	38332	1.9	1.0E-118	BE006676.1	EST_HUMAN	601489514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11887	24768	38335	1.51	1.0E-118	BF036687.1	EST_HUMAN	QVQ-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
11887	24768	38336	1.51	1.0E-118	BF036687.1	EST_HUMAN	QVQ-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
12036	24911	1038	1.58	1.0E-118	6325465.NT	NT	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA
10338	19557	27034	1.75	1.0E-119	7705607.NT	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1050	14873	27072	2.88	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
3119	16178	22097	0.93	1.0E-119	8822205.NT	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3254	16308		0.68	1.0E-119	AA916760.1	EST_HUMAN	CE01214 ;
3875	17015	29929	1.12	1.0E-119	4504116.NT	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5410	18513	31391	2.79	1.0E-119	AU133369.1	EST_HUMAN	AU133369 NT28P4 Homo sapiens cDNA clone NT28P4001881 5'
5423	18528	31404	14.88	1.0E-119	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5428	18631	31411	2.88	1.0E-119	BE5936121.1	EST_HUMAN	RC1-NN0073-280800-078-g08 NN0073 Homo sapiens cDNA
5508	18638	31538	1.55	1.0E-118	AV693731	EST_HUMAN	AV693731 GKGC Homo sapiens cDNA clone GKCDH803 5'
5671	18766	31937	0.68	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: tme12) Homo sapiens cDNA clone DKFZp762M0710 5'
5671	18766	31938	0.68	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_r1 762 (synonym: tme12) Homo sapiens cDNA clone DKFZp762M0710 5'
6290	19323	32553	7.38	1.0E-119	AI150703.1	EST_HUMAN	qb77609.x1 Soares_fetal_heart_NHHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW_KTCJ_MOUSE P02535 KERATIN, TYPE I (CYTOSKELETAL 10 ;
8415	19483	32730	0.69	1.0E-119	AF315693.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
8415	19483	32731	0.69	1.0E-119	AF315693.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
8468	19500	32778	1	1.0E-119	AI478732.1	EST_HUMAN	In23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
8604	19683	32836	2.67	1.0E-119	X06292.1	NT	Human c-fos-like proto-oncogene
6919	19974	32932	4.98	1.0E-119	AW974183.1	EST_HUMAN	EST386268 MAGC resequences, MAGM Homo sapiens cDNA
7540	20620	33994	1.3	1.0E-119	BE786614.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945081 5'
9009	21975	35356	1.15	1.0E-119	BE16150.1	EST_HUMAN	601280584F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622828 5'
10113	23039	36618	0.5	1.0E-119	11645821.NT	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
10287	23192	36678	1.1	1.0E-119	11036943.NT	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10508	23530	37025	5.31	1.0E-119	AA465124.1	EST_HUMAN	aa3205.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814077 5'
10870	23760	37280	37280	1.12	1.0E-119	AJ297701.1	NT
10871	23831	37344	1.73	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10871	23831	37346	0.73	1.0E-119	11428837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10885	23905	37419	0.78	1.0E-119	AB032261.1	NT	Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds
11394	24340	37870	1.88	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11394	24340	37871	1.86	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11835	24476		13.43	1.0E-119	BF565671.1	EST_HUMAN	602160072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
12486	25001		3.21	1.0E-119	AW847519.1	EST_HUMAN	RC3-C10212-240399-011-003_C10212 Homo sapiens cDNA
301	13395	26522	0.99	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1042	14088	27040	1.6	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1042	14088	27041	1.6	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1422	14455	27426	2.56	1.0E-120	N44873.1	EST_HUMAN	xy40g12.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273765 5'
1605	14637	27614	2.5	1.0E-120	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1823	14850	27844	1.4	1.0E-120	4557280	NT	Homo sapiens aequorin 4 (AQP4), splice variant b, mRNA
2534	15537	28558	1.08	1.0E-120	4755124	NT	Homo sapiens aequorin 1 (SYNJ1), mRNA
3318	13395	26522	1.34	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4385	17413	30287	1.81	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4385	17413	30288	1.81	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4691	17712	30806	2.87	1.0E-120	AF059463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4691	17712	30807	2.87	1.0E-120	AF059463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5825	18915	32068	13.85	1.0E-120	BF568222.1	EST_HUMAN	602163994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5825	18915	32069	13.85	1.0E-120	BF568222.1	EST_HUMAN	602163994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6583	18943	32910	0.63	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
6583	18943	32911	0.63	1.0E-120	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exons 6 and 7
7823	20771	34147	1.84	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8228	21195	34602	1.78	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8228	21195	34603	1.78	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8676	21643	35068	2.82	1.0E-120	BF337599.1	EST_HUMAN	602035532F1 NCI CGAP_Brm54 Homo sapiens cDNA clone IMAGE:4183333 5'
8747	21715	35139	0.75	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8747	21715	35139	0.75	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8761	21719	35141	2.6	1.0E-120	AB007654.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8761	21719	35142	2.5	1.0E-120	AB007654.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8796	21763	35185	1.13	1.0E-120	AB007634.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9859	22795	36247	4.14	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9859	22795	36248	4.14	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
10102	23028	36249	3.99	1.0E-120	BF300541.1	EST_HUMAN	60188959F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
10118	23044	36524	7.33	1.0E-120	AU133205.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone NT2RP4001541 5'
10135	23051	36539	0.67	1.0E-120	AL048901.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10252	23177		0.51	1.0E-120	AB04151.1	EST_HUMAN	GM-BT043-06029-078 BT043 Homo sapiens cDNA
10436	23358	36846	3.02	1.0E-120	AB028000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11461	24404	37952	19.45	1.0E-120	BE299397.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11672	24638	38216	2.5	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11672	24638	38217	2.3	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11663	24842	38436	2.23	1.0E-120	U64774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
12632	25318	31785	1.45	1.0E-120	11417662	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
74	13191	26113	0.97	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
378	13462	26592	1.62	1.0E-121	AU134663.1	EST_HUMAN	AU134663 PLACE1 Homo sapiens cDNA clone PLACE100869 5'
725	15948	28721	1.83	1.0E-121	5032162	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1983	15004	28007	1.17	1.0E-121	4756139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (NIPP4A), splice variant a, mRNA
1983	15004	28008	1.17	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (NIPP4A), splice variant a, mRNA
2112	15129	28149	1.36	1.0E-121	L76631.1	NT	Homo sapiens melastatin-like receptor 1 beta (MLUR1beta) mRNA, complete cds
2980	16038	28961	1.69	1.0E-121	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds, and unknown genes
3097	16154	29067	3.41	1.0E-121	Y19203.1	NT	Homo sapiens HH33 gene for hair keratin, exons 1 to 9
3097	16154	29068	3.41	1.0E-121	Y19203.1	NT	Homo sapiens HH33 gene for hair keratin, exons 1 to 9
3547	16593	29518	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3547	16593	29519	0.84	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3690	16733	29846	8.83	1.0E-121	AF155156.2	NT	Homo sapiens epsilon subunit of protein complex AP-4 epsilon subunit mRNA, complete cds
4358	17365	30267	1.39	1.0E-121	AF263294.1	EST_HUMAN	qx571001.x1 NCI_OGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
5012	18026	30911	3.4	1.0E-121	X91837.1	NT	H sapiens ECE-1 gene (exon 17)
5162	18191	31067	0.93	1.0E-121	4607334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
5340	18445	31198	0.86	1.0E-121	BE22250.1	EST_HUMAN	Hu09008.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168119 3'
5641	18737	31901	0.96	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3304620 5'
7072	20094		0.7	1.0E-121	AL271736.1	NT	Homo sapiens Xq pseudocentromeric region, segment 2/2
7165	18397	31200	0.82	1.0E-121	AW689068.1	EST_HUMAN	RC3-NN0066-270400-011-602 NN0066 Homo sapiens cDNA
7165	18397	31231	0.82	1.0E-121	AW689068.1	EST_HUMAN	RC3-NN0066-270400-011-602 NN0066 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8269	21238	34649	1.57	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8273	21242	34853	2.22	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8273	21242	34654	2.22	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10217	23142	36630	0.79	1.0E-121	AW58358.1	EST_HUMAN	h03g05.v1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA :
10217	23142	36631	0.79	1.0E-121	AW58358.1	EST_HUMAN	h03g05.v1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA :
11130	24090	37619	1.87	1.0E-121	11427768	NT	Homo sapiens COX11 (yeast) homologue, cytochrome c oxidase assembly protein (COX11), mRNA
11138	24096	37625	1.52	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E459 allele, complete cds
11316	24295	37763	3.61	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11340	24290	37615	3.42	1.0E-121	N58624.1	EST_HUMAN	W74001.3t Soares fetal liver spleen TNF-LS Homo sapiens cDNA clone IMAGE:248448 3'
11664	24600	38175	4.22	1.0E-121	AU119320.1	EST_HUMAN	AU119320 HEMBA1 Homo sapiens cDNA clone HEMBA1005636 5'
267	13363	26287	2.23	1.0E-122	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
336	13423	26347	3.36	1.0E-122	AF114488.1	NT	Homo sapiens intercedin short isoform (ITSN) mRNA, complete cds
358	13445	26372	2.1	1.0E-122	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
883	13938	26897	3.29	1.0E-122	AF114488.1	NT	Homo sapiens intercedin short isoform (ITSN) mRNA, complete cds
1224	14262	27219	16.65	1.0E-122	N20707.1	NT	Human leucine-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa I)
1702	14732	27714	1.02	1.0E-122	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1725	14755	27741	1.67	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1725	14755	27742	1.67	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1831	14858	27856	5.11	1.0E-122	BE960024.1	EST_HUMAN	801497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895359 5'
2489	15002	28528	8.16	1.0E-122	BF316170.1	EST_HUMAN	801898173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2489	15002	28529	8.16	1.0E-122	BF316170.1	EST_HUMAN	801898173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2851	15911	28834	0.91	1.0E-122	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4883	17900	30789	1.03	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA
5025	18039	31903	1.4	1.0E-122	AW504645.1	EST_HUMAN	U14H-BND-ala-03-0-UTR1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076948 5'
5943	18739	31904	1.31	1.0E-122	BE256039.1	EST_HUMAN	801113597F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6920	18739	31904	7.59	1.0E-122	BE256039.1	EST_HUMAN	801113597F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7422	20380	33740	0.6	1.0E-122	AA868571.1	EST_HUMAN	ak091008.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8135	21072	34471	0.51	1.0E-122	AA224250.1	EST_HUMAN	z15a03.r1 Stralagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINO CYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;
8135	21072	34472	0.51	1.0E-122	AA224250.1	EST_HUMAN	z15a03.r1 Stralagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:663436 5' similar to TR:G940370 G940370 1-AMINO CYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;
9148	22714	35539	0.56	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9383	22348	35780	1.17	1.0E-122	11424216	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
8878	22631	36086	0.78	1.0E-122	AJ359818.1	EST_HUMAN	q52h07.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1 ;
8878	22631	36087	0.78	1.0E-122	AJ359818.1	EST_HUMAN	q52h07.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1 ;
10483	23415	36913	0.77	1.0E-122	AL117294.1	NT	Novel human gene mapping to chromosome X, isoform of ddb1 (proto-oncogene)
11714	24677	38255	6.11	1.0E-122	AB024083.1	NT	Homo sapiens gene for B120, exon 10
12102	24973	36570	1.5	1.0E-122	11434816	NT	Homo sapiens thyroid hormone receptor interactor 11 (TRIP11), mRNA
12228	25053		5.83	1.0E-122	11418187	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase 1 (PIPK2B), mRNA
13107	14262	27219	3.03	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22-4) variable region (subgroup V kappa II)
769	13828	26772	1.18	1.0E-123	BF345274.1	EST_HUMAN	002018058FT NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
769	13828	26773	1.18	1.0E-123	BF345274.1	EST_HUMAN	002018058FT NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1015	14083	27014	5.55	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1024	14070	27021	2.2	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1243	14278	27241	5.25	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIPK2B) mRNA, and translated products
1243	14278	27242	5.25	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIPK2B) mRNA, and translated products
1449	14482	27459	83.95	1.0E-123	AJ388641.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2109	15126	28143	2.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2109	15126	28143	2.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2109	16128	28147	2.75	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
3264	15334	15334	3.14	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3264	16318	29239	1.52	1.0E-123	6912617	NT	Homo sapiens glutaminyl-peptidyl cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5522	18621	31555	1.58	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds
5522	18621	31559	1.58	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds
5691	18757	31925	1.31	1.0E-123	BE799746.1	EST_HUMAN	001591108FT NIH MGCC 7 Homo sapiens cDNA clone IMAGE:3945493 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6613	19671	32949	1.97	1.0E-123	AU18435.1	EST_HUMAN	AU18435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7196	20223	33554	0.83	1.0E-123	H63168.1	EST_HUMAN	Y68403.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14980 PROTEIN KINASE YAK1
7212	20235	33569	1.24	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7400	20368	33721	0.57	1.0E-123	U65268.1	NT	Human HBRVONIN-CAM precursor (HBRVONIN-CAM) gene, complete cds
7632	20592	33855	0.9	1.0E-123	11525533	NT	Homo sapiens heparan sulfate (glucosaminide) 3-O-sulfotransferase 2 (HSSST2), mRNA
7604	20847	34232	1.29	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7913	20895	34244	1.87	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509182 5'
8083	21020	34419	0.71	1.0E-123	N35841.1	EST_HUMAN	y689d11.1 Soares melanocyte 2NHHM Homo sapiens cDNA clone IMAGE:266917 5' similar to PIR:S46611
8083	21020	34419	0.71	1.0E-123	N35841.1	EST_HUMAN	S49611 protein kinase PkqA - Phycomyces blakesleeanus
8083	21020	34419	0.71	1.0E-123	N35841.1	EST_HUMAN	y689d11.1 Soares melanocyte 2NHHM Homo sapiens cDNA clone IMAGE:266917 5' similar to PIR:S46611
8248	21217	34628	0.5	1.0E-123	AU131881.1	EST_HUMAN	S49611 protein kinase PkqA - Phycomyces blakesleeanus
8248	21217	34627	0.5	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8880	21847		1.43	1.0E-123	AW371924.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8724	22752	36205	2.03	1.0E-123	AB007623.1	NT	RC4-BT0311-251169-012-407 BT0311 Homo sapiens cDNA
8863	22769	36233	31.72	1.0E-123	U09823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10370	22893		0.44	1.0E-123	4504808	NT	Oryzolepis cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
12029	24905	39489	5.3	1.0E-123	BF677292.1	EST_HUMAN	Homo sapiens jerky (mouse) homolog-like (JRLK), mRNA
12029	24905	39500	5.3	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
268	13364	25288	1.18	1.0E-124	4507500	NT	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
268	13364	25289	1.18	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
274	13370		0.78	1.0E-124	D87676.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
486	13559	26465	2.11	1.0E-124	AL163246.2	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
692	13754	26963	8.04	1.0E-124	AA397551.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210046
692	13754	26964	8.04	1.0E-124	AA397551.1	EST_HUMAN	z81b04.11 Striatum schizo brain S11 Homo sapiens cDNA clone IMAGE:728716 5' similar to TR:G300482
759	13818	28763	6.08	1.0E-124	AF155954.1	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)
809	13967	28916	1.34	1.0E-124	4507500	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT)
505	13960	28916	4.34	1.0E-124	7705448	NT	Human putative ribosomal protein S1 mRNA
1349	14384	27352	12.68	1.0E-124	AF274892.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1349	14384	27353	12.68	1.0E-124	AF274892.1	NT	Homo sapiens hypodermal protein (HSPC088), mRNA
1349	14384	27353	12.68	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1349	14384	27353	12.68	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1832	14859	27857	2.84	1.0E-124	AIJ31712.1	NT	Homo sapiens mRNA for nuclear RNA-helicase (nhH61 gene)
2078	15093	28110	1.99	1.0E-124	BE975524.1	EST_HUMAN	607491751F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3893954 5'
2463	15487	28490	1.29	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
3502	16549	29476	0.81	1.0E-124	S78584.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3502	16549	29476	0.81	1.0E-124	S78584.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3915	16955	29887	0.84	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4102	17139	30031	0.95	1.0E-124	4504118	EST_HUMAN	h39607.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175783 3'
4772	17792	30683	0.81	1.0E-124	BE220437.1	NT	Homo sapiens gene for B120, exon 11
4775	17795	30687	1.97	1.0E-124	AB024069.1	NT	Homo sapiens hypodermal protein FL10300 (FL10300) mRNA
5370	18475	31348	10.26	1.0E-124	8622337	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
5755	18949	32029	1.03	1.0E-124	4506766	NT	602124644F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4281635 5'
5989	19074	32272	6.53	1.0E-124	BF696135.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CuaADF07 5'
6253	19365	32604	0.97	1.0E-124	AV711263.1	EST_HUMAN	
6572	19632	32899	0.78	1.0E-124	11420854	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Xrosophila fat facets related) (USP9X) mRNA
7208	20231	33584	2.95	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
7344	20315	33659	1.04	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7344	20315	33680	1.04	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2966585 5'
7801	20753	34120	2.50	1.0E-124	AA630331.1	EST_HUMAN	sc08105.x1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:355597 3'
8128	21065	34464	1.78	1.0E-124	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
8128	21065	34465	1.78	1.0E-124	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
8901	21560	34985	13.39	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8906	21773	35198	1.25	1.0E-124	AW612108.1	EST_HUMAN	hg04099.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162
8906	21773	35198	1.25	1.0E-124	AW612108.1	EST_HUMAN	095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
8917	22480	35524	0.92	1.0E-124	AI799864.1	EST_HUMAN	hg04099.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:095162
8917	22480	35525	0.92	1.0E-124	AI799864.1	EST_HUMAN	095162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
9846	22782	36236	1.95	1.0E-124	AV645633.1	EST_HUMAN	wc4303.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:2321428 3'
9846	22782	36237	1.95	1.0E-124	AV645633.1	EST_HUMAN	wc4303.x1 NCI CGAP_P728 Homo sapiens cDNA clone IMAGE:2321428 3'
9846	22782	36237	1.95	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9837	22964	36326	0.96	1.0E-124	AF022055.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9837	22964	36326	0.96	1.0E-124	AF022055.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9867	22994	36356	8.08	1.0E-124	AI767133.1	EST_HUMAN	Homo sapiens cap250 centrosome associated protein mRNA, complete cds
9867	22994	36356	8.08	1.0E-124	AI767133.1	EST_HUMAN	Homo sapiens cap250 centrosome associated protein mRNA, complete cds
9867	22994	36356	8.08	1.0E-124	AI767133.1	EST_HUMAN	w6302.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9867	22994	36357	8.08	1.0E-124	AI767133.1	EST_HUMAN	w6302.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'



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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10230	23155	36846	1.75	1.0E-124	AW503755.1	EST_HUMAN	ULHF-BNO-alc-b-04-0-J1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
11388	24333	37892	1.36	1.0E-124	U94778.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exon 8 through 17
11860	24596	38169	5.95	1.0E-124	AA655663.1	EST_HUMAN	H05006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809003 3'
11801	23958	37479	2.06	1.0E-124	AI446455.1	EST_HUMAN	H19603.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141680 3' similar to TR:O31662 O31662
11801	23958	37480	2.06	1.0E-124	AI446455.1	EST_HUMAN	H19603.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141680 3' similar to TR:O31662 O31662
12305	13754	26683	4.06	1.0E-124	AA397551.1	EST_HUMAN	ZB1604.r1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
12305	13754	26684	4.06	1.0E-124	AA397551.1	EST_HUMAN	ZB1604.r1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
12730	25393	31749	1.36	1.0E-124	AB028016.1	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) :
12993	25852	31436	1.67	1.0E-124	11417862	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) :
12993	25852	31437	1.67	1.0E-124	11417862	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
319	13411	26019	10.43	1.0E-125	AB032693.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
428	13121	26019	5.43	1.0E-125	BE743922.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
645	13711	26632	1.26	1.0E-125	AI110656.1	EST_HUMAN	90167793TFT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926865 5'
845	13711	26633	1.26	1.0E-125	AI110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
728	13790	26725	2.34	1.0E-125	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
861	13917	26875	1.61	1.0E-125	AA042813.1	EST_HUMAN	Z65307.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:485540 3' similar to
1000	14051	27003	1.16	1.0E-125	AL163210.2	NT	gb-X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HOMPOTE (HUMAN);
1166	14198	27148	2.2	1.0E-125	7662270	NT	Homo sapiens chromosome 21 segment HS21C010
1682	15974	27692	1.99	1.0E-125	7661687	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1817	14844	27836	1.65	1.0E-125	U76027.1	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1828	14855	27852	2.84	1.0E-125	AF015450.1	NT	Homo sapiens Brunt's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
1828	14855	27853	2.84	1.0E-125	AF015450.1	NT	(L44), and FTP3 (FTP3) genes, complete cds
2368	15374	28395	1.78	1.0E-125	AA01278.1	EST_HUMAN	Homo sapiens Ueuphr-alpha mRNA, complete cds
2504	15804	28626	1.19	1.0E-125	4504696	NT	Homo sapiens Ueuphr-alpha mRNA, complete cds
2604	15904	28627	1.19	1.0E-125	4504696	NT	201p08.11 Soares_fetal_liver_spleen_1NF.L.S_51 Homo sapiens cDNA clone IMAGE:429568 5'
3022	48311	29001	1.19	1.0E-125	BE018009.1	EST_HUMAN	Homo sapiens inhibin, alpha (NHHA) mRNA
							bb74065.V1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:O95604 O95604
							ZINC FINGER PROTEIN. ;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3872	16911	29821	1.11	1.0E-125	AA042813.1	EST_HUMAN	243307.s7 Soares_pregnant_uterus_NH4PU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:XB5857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGNM07E (HUMAN);
4580	17802	30498	1.88	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4580	17802	30499	1.86	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4648	17689	30358	1.67	1.0E-125	BE315412.1	EST_HUMAN	607141152FT NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140786 5'
5973	18058	32259	1.47	1.0E-125	11439448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
5984	18078	32276	1.01	1.0E-125	BE176160.1	EST_HUMAN	QV2-HT0577-070500-165506 HT0577 Homo sapiens cDNA
6041	19123	32328	3.56	1.0E-125	BE982860.1	EST_HUMAN	601493472FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6086	19166	32378	0.8	1.0E-125	A1679604.1	EST_HUMAN	b67c07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2258108 3' similar to WP:CA4639.2
6413	19491	32726	0.88	1.0E-125	BE736055.1	EST_HUMAN	60135870FT NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3640067 5'
6733	19789	33068	1.29	1.0E-125	BE952526.1	EST_HUMAN	60135828FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689780 5'
6733	19789	33069	1.29	1.0E-125	BE952526.1	EST_HUMAN	60135828FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689780 5'
7263	19998	33286	5.05	1.0E-125	X03427.1	NT	Homo sapiens (GE-II) gene, exon 5
7263	19998	33297	5.05	1.0E-125	X03427.1	NT	Homo sapiens (GE-II) gene, exon 5
7776	20728	34100	1.04	1.0E-125	BE278523.1	EST_HUMAN	601159076FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3605603 5'
8032	20959	34363	0.84	1.0E-125	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8891	21857	35278	0.89	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenergicodystrophy (ALD) gene segment containing exons 8-10
8891	21857	35279	0.89	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenergicodystrophy (ALD) gene segment containing exons 8-10
9473	22437	35975	12.5	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0538-070500-191-d12 HT0538 Homo sapiens cDNA
9473	22437	35976	12.5	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0538-070500-191-d12 HT0538 Homo sapiens cDNA
9736	22764	36219	0.93	1.0E-125	A1655986.1	EST_HUMAN	h52b03.x1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10819	23740	37242	0.85	1.0E-125	BE764576.1	EST_HUMAN	HYPOPHYSICAL PROTEIN
10860	23760	37280	0.74	1.0E-125	AB002296.1	NT	Human mRNA for KIAA0300 gene, partial cds
11042	24006	37333	2.64	1.0E-125	AFC043458.1	NT	Homo sapiens LREL gene, exon 5
11124	24084	37810	1.97	1.0E-125	AW131202.1	EST_HUMAN	x5902.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
11124	24084	37811	1.97	1.0E-125	AW131202.1	EST_HUMAN	LAMBDA/OTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
11471	24414	37983	2.98	1.0E-125	AB014597.1	NT	x5902.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284
11621	24559	38121	2.06	1.0E-125	7669505	NT	LAMBDA/OTA PROTEIN KINASE C-INTERACTING PROTEIN. [1];
							Homo sapiens mRNA for KIAA0667 protein, partial cds
							Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11628	24564	38128	5	1.0E-126	AF028029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11729	24615	38192	1.08	1.0E-128	AW812899.1	EST_HUMAN	RC3-370168-250200-078-c11 ST0188 Homo sapiens cDNA
11830	24713	38208	4.32	1.0E-126	BE072397.1	EST_HUMAN	QV3-8710569-020200-075-g09 BT05589 Homo sapiens cDNA
11830	24713	38297	4.32	1.0E-126	BE074287.1	EST_HUMAN	QV3-8710569-020200-075-g09 BT05589 Homo sapiens cDNA
12108	18942	32127	1.48	1.0E-128	BF683645.1	EST_HUMAN	602138874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
775	13834	25780	6.16	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
920	13974	26926	0.8	1.0E-126	X68735.1	NT	H. sapiens gene for alphas1-antichymotrypsin, exon 3
2352	15361	28383	0.91	1.0E-126	89230559	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2352	15361	28384	0.91	1.0E-126	89230558	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2805	15505	28028	1.41	1.0E-126	6932078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3087	16145	29058	7.58	1.0E-126	AA160709.1	EST_HUMAN	2672c03.r1 Stratagene pancreas (8937208) Homo sapiens cDNA clone IMAGE:592420 6'
3087	16145	29059	7.58	1.0E-126	AA160709.1	EST_HUMAN	2672c03.r1 Stratagene pancreas (8937208) Homo sapiens cDNA clone IMAGE:592420 5'
3088	16146	29060	1.02	1.0E-126	BF510408.1	EST_HUMAN	U1-H-BK-acc-b-05-0-UJ.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3088	16146	29061	1.02	1.0E-126	BF510408.1	EST_HUMAN	U1-H-BK-acc-b-05-0-UJ.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084608 3'
3845	16888	29803	0.76	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3668	18711	29826	2.09	1.0E-126	X63941.1	NT	Homo sapiens death receptor 6 (DR6), mRNA
4826	17843	30741	1.15	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4826	17843	30742	1.15	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4872	17889	30777	1.38	1.0E-126	N34078.1	EST_HUMAN	X78006.r1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:267850 5'
5767	18979	32081	0.71	1.0E-126	T69898.1	EST_HUMAN	y62b212.at Soares fetal liver spleen TNFHS Homo sapiens cDNA clone IMAGE:36627 3'
6360	19429	32672	3.23	1.0E-126	AA460075.1	EST_HUMAN	265603.r1 Soares, total, fetus, NB2HFE_gw Homo sapiens cDNA clone IMAGE:786444 5' similar to TR-G1145890 G1145890 TITN:
6422	19489	32738	3.5	1.0E-126	AB040688.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6422	19489	32740	3.5	1.0E-126	AB040688.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7742	20596	34061	0.98	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7742	20596	34062	0.98	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7869	22008	34296	0.64	1.0E-126	AU136463.1	EST_HUMAN	AU136463 PLACE1 Homo sapiens cDNA clone PLACE1004325 5'
8031	20968	34362	0.68	1.0E-126	AB06483.1	EST_HUMAN	W0801.xt Soares_NFL_1_OBC.S1 Homo sapiens cDNA clone IMAGE:2350009 3' similar to SWMPF2
8210	21179	34587	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8210	21179	34588	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8320	21289	34703	4.9	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.)

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8524	21492	34607	1.02	1.0E-126	AA483368.1	EST_HUMAN	nr74b12.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:908983 similar to SW:TSBG_HUMAN
10165	23080	36555	0.44	1.0E-126	4505424	NT	P98066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-4 PRECURSOR ;
11203	24162	37692	4.45	1.0E-126	BF683175.1	EST_HUMAN	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11848	24728	38315	2.98	1.0E-126	BE281680.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288240 5'
12766	18352	13787	1.37	1.0E-126	BE743622.1	EST_HUMAN	60114604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
173	13275	26201	1.78	1.0E-127	AB024597.1	EST_HUMAN	60157681F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
173	13275	26202	1.37	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
174	13275	26201	1.7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
174	13275	26202	1.7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
273	13360	26236	0.9	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
273	13360	26237	0.9	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
882	13937	26896	0.98	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
917	13971	26925	2.94	1.0E-127	U72821.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1700	14730	27712	1.18	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2080	15097	28113	4.83	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LLRA1), mRNA
2080	15097	28114	4.83	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LLRA1), mRNA
2210	15225	28248	10.89	1.0E-127	4506920	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2349	15358	29330	3.28	1.0E-127	AF245505.1	NT	Homo sapiens adiclin mRNA, complete cds
2617	15615	29840	2.23	1.0E-127	X12881.1	NT	Human mRNA for cyclophilin 18
2628	15627	29851	1.15	1.0E-127	AA450131.1	EST_HUMAN	242402.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789038 5'
2628	15627	29852	1.15	1.0E-127	AA450131.1	EST_HUMAN	242402.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789038 5'
3702	16745	29653	0.98	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3824	18884	29768	0.81	1.0E-127	AW461287.1	EST_HUMAN	af0609.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to
4249	17278	30159	0.84	1.0E-127	AL163247.2	NT	TR015170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element ;
4282	17311	30189	20.15	1.0E-127	7706239	NT	Homo sapiens chromosome 21 segment HS21C047
4282	17311	30190	20.15	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594) mRNA
4523	17548	30458	1.42	1.0E-127	AF58297.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594) mRNA
4523	17548	30458	1.42	1.0E-127	AF58297.1	NT	Homo sapiens cyclochrome P450 reductase metabolizing protein P450RA-2 mRNA, complete cds
4833	17654	30541	5.27	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products

Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4683	17684		2.42	1.0E-127	AL165288.2	NT	Homo sapiens chromosome 21 segment HS21C068
4700	17721	30814	1.32	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5791	18853	32065	1.46	1.0E-127	W03547.1	EST_HUMAN	zao1a10.r1 Scarsa melanocyte 2NHM Homo sapiens cDNA clone IMAGE:391258 5' similar to SW-PIP6 RAT P10688 1-PHOSPHATIDYLINOSITOL-4-5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5828	18916	32100	2.07	1.0E-127	4828683	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
5900	18987	32178	4.61	1.0E-127	X85764.1	NT	H. sapiens NOS2 gene, exon 6
6286	19358	32584	1.95	1.0E-127	X84080.1	NT	H. sapiens TOF11 gene, exon 3-6
6454	19519	32763	5.46	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8), mRNA
6816	19699	33168	0.91	1.0E-127	11421695	NT	Homo sapiens integrin, beta 8 (ITGB8), member 3 (IGSF3), mRNA
7264	19999	33298	1.05	1.0E-127	4820977	NT	Homo sapiens reelin (RELN), mRNA
8068	21003	34400	1.34	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8066	21003	34401	1.34	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
8076	21013	34413	0.58	1.0E-127	BF971355.1	EST_HUMAN	602151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
8078	21016	34416	0.8	1.0E-127	AW696592.1	EST_HUMAN	QV3-BN0046-150300-121-H11 BN0040 Homo sapiens cDNA
9239	22205	35637	1.12	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9239	22205	35638	1.12	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9908	22925	36390	4.83	1.0E-127	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9986	22925	36391	4.83	1.0E-127	AF274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10232	23157	36646	0.76	1.0E-127	AI298932.1	EST_HUMAN	qim94h09.x1 NC1 CGAP Lusi Homo sapiens cDNA clone IMAGE:1896449 3'
10708	23630	37126	1.88	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11492	24435	37883	6.72	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein BB (mortalin-2) (H. sapiens) (LOC83184), mRNA
11492	24435	37884	6.72	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein BB (mortalin-2) (H. sapiens) (LOC83184), mRNA
11949	24928	38423	2.78	1.0E-127	BE955415.1	EST_HUMAN	801434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918917 5'
11949	24928	38424	2.78	1.0E-127	BE955415.1	EST_HUMAN	801434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918917 5'
12089	21003	34400	2.11	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
12089	21003	34401	2.11	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
12532	13275	26201	1.39	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12532	13275	26202	1.39	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12721	26376	31776	2.4	1.0E-127	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
13062	29580		1.47	1.0E-127	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
460	13533	26460	3.35	1.0E-128	BE385617.1	EST_HUMAN	801278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618922 5'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1159	14200	27160	2.18	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1158	14200	27161	2.18	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2084	15101	28117	0.34	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, intronucleotide repeat regions
2084	15101	28118	0.34	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, intronucleotide repeat regions
2219	15233	28237	31.4	1.0E-128	4608718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2451	15456		1.49	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3405	18434	29377	1.23	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4893	17714	30509	5.95	1.0E-128	11428873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5624	18720	31879	0.84	1.0E-128	X68539.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6558	19818	32883	1.84	1.0E-128	11420905	NT	Homo sapiens phospholipase 1C, calcium-dependent (70kD) (PDE1C), mRNA
7119	20050	33353	8.42	1.0E-128	BF224345.1	EST_HUMAN	7485610.X1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3805784.5
7661	20821	33988	0.80	1.0E-128	BE614105.1	EST_HUMAN	601503846FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3805784.5
7983	20922	34313	0.53	1.0E-128	BF526931.1	EST_HUMAN	602042322FT NC1 CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179888.5
7983	20922	34314	0.53	1.0E-128	BF526931.1	EST_HUMAN	602042322FT NC1 CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179888.5
7983	20922	34315	0.53	1.0E-128	BF526931.1	EST_HUMAN	602042322FT NC1 CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179888.5
8080	21017	34417	0.92	1.0E-128	11543923	NT	Homo sapiens putative ABC transporter (WHITE2), mRNA
8139	21076	34476	0.49	1.0E-128	AB046856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
8139	21076	34477	0.49	1.0E-128	AB046856.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
8893	21859	35281	0.5	1.0E-128	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8893	21859	35282	0.5	1.0E-128	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
10498	23418	35917	1.73	1.0E-128	AA635198.1	EST_HUMAN	nc044111 NC1 CGAP_Ewt Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
11065	24028	37652	3.42	1.0E-128	11425284	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11073	24035	37659	3.84	1.0E-128	AA929559.1	EST_HUMAN	on088008.s1 NC1 CGAP_G04 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X94941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
11149	24108	37635	1.48	1.0E-128	AL250690.1	NT	Homo sapiens mRNA for TRABID protein (TRABID gene)
11202	24158	37687	2.69	1.0E-128	BE384475.1	EST_HUMAN	601277626FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750.5
12400	25174		8.88	1.0E-128	AW955290.1	EST_HUMAN	EST1367360 IMAGE resequencing, MAGC Homo sapiens cDNA
122	13486	28423	0.89	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1018 nt, segment 2 of 4]
413	13486	28423	1	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1018 nt, segment 2 of 4]
1731	14751	27145	3.06	1.0E-128	AL065880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1736	14766	27750	2.5	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1796	14766	27751	2.5	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1863	14898	27895	2.86	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3145	16202	29113	1.33	1.0E-129	Q14565	SWISSPROT	ZINC FINGER PROTEIN HZF10
3145	16202	29114	1.33	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3145	16202	29115	1.33	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4192	17223	30112	1.87	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4309	17338	30216	1.86	1.0E-129	AW755254.1	EST_HUMAN	OMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to OMYA5 Cardiomyopathy associated gene 5
4309	17338	30217	1.86	1.0E-129	AW755254.1	EST_HUMAN	OMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to OMYA5 Cardiomyopathy associated gene 5
6210	19284	32516	4.28	1.0E-129	ALJ006345.1	NT	Homo sapiens KVLQ11 gene
6874	19731	33007	0.54	1.0E-129	BE888594.1	EST_HUMAN	901513561 F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE3915350 5'
7334	20305	33549	4.07	1.0E-129	ALJ006345.1	NT	Homo sapiens KVLQ11 gene
7366	20364	33716	0.8	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63694], mRNA
7771	20724	34095	0.78	1.0E-129	AF041055.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
7771	20724	34096	0.78	1.0E-129	AF041055.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8661	21629	36850	4.37	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10439	23361	36850	0.79	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10439	23361	36851	0.79	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10878	23768	37259	0.48	1.0E-129	AI199117.1	EST_HUMAN	q40d08.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:185859 3' similar to TR:Q14840 Q14840 MITOGEN INDUCIBLE GENE MIG-2;
10878	23768	37300	0.48	1.0E-129	AI199117.1	EST_HUMAN	q40d08.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:185859 3' similar to TR:Q14840 Q14840 MITOGEN INDUCIBLE GENE MIG-2;
11567	24487	38053	2.89	1.0E-129	IA025528.1	EST_HUMAN	ar7207.r1 Soares NIH/MPU-ST Homo sapiens cDNA clone IMAGE:1047569 5'
11630	20364	33716	6.2	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) [LOC63694], mRNA
12366	25164		4.21	1.0E-129	H83155.1	EST_HUMAN	y49d05.r1 Soares fetal liver spleen TNFHS Homo sapiens cDNA clone IMAGE:190112 5' similar to SP-B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS-ASIAN;
12758	25401		2.63	1.0E-129	AL120739.1	EST_HUMAN	DKFZp762K171.1 762 (synonym: hmd2) Homo sapiens cDNA clone DKFZp762K171 5'
77	13194	28117	0.65	1.0E-130	7705530	NT	Homo sapiens hypothetical protein (HSP-C242), mRNA
1174	14215	27170	5.65	1.0E-130	AB037895.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1875	14707	27685	13.33	1.0E-130	BE275192.1	EST_HUMAN	901121965 F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3346365 5'
1875	14707	27686	13.33	1.0E-130	BE275192.1	EST_HUMAN	901121965 F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3346365 5'
2000	15021		3.15	1.0E-130	X04092.1	NT	Human gene for cellulase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2781	15773		8.37	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2880	15949	28854	1.3	1.0E-130	BE664219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
2880	15949	28865	1.3	1.0E-130	BE664219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3561	16638	29556	1.27	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3779	15949	28864	4.85	1.0E-130	BE664219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3779	15949	28865	4.56	1.0E-130	BE664219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3957	16997	29812	1.41	1.0E-130	AF503580.1	EST_HUMAN	U1HF-BND-alky-g-96-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4059	17133	30027	1	1.0E-130	N97710.1	NT	Human T-cell receptor (alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
4569	17592	30485	8.22	1.0E-130	AW843693.1	EST_HUMAN	GM4-CN0045-160200-511-402 CN0045 Homo sapiens cDNA
5133	18142	31021	1.53	1.0E-130	AW363299.1	EST_HUMAN	RQ0-CT0318-201169-031-att1 CT0318 Homo sapiens cDNA
5133	18142	31022	1.53	1.0E-130	AW363299.1	EST_HUMAN	RQ0-CT0318-201169-031-att1 CT0318 Homo sapiens cDNA
6891	18943	33239	0.63	1.0E-130	X57825.1	NT	Human germline immunoglobulin lambda light chain pseudogene (VII.1)
6894	20120	33433	0.89	1.0E-130	AW843875.1	EST_HUMAN	GM4-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6894	20120	33434	0.89	1.0E-130	AW843875.1	EST_HUMAN	GM4-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
7010	20136	33452	0.88	1.0E-130	11428448	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7466	20432	33789	2.06	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7674	20536	33594	0.65	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7674	20536	33595	0.65	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8030	21998		0.8	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARKT) mRNA, complete cds
9171	22137	35563	2.81	1.0E-130	AF956242.1	EST_HUMAN	EST368312 IMAGE sequences, MAGD Homo sapiens cDNA
9559	22531	35581	1.74	1.0E-130	AB037756.1	NT	X35805x1 NC1 CGAP_Q223 Homo sapiens cDNA clone IMAGE:2565874 3'
10293	23218		1.29	1.0E-130	AW103454.1	EST_HUMAN	Homo sapiens glutamate receptor, metabotropic 5 (GRM5) mRNA
12015	24892	38489	1.71	1.0E-130	4504142	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
13046	15773		1.44	1.0E-130	AJ010230.1	NT	z58d04.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667690 5' similar to TR:G222811
4	13125	28023	2.04	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
4	13125	28024	2.64	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN ;
8	13128	28028	2.59	0.0E+00	4885138	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
16	13136	28034	0.60	0.0E+00	8923348	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
16	13136	28035	0.88	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13143	28042	1.8	0.0E+00	D83327.1	NT	Homo sapiens DCR1 mRNA, partial cds
23	13143	28043	1.8	0.0E+00	D83327.1	NT	Homo sapiens DCR1 mRNA, partial cds



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
29	13149	26048	51.1	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
38	13150	26060	0.87	0.0E+00	M59600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
42	13162	26065	4.85	0.0E+00	6857826	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNP51), mRNA
59	13176	26080	2.13	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	13176	26081	2.13	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	13180	26095	1.27	0.0E+00	D78904.1	EST_HUMAN	HUM151610B8 Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-516H08 5'
61	13180	26096	1.27	0.0E+00	D78904.1	EST_HUMAN	HUM151610B8 Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-516H08 5'
62	13181	26097	25.34	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
64	13183	26100	11.49	0.0E+00	AW069534.1	EST_HUMAN	cr48607.x1 Jia bone marrow sarcoma Homo sapiens cDNA clone HBMSC.cr48607 3'
64	13183	26101	11.49	0.0E+00	AW069534.1	EST_HUMAN	cr48607.x1 Jia bone marrow sarcoma Homo sapiens cDNA clone HBMSC.cr48607 3'
66	13186		1.18	0.0E+00	M90978.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
70	13193	26115	4.09	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
76	13193	26116	4.06	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
79	13193	26115	2.97	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
79	13193	26116	2.97	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	13198	26122	0.79	0.0E+00	4501850	NT	Homo sapiens enololide binding protein 1 (entire oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
83	13199		18.85	0.0E+00	4504444	NT	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
91	13207	26131	80.78	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
94	13210	26134	18.95	0.0E+00	U89277.1	NT	Human polyomodelo 1 homolog (HPH1) mRNA, partial cds
101	13217	26141	2.55	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
102	13218	26142	1.19	0.0E+00	A9037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
118	13227	26151	0.83	0.0E+00	A1623701.1	EST_HUMAN	ts3805.x1 NCI CGAP J14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q98551 Q98551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
117	13227	26151	0.78	0.0E+00	A1623701.1	EST_HUMAN	ts3805.x1 NCI CGAP J14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q98551 Q98551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
118	13229	26152	0.84	0.0E+00	N36040.1	EST_HUMAN	Y01103.1t Soares melanocyte 2N3H1M Homo sapiens cDNA clone IMAGE:270017 5'
118	13229	26153	0.84	0.0E+00	N36040.1	EST_HUMAN	Y01103.1t Soares melanocyte 2N3H1M Homo sapiens cDNA clone IMAGE:270017 5'
121	13230	26158	0.95	0.0E+00	4505458	NT	Homo sapiens neurexin 2 (NRX2) mRNA
131	13236	26166	5.49	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
131	13236	26167	5.49	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
139	13474	26407	0.65	0.0E+00	4503580	NT	Homo sapiens IgG Fc binding protein (FCG/GAMMA/BP) mRNA
141	13244	26174	0.85	0.0E+00	T69545.1	EST_HUMAN	y68304.2 Striatogene fetal spleen (6637205) Homo sapiens cDNA clone IMAGE:68310 5'
141	13244	26175	0.85	0.0E+00	T69545.1	EST_HUMAN	y68304.2 Striatogene fetal spleen (6637205) Homo sapiens cDNA clone IMAGE:68310 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
154	13297		64.2	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
158	13291	26188	4.4	0.0E+00	BFO39881.1	EST_HUMAN	601460375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803.5
160	13293		30.14	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
163	13298	26191	0.92	0.0E+00	AF111188.2	NT	Homo sapiens cathepalmidyl transferase, subunit II gene, complete cds; and unknown genes
165	13298	26192	0.74	0.0E+00	BE259973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:5529864.5
166	13298	26192	1.17	0.0E+00	BE259973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864.5
167	13296	26193	2.37	0.0E+00	W73973.1	EST_HUMAN	z66206.6.1 Soares fetal heart, NHH19W Homo sapiens cDNA clone IMAGE:345201.6 similar to gb:U18282.cds ZINC FINGER PROTEIN CLONE 647 (HUMAN);
168	13270	26194	0.85	0.0E+00	BE162632.1	EST_HUMAN	QV5-HT0457.440200-088-004 HT0457 Homo sapiens cDNA
168	13270	26195	0.85	0.0E+00	BE162632.1	EST_HUMAN	QV5-HT0457.740200-088-004 HT0457 Homo sapiens cDNA
169	13271	26199	1.59	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
172	13274	26199	14.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
172	13274	26200	14.16	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
182	13282	26207	4.87	0.0E+00	BEQ18970.1	EST_HUMAN	b024e12.Y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854.5 similar to WP:V57A10A.2 CEZ2831.1
182	13282	26208	4.87	0.0E+00	BEQ18970.1	EST_HUMAN	b024e12.Y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854.5 similar to WP:V57A10A.2 CEZ2831.1
187	13287	26211	4.35	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
187	13287	26212	4.35	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	13298	26213	3.09	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
188	13298	26214	3.06	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
195	13297	26225	268.4	0.0E+00	D50699.1	NT	Human gamma-cytoplasmic actin (ACTG9) pseudogene
200	13301	26228	4.35	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4-3 mRNA, complete cds
200	13301	26230	4.35	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4-3 mRNA, complete cds
202	13303	26232	3.93	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X NSL3.2 protein mRNA, complete cds
202	13303	26233	3.93	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X NSL3.2 protein mRNA, complete cds
211	15835	26239	51.32	0.0E+00	AI897308.1	EST_HUMAN	tq0408.X1 NCI_CGAP_U18 Homo sapiens cDNA clone IMAGE:2207847.3 similar to gb:03191 PROFLIN1 (HUMAN);
211	15835	26240	51.32	0.0E+00	AI897308.1	EST_HUMAN	tq0408.X1 NC_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847.3 similar to gb:03191 PROFLIN1 (HUMAN);
213	13313	26242	1.57	0.0E+00	AF196668.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
218	13316		43.74	0.0E+00	4500632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
217	13317		6.45	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
223	13323	26248	1.15	0.0E+00	AF014264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
224	13323	26248	1.81	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
225	13324	26249	3.11	0.0E+00	6978444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tepyl), mRNA
239	13338	26264	3.14	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
240	13336		6.19	0.0E+00	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
247	13344	26269	3.46	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
249	13346	26272	2.06	0.0E+00	X89772.1	NT	H sapiens mRNA for Interferon alphabeta receptor (long form)
257	13364		9.67	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
269	13365	26290	1.2	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	13365	26291	1.2	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
271	13367	26293	3.56	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
282	13377		1.56	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
283	13378	26306	1.75	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
283	13378	26307	1.75	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
284	13379		0.69	0.0E+00	AF184528.1	EST_HUMAN	IL2 CT0031-181189-020-303 CT0031 Homo sapiens cDNA
283	13387	26314	7.75	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
283	13387	26315	7.75	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
304	13398	26325	3.69	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
305	13399	26326	15.06	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
308	13638		12.15	0.0E+00	450728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
307	13400	26327	0.8	0.0E+00	45039114	NT	Homo sapiens phosphoribosylglycylamide formyltransferase, phosphoribosylamidoimidazole synthetase (GART) mRNA
308	13401		1.85	0.0E+00	AA480002.1	EST_HUMAN	av18065.11 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:753984 5'
309	13402	26328	23.16	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
310	13402	26328	22.55	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
314	13406	26332	1.76	0.0E+00	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
327	13418	26341	2.84	0.0E+00	O14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
327	13418	26342	2.84	0.0E+00	O14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
328	13419	26343	4.94	0.0E+00	7657213	NT	Homo sapiens homonally upregulated nec tumor-associated kinase (HUNK), mRNA
329	13419	26343	1.14	0.0E+00	7657213	NT	Homo sapiens homonally upregulated nec tumor-associated kinase (HUNK), mRNA
							Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (Hlthorax (Drosophila) homolog), translocated to 4 (MLL14) mRNA
344	13433	26355	0.86	0.0E+00	5174574	NT	Homo sapiens moesin (MSN), mRNA
345	13434	26356	2.48	0.0E+00	4505266	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
346	13437	26360	3.07	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
351	13440	26365	1.24	0.0E+00	U71600.1	NT	Human zinc finger protein Zfp31 (Zf31) mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
356	13444	26359	2.64	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	13444	26370	2.64	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
357	15639	26371	2.87	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
359	13446	26373	0.87	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
361	13448	26376	0.9	0.0E+00	4503954	NT	Homo sapiens GAB-binding protein transcription factor, alpha subunit (GABPA), mRNA
362	13449	26377	1.81	0.0E+00	D80006.1	NT	Human mRNA for KIA0184 gene, partial cds
363	13449	26377	1.41	0.0E+00	D80008.1	NT	Human mRNA for KIA0184 gene, partial cds
365	13451	26378	0.63	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
376	13460	26390	2.41	0.0E+00	AU134683.1	EST_HUMAN	AU134683 PLACE1 Homo sapiens cDNA clone IMAGE2018457 3' similar to gb:U54199
387	13500	26433	7.68	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
388	13501	26434	2.78	0.0E+00	AI353014.1	EST_HUMAN	qy87H05.x1 NCL CGAP_Bin28 Homo sapiens cDNA clone IMAGE2018457 3' similar to gb:U54199
392	13467	26397	2.88	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
395	13469	26400	1.3	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
398	13470	26401	2.24	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
396	13470	26402	2.24	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
397	13471	26403	1.22	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
398	13472	26404	1.27	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
398	13472	26405	1.27	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
399	13473	26406	3.09	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
400	13474	26407	0.87	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein [FC(GAMMA)BP] mRNA
401	13475	26408	2.69	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
401	13475	26409	2.69	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
402	13475	26408	2.37	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
402	13475	26409	2.37	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-28
406	13478	26409	25.98	0.0E+00	4506908	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
420	13115	26013	1.44	0.0E+00	R17795.1	EST_HUMAN	Homo sapiens phosphoribosylpyrimidine formyltransferase, phosphoribosylglycinamide synthetase, xq90a02.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE31652 5'
428	13502	26435	2.15	0.0E+00	4503914	NT	phosphoribosylaminoimidazole synthetase (GART) mRNA
428	13503	26436	15.71	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
430	13504	26436	1.89	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
431	13505	26437	3.68	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
431	13505	26438	3.68	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
432	13506	26439	4.53	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13517		1.27	0.0E+00	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
446	13519	28452	6.45	0.0E+00	4857876	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
451	13524		0.75	0.0E+00	AA324282.1	EST_HUMAN	EST127054 Carcibulum II Homo sapiens cDNA 5' end
452	13525		1.28	0.0E+00	BE254447.1	EST_HUMAN	60111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362348 5'
488	13641	26468	3.47	0.0E+00	4504532	NT	Homo sapiens 3-hydroxyisoprenaline (serotonin) receptor 1B (HTR1B) mRNA
489	13641	26467	3.47	0.0E+00	4504532	NT	Homo sapiens 3-hydroxyisoprenaline (serotonin) receptor 1B (HTR1B) mRNA
474	13546	26475	2.84	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
474	13546	26478	2.84	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
484	13597	26482	2.68	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	13598	26483	6.81	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	13598	26484	6.81	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
484	13598	26489	3.92	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
495	13598	26491	1.83	0.0E+00	AL132893.1	EST_HUMAN	AL132898 NT2R24 Homo sapiens cDNA clone NT2R2400837 5'
504	13676	26497	1.58	0.0E+00	BE385744.1	EST_HUMAN	60127495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615758 5'
505	13642	26498	1.88	0.0E+00	AW93825.1	EST_HUMAN	PMO-DT0066-130400-002-008 DT0068 Homo sapiens cDNA
508	13579	26500	1.47	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
509	13580	26501	0.9	0.0E+00	8923955	NT	Homo sapiens PC328 protein (PC328) mRNA
513	13584		0.82	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-507 FT0159 Homo sapiens cDNA
520	13591	26511	5.32	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
527	13643	26515	1.15	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
532	13603	26521	1.61	0.0E+00	BE028005.1	EST_HUMAN	60176455F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996598 5'
538	13609	26528	2.23	0.0E+00	AB040309.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
541	13612	26531	10.84	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII) polypeptide 1-like (TCEB1L) mRNA
542	13613	26532	4.48	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
542	13613	26533	4.46	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
544	13616	26536	0.99	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443) mRNA
545	13616	26538	1.2	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443) mRNA
545	13616	26537	1.2	0.0E+00	8923831	NT	Homo sapiens X-linked arthritic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
550	13620		5.14	0.0E+00	AF003528.1	NT	U1H-B1-ach-h-04-04-U1.s1 NC1_QGAP_Su303 Homo sapiens cDNA clone IMAGE:2713957 3'
558	13628	26546	1.55	0.0E+00	AW135204.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
568	13638		2.54	0.0E+00	DT0083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UOCRF51), nuclear gene
588	13656	26571	2.72	0.0E+00	5174742	NT	encoding mitochondrial protein, mRNA

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
601	13668		15.19	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
604	13671	26595	1.83	0.0E+00	BF104838.1	EST_HUMAN	801822627F1 NIH_MGC 75 Homo sapiens cDNA clone IMAGE:4045447 5'
606	13673	26587	0.77	0.0E+00	8823631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
608	13675	26588	0.77	0.0E+00	8823631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
611	13678	26591	0.89	0.0E+00	4501854	NT	Homo sapiens acyl-Coenzyme A carboxylase beta (ACACB), mRNA
616	13681	26597	1.6	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
618	13681	26598	1.6	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
621	13683	26605	1.86	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
625	13680	26608	1.83	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
627	13692	26609	0.85	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
628	13693	26610	1.65	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
628	13693	26611	1.55	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
629	13694	26612	1.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
629	13694	26613	1.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
636	13702	26623	1.35	0.0E+00	AA3369488.1	EST_HUMAN	260007.1 Soares, Jests_NHT Homo sapiens cDNA clone IMAGE:728732 5'
640	13706	26627	4.81	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
644	13710	26630	1.86	0.0E+00	W78811.1	EST_HUMAN	zh51604.1 Soares, Jests_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
644	13710	26631	1.86	0.0E+00	W78811.1	EST_HUMAN	zh51604.1 Soares, Jests_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:415587 5' similar to gb-A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
647	13713		5.61	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
654	13720	26643	2.78	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
656	13722	26646	2.3	0.0E+00	5331624	NT	Homo sapiens CCAAT box-binding transcription factor (CBF2) mRNA
659	13726	26650	3.11	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
663	13729	26653	0.99	0.0E+00	AF108388.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
663	13729	26654	0.99	0.0E+00	AF108388.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
668	13734	26659	4.94	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
668	13734	26660	4.94	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
675	16946		3.3	0.0E+00	X57147.1	NT	Human endogenous retrovirus PHE-1 (ERV9)
683	13746	26673	9.59	0.0E+00	4904424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMGT1) mRNA
688	13751	26677	4.6	0.0E+00	AB026012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
698	13760	26682	17.83	0.0E+00	7557468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
710	13772	26706	15.52	0.0E+00	AA814537.1	EST_HUMAN	np4901.1 NCI CGAP_Brl.1 Homo sapiens cDNA clone IMAGE:1129833 3' similar to gb-X67052 INTERFERON-INDUCIBLE PROTEIN 1-80 (HUMAN);

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
714	13778	28770	4.91	0.0E+00	M80675.1	NT	Human von Willebrand factor gene, exons 23 through 34
714	13778	28771	4.91	0.0E+00	M80675.1	NT	Human von Willebrand factor gene, exons 23 through 34
724	13786	28770	2.21	0.0E+00	S032192	NT	Human sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
730	13791	28726	4.69	0.0E+00	AF284750.1	NT	Human sapiens ALR-like protein mRNA, partial cds
730	13791	28727	4.69	0.0E+00	AF284750.1	NT	Human sapiens ALR-like protein mRNA, partial cds
732	13793	28730	11.39	0.0E+00	U1545900	NT	Human sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
738	13798	28738	2.31	0.0E+00	BE241577.1	EST_HUMAN	TCAP-1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) BAYOR-HGSC project-TCAP Homo sapiens cDNA clone TCAP0779
757	13817	28761	2.09	0.0E+00	AF226900.2	NT	Human sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
757	13817	28762	2.09	0.0E+00	AF226900.2	NT	Human sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
759	13819	28764	0.89	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
759	13819	28765	0.89	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
762	13822	28766	2.01	0.0E+00	AB037780.1	NT	Human sapiens mRNA for KIAA1339 protein, partial cds
763	13823	28767	0.66	0.0E+00	6912748	NT	Human sapiens zinc finger protein 212 (ZNF212), mRNA
765	13850	28769	3.03	0.0E+00	D30812.1	NT	Human sapiens mRNA for repressor protein, partial cds
766	13825	28770	1.78	0.0E+00	BE869735.1	EST_HUMAN	601448947F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE3849803 5'
770	13828	28774	3.69	0.0E+00	R48915.1	EST_HUMAN	y88g08.r1 Soares breast 2NB-Hst Homo sapiens cDNA clone IMAGE154046 5'
771	13830	28775	2.14	0.0E+00	S032086	NT	Human sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
779	13838	28783	1.88	0.0E+00	AB011390.1	NT	Human sapiens gene for A-E-g, complete cds
782	13842	28787	2.77	0.0E+00	F691968	NT	Human sapiens KIAA0170 gene product (KIAA0170), mRNA
783	13852	28799	2.38	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
789	13852	28800	2.38	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
793	13857	28804	2.72	0.0E+00	X89772.1	NT	H sapiens mRNA for interferon alpha/helix receptor (long form)
802	13861	28808	3.38	0.0E+00	AB020717.1	NT	Human sapiens mRNA for KIAA0910 protein, partial cds
807	13867	28809	3.38	0.0E+00	AB020717.1	NT	Human sapiens mRNA for KIAA0910 protein, partial cds
807	13866	28816	10.76	0.0E+00	5174478	NT	Human sapiens perlecanin (PCNT1) mRNA
809	13869	28816	9.63	0.0E+00	4507500	NT	Human sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
828	13883	28836	1.59	0.0E+00	7657213	NT	Human sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
828	13884	28837	2.57	0.0E+00	7657213	NT	Human sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
828	13886	28839	1.82	0.0E+00	4557668	NT	Human sapiens potassium voltage-gated channel, beta-related family, member 1 (KCNE1) mRNA
834	13891	28845	3.12	0.0E+00	AF108930.1	NT	Human sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
834	13891	28846	3.12	0.0E+00	AF108930.1	NT	Human sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
835	13892	28847	1.34	0.0E+00	AF108930.1	NT	Human sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
840	13897	28852	2.18	0.0E+00	4503854	NT	Human sapiens G4-binding protein transcription factor, alpha subunit (90KD) (GASBP4), mRNA

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
844	13900	26857	1.23	0.0E+00	4807600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
844	13900	26858	1.23	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
851	13907		1.78	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
855	13911	26868	4.48	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
855	13911	26870	4.48	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
855	13912	26871	10.69	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
857	13913	26872	4.54	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
858	13914	26873	14.11	0.0E+00	4509728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
858	13918	26876	1.18	0.0E+00	AB020777.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
858	13918	26877	1.18	0.0E+00	AB020777.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
863	13919	26878	1.8	0.0E+00	AA533272.1	EST_HUMAN	hlg607.s1 NC1 CGAP P170 Homo sapiens cDNA clone IMAGE:897453
863	13919	26879	1.8	0.0E+00	AA533272.1	EST_HUMAN	hlg607.s1 NC1 CGAP P170 Homo sapiens cDNA clone IMAGE:897453
864	13920		10.08	0.0E+00	BF677694.1	EST_HUMAN	802085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4245973 5'
868	13924	26880	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
868	13924	26881	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	13925	26882	1.95	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	13925	26883	1.95	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
892	13947	26906	0.86	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
899	13954	26911	1.72	0.0E+00	BE085622.1	EST_HUMAN	QV0-BT0703-280400-21-1-g11 BT0703 Homo sapiens cDNA
899	13954	26912	1.72	0.0E+00	BE085622.1	EST_HUMAN	QV0-BT0703-280400-21-1-g11 BT0703 Homo sapiens cDNA
909	13954	26921	1.89	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C008
919	13973		63.74	0.0E+00	4504658	NT	Homo sapiens laminin receptor 1 (67KD, ribosomal protein SA) (LAMR1), mRNA
921	13973		24.73	0.0E+00	4504658	NT	Homo sapiens laminin receptor 1 (67KD, ribosomal protein SA) (LAMR1), mRNA
922	13975	26927	0.71	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
923	13976	26928	2.39	0.0E+00	Z8101.1	NT	Homo sapiens alpha-1-antitrypsin heavy chain gene
925	13978	26930	0.84	0.0E+00	Z20659.1	NT	Homo sapiens alpha-1-antitrypsin heavy chain gene
926	13978	26931	0.84	0.0E+00	Z20659.1	NT	Homo sapiens alpha-1-antitrypsin heavy chain gene
926	13978	26932	0.83	0.0E+00	Z20659.1	NT	Homo sapiens alpha-1-antitrypsin heavy chain gene
928	13979	26933	0.83	0.0E+00	Z20659.1	NT	Homo sapiens alpha-1-antitrypsin heavy chain gene
946	13989	26950	2.86	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0894 protein, partial cds
946	13989	26951	2.86	0.0E+00	AB023211.1	NT	Homo sapiens mRNA for KIAA0894 protein, partial cds
952	14005	26957	0.88	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
953	14006	26958	8.74	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end
954	14007	26959	0.72	0.0E+00	M37180.1	NT	Human ras inhibitor mRNA, 3' end





Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1068	14111	27060	2.13	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1069	14111	27061	2.13	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1070	14115	27065	3.18	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1070	14115	27066	3.18	0.0E+00	8923824	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1071	14116	27067	28.45	0.0E+00	AJ245922.1	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1073	14118	27069	0.82	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1075	14120	27071	3.85	0.0E+00	6174384	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1084	14126	27082	1.91	0.0E+00	4759117	NT	Homo sapiens Desitin associated protein 3 (DAP3) mRNA
1098	14142	27092	2.82	0.0E+00	BE005208.1	EST_HUMAN	hRC-BNO115-203300-003-n08 BN0115 Homo sapiens cDNA
1121	14165	27116	5.64	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1121	14165	27117	5.54	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1134	14177	27127	0.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1134	14177	27128	0.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1135	14178	27129	33.54	0.0E+00	4505712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1137	14180	27131	2.34	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1140	14183	27134	8.07	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1142	14185	27135	20.89	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1143	14186	27136	5.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1143	14188	27137	5.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1147	14189	27140	1.84	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1148	14190	27141	0.76	0.0E+00	X95926.1	NT	H. sapiens ART 4 gene
1148	14190	27142	0.76	0.0E+00	X95926.1	NT	H. sapiens ART 4 gene
1149	14191	27143	1.25	0.0E+00	A147660.1	EST_HUMAN	q22d10.x1 Scores, pregnant uterus, NHPRU Homo sapiens cDNA clone IMAGE:169701.3'
1151	14193	27145	1.68	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1160	14202	27154	3.19	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1160	14202	27155	3.19	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1161	14203	27156	0.89	0.0E+00	6989844	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
1172	14213	27167	8.28	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 87kD) (GAD1), transcript variant GAD25, mRNA
1172	14213	27168	8.28	0.0E+00	7305078	NT	Homo sapiens glutamate decarboxylase 1 (brain, 87kD) (GAD1), transcript variant GAD25, mRNA
1185	14216	27171	1.08	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1182	14223	27180	1.21	0.0E+00	4557887	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1198	14236	27191	0.64	0.0E+00	AF073299.1	NT	Homo sapiens Na <sup>+</sup> /H <sup>+</sup> exchanger, isoform 2 (NHE2) mRNA, complete cds
1214	14252	27201	1.24	0.0E+00	7657336	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1230	14268	27226	1.18	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1230	14268	27226	1.18	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1231	14269	27227	1.6	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1232	15861	27228	1.7	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1251	14267	27253	6.18	0.0E+00	AF103718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1252	14268	27254	0.98	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (telomere-associated) (CSPG4), mRNA
1282	14267	27260	0.73	0.0E+00	4505740	NT	Homo sapiens pifecidin 4 (PFND4) mRNA
1271	14308		2.04	0.0E+00	Y16000.1	NT	Homo sapiens NF2 gene
1278	14314	27275	48.44	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1286	14321	27284	4.02	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSOR9) mRNA, complete cds
1282	14327	27286	1.08	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1282	14327	27286	1.08	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1303	14339	27302	2	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1303	14339	27303	2	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1303	14339	27304	2	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1304	14340		3.46	0.0E+00	AF066196.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1314	15863	27316	1.26	0.0E+00	7657529	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
1314	15863	27317	1.26	0.0E+00	7657529	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
1316	14354	27322	6.23	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1320	14356	27323	0.81	0.0E+00	4509004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1322	14357	27324	6.68	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1323	14358	27325	33.1	0.0E+00	4509004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1325	14360	27327	4.74	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0517 protein, complete cds
1326	14361	27328	6.7	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1327	14362	27329	8.47	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1328	14363	27330	5.14	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1328	14363	27331	5.14	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1340	14374	27344	2.17	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1407	14440	27410	1.34	0.0E+00	AJ250074.1	NT	Homo sapiens mRNA for Familial Oculodentodysplasia cld gene
1416	14448	27421	1.79	0.0E+00	AI208758.1	EST_HUMAN	gg88066.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1837427 3 similar to WP:T27A1.5 CE14213
1416	14449	27422	32.64	0.0E+00	6042208	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1423	14456	27430	1.31	0.0E+00	4505946	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1423	14456	27431	1.31	0.0E+00	4505946	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1425	14468	27434	2.29	0.0E+00	7705568	NT	Homo sapiens KIAA11114 protein (KIAA11114), mRNA
1425	14458	27435	2.29	0.0E+00	7705568	NT	Homo sapiens KIAA11114 protein (KIAA11114), mRNA
1427	14460	27436	6.81	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1434	14468	27446	2.91	0.0E+00	AF038260.1	NT	Homo sapiens alpha1-fucosyltransferase (alpha1-6FucT) gene, exon 7
1447	14480	27466	1.01	0.0E+00	U58337.1	NT	Human nebulin mRNA, partial cds
1447	14480	27457	1.01	0.0E+00	U56337.1	NT	Human nebulin mRNA, partial cds
1457	14492	27464	3.14	0.0E+00	AL132896.1	NT	Novel human gene on chromosome 20
1459	14482	27465	2.5	0.0E+00	AL13764.1	NT	Novel human gene mapping to chromosome 1
1463	14486	27470	1.59	0.0E+00	DB7077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1468	14469	27473	5.38	0.0E+00	6912467	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1468	14501	27475	1.7	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1468	14501	27476	1.7	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1469	14502		1.04	0.0E+00	Y07828.2	NT	Homo sapiens RFB30 gene for RING finger protein
1513	14545	27516	2.11	0.0E+00	7708434	NT	Homo sapiens PHD3 for homolog of Drosophila headcase (LOC81698), mRNA
1528	14581	27532	1.84	0.0E+00	AA481172.1	EST_HUMAN	aa340371 NC1 CGAP GC87 Homo sapiens cDNA clone IMAGE816110 5'
1534	14587	27536	29.54	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1534	14587	27537	29.54	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1536	14589	27540	1.37	0.0E+00	AW976097.1	EST_HUMAN	EST1383205 IMAGE ressequences, MAGN Homo sapiens cDNA
1536	14589	27541	1.37	0.0E+00	AW976097.1	EST_HUMAN	EST1383205 IMAGE ressequences, MAGN Homo sapiens cDNA
1538	14571		2.22	0.0E+00	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F1P3 (F1P3) genes, complete cds
1539	14572	27544	2.25	0.0E+00	M16768.1	NT	Human T-cell receptor gamma chain VJCI-CII region mRNA, complete cds
1540	14573	27546	2.04	0.0E+00	4605404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1540	14573	27546	2.04	0.0E+00	4605404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1541	14574	27547	3.31	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1542	14575		7.04	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1549	14581	27553	2.45	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1551	14584	27555	1.24	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1551	14584	27556	1.24	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1552	14585	27557	19.78	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1553	14585	27557	26.31	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epilope) mRNA, 5' end
1563	14596	27571	0.94	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1563	14596	27572	0.94	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1565	14598	27573	10.15	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanin-associated) (CSPG4), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1583	14616	27586	9.8	0.0E+00	Z83733.1	NT	H.sapiens H2B1 gene
1584	14617	27590	1.81	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1584	14617	27591	1.81	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1585	14618	27592	12.82	0.0E+00	AV690361.1	EST_HUMAN	AV690361 GKX Homo sapiens cDNA clone GKCBQF02 5'
1585	14618	27593	12.82	0.0E+00	AV690361.1	EST_HUMAN	AV690361 GKX Homo sapiens cDNA clone GKCBQF02 5'
1588	15872	27596	2.64	0.0E+00	AB040505.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1592	14624	27597	1.24	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1594	14628	27600	4.83	0.0E+00	7692183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1594	14628	27601	4.83	0.0E+00	7692183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1596	14628	27602	26.26	0.0E+00	5729876	NT	Homo sapiens heat shock 70KD protein 10 (HSC71) (HSPA10), mRNA
1596	14628	27603	26.26	0.0E+00	5729876	NT	Homo sapiens heat shock 70KD protein 10 (HSC71) (HSPA10), mRNA
1598	14630	27605	1.56	0.0E+00	M97803.1	NT	Human sodium channel mRNA
1613	14645	27621	7.01	0.0E+00	H28973.1	EST_HUMAN	yo76205.ct Scores adult brain N2x4H85Y Homo sapiens cDNA clone IMAGE:183848 3'
1622	14655	27632	2.31	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1622	14655	27633	2.31	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1644	14678	27649	1.04	0.0E+00	AW444637.1	EST_HUMAN	U1H-B13-qjw-c-D4-Q-U1 st NCI_CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1673	14705	27682	1.19	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191189-004-b11 HT0166 Homo sapiens cDNA
1673	14705	27683	1.19	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191189-004-b11 HT0166 Homo sapiens cDNA
1677	14709	27687	1.84	0.0E+00	AI768104.1	EST_HUMAN	wg81607.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 082788 CYS2HIS2 ZINC FINGER PROTEIN. ;
1678	14710	27688	1.44	0.0E+00	47558513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1679	14711	27689	3.61	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1683	14714	27693	1.72	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1683	14714	27694	1.72	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1685	14716	27696	1.63	0.0E+00	4557887	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1688	14717	27697	2.12	0.0E+00	7657065	NT	Homo sapiens keratin 18 (KRT18) mRNA
1688	14717	27697	2.12	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1690	14721	27700	1.27	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCI_CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O65147 065147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1690	14721	27701	1.27	0.0E+00	BE222374.1	EST_HUMAN	hu11405.x1 NCI_CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O65147 065147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1693	14723	27705	5.17	0.0E+00	H30132.1	EST_HUMAN	yo59a03.r1 Scores breast 3NH8Bat Homo sapiens cDNA clone IMAGE:192246 5' similar to gb:M64089
1693	14723	27705	5.17	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1693	14723	27706	5.17	0.0E+00	H30132.1	EST_HUMAN	yo59a03.r1 Scores breast 3NH8Bat Homo sapiens cDNA clone IMAGE:192246 5' similar to gb:M64089
1693	14723	27706	5.17	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1685	14726		0.94	0.0E+00	A149880.1	EST_HUMAN	qf4309.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752009 3'
1686	14726	27708	7.26	0.0E+00	Z80780.1	NT	H.sapiens H2B1h gene
1686	14726	27709	7.26	0.0E+00	Z80780.1	NT	H.sapiens H2B1h gene
1689	14729		28.3	0.0E+00	6031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1708	14739	27721	0.91	0.0E+00	AF169883.1	NT	Homo sapiens WNT16 protein (WNT16) mRNA, complete cds
1710	14740	27724	5.35	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1713	14743	27727	1.03	0.0E+00	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1716	14746	27731	0.86	0.0E+00	M7580.1	NT	Human hepatocyte growth factor gene, exon 15
1716	14746	27732	0.86	0.0E+00	M7580.1	NT	Human hepatocyte growth factor gene, exon 15
1720	14750	27736	1.37	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1728	14758		20.03	0.0E+00	AB028542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1737	14767	27752	2.59	0.0E+00	S84400.1	NT	TCR zeta [human, Genomic]mRNA, 365 nt, segment 1 of 6
1744	15976	27759	0.97	0.0E+00	4557538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA
1760	14788	27775	1.21	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1800	15877		2.63	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1800	15877		35.79	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1805	14833	27821	2.42	0.0E+00	4507568	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1805	14833	27822	2.42	0.0E+00	4507568	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1807	14835	27825	2.05	0.0E+00	U63993.1	NT	Human GSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1810	14836		1.32	0.0E+00	W76571.1	EST_HUMAN	Z86690.r1 Soares_testis_NHT LNH2.H16W Homo sapiens cDNA clone IMAGE:345664 5'
1811	15378	27829	3.9	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1812	14839	27830	1.13	0.0E+00	AA113030.1	EST_HUMAN	z165c03.a1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563056 3'
1824	14851	27845	14.85	0.0E+00	U14687.1	NT	Human ribosomal protein L21 mRNA, complete cds
1828	14853	27848	5.94	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0393 gene, partial cds
1827	14854	27849	6.64	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1827	14854	27850	6.64	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1827	14854	27851	6.64	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1861	14877	27872	6.56	0.0E+00	6005655	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1861	14877	27873	6.56	0.0E+00	6005655	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1861	14887	27883	1.34	0.0E+00	AB032378.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1861	14887	27884	1.34	0.0E+00	AB032378.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1865	14890	27889	3.28	0.0E+00	4820789	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1865	14890	27887	3.28	0.0E+00	4820789	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1865	14891	27888	6.86	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1865	14891	27889	6.86	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1869	14884	27892	1.48	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-4in-407-Q11et NCI_CGAP Sub3 Homo sapiens cDNA clone IMAGE:2772333 3'
1869	14894	27893	1.48	0.0E+00	AW207280.1	EST_HUMAN	UI-H-B11-4in-407-Q11et NCI_CGAP Sub3 Homo sapiens cDNA clone IMAGE:2772333 3'
1892	14917	27912	3.46	0.0E+00	BE277466.1	EST_HUMAN	G01179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1892	14917	27913	3.46	0.0E+00	BE277466.1	EST_HUMAN	G01179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1899	14910	27956	0.93	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1899	14910	27957	0.93	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1836	14880	27967	2.02	0.0E+00	4908384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1839	14953	27969	2.02	0.0E+00	4908384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1839	14953	27969	2.02	0.0E+00	4908384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1948	14972	27970	1.13	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1949	15881	27970	1.41	0.0E+00	M8478.1	NT	Human transglutaminase mRNA, complete cds
1949	15881	27971	1.41	0.0E+00	M8478.1	NT	Human transglutaminase mRNA, complete cds
1949	15881	27971	1.41	0.0E+00	M8478.1	NT	Human transglutaminase mRNA, complete cds
1954	14977	27978	2.02	0.0E+00	4307484	NT	Homo sapiens transforming growth factor, beta 3 (TGFβ3), mRNA
1954	14977	27979	2.02	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGFβ3), mRNA
1957	14976	27981	1.06	0.0E+00	7657038	NT	Homo sapiens death receptor 8 (DR8), mRNA
1957	14976	27981	1.06	0.0E+00	7657038	NT	Homo sapiens death receptor 8 (DR8), mRNA
1957	14976	27981	1.06	0.0E+00	7657038	NT	Homo sapiens death receptor 8 (DR8), mRNA
1959	14981		5.63	0.0E+00	AF240788.1	NT	Homo sapiens gliothione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1959	14981		5.63	0.0E+00	AF240788.1	NT	Homo sapiens gliothione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1964	14986		2.83	0.0E+00	M55932.1	NT	Human topoisomerase 1 pseudogene 1
1965	15892	27983	1.46	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTNSA2), mRNA
1973	14984	27985	1.88	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1973	14984	27985	1.88	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1973	14984	27986	1.88	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1984	15005		0.9	0.0E+00	AL183252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1988	15007	28010	1.81	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1988	15007	28011	1.81	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1988	15007	28011	1.81	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1987	15008	28012	2.97	0.0E+00	4826838	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1987	15008	28013	2.87	0.0E+00	4826838	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1997	15018	28025	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIA04780 protein, partial cds
1997	15018	28025	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIA04780 protein, partial cds
1997	15018	28026	1.05	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIA04780 protein, partial cds
2003	15024	28030	1.58	0.0E+00	M33762.1	NT	Human TEEB protein KIAA0790, partial cds

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2003	15024	28031	1.59	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2005	15026	28032	1.29	0.0E+00	AW183024.1	EST_HUMAN	X69601.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2678913 3'
2005	15028	28033	1.29	0.0E+00	AW183024.1	EST_HUMAN	X69601.x1 NCI_CGAP_Pant Homo sapiens cDNA clone IMAGE:2678913 3'
2006	15027	28034	6.16	0.0E+00	6512457	NT	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
2006	15027	28036	6.16	0.0E+00	6512457	NT	Homo sapiens calcineurin binding protein 1 (KIA0330), mRNA
2008	15029	28037	1.33	0.0E+00	AB011149.1	NT	Homo sapiens protein, complete cds
2009	15030	28038	1.36	0.0E+00	Z47558.1	NT	H.sapiens genes for semenogelin I and semenogelin II
2009	15030	28039	1.36	0.0E+00	Z47558.1	NT	H.sapiens genes for semenogelin I and semenogelin II
2016	15037	28048	3.07	0.0E+00	AB040948.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2036	15055	28072	1.16	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2036	15055	28073	1.16	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2069	15086	28104	1.04	0.0E+00	7706742	NT	Homo sapiens TP53 T33a (TP53T33a), mRNA
2074	15091	28108	0.92	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2075	15092	28109	4.79	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2077	15094	28111	1.69	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2077	15094	28112	1.69	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2079	15098		3.76	0.0E+00	7857458	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2081	15098		1.64	0.0E+00	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2083	15100		1.7	0.0E+00	A1244247.1	EST_HUMAN	q80008.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:198871 3' similar to contains Alu repetitive element
2088	15105	28123	3.3	0.0E+00	BE677225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2089	15106	28124	1.88	0.0E+00	BF316325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2089	15106	28125	1.88	0.0E+00	BF316325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2093	15110	28129	2.38	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2093	15110	28130	2.38	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2098	15115	28136	2.35	0.0E+00	LD0820.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 2 (AP2B2) mRNA, complete cds
2098	15115	28137	2.35	0.0E+00	LD0820.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 2 (AP2B2) mRNA, complete cds
2103	15120	28147	2.29	0.0E+00	LD06520.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2122	15139		3.16	0.0E+00	BE767963.1	EST_HUMAN	GV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2123	15140		1.29	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 8 and complete cds
2125	15142	28159	3.87	0.0E+00	BF027582.1	EST_HUMAN	601672056F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3964785 5'
2126	15143	28160	1.42	0.0E+00	BE072624.1	EST_HUMAN	PM0-B10647-210300-004-F04 B10647 Homo sapiens cDNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2128	15145	28161	1.20	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2131	15149	28163	2.95	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT10219-27.059-022-Q10 C10219 Homo sapiens cDNA
2133	15160	28165	4.92	0.0E+00	A090480.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2133	15150	28166	4.92	0.0E+00	A090460.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2191	15206		1.37	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2166	15211	28229	0.63	0.0E+00	BE274698.1	EST_HUMAN	601122338FT NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3346988 5'
2198	15213	28232	19.22	0.0E+00	AV739288.1	EST_HUMAN	AV739288 CB Homo sapiens cDNA clone CBNBDE08 5'
2198	15213	28233	18.22	0.0E+00	AV739288.1	EST_HUMAN	AV739288 CB Homo sapiens cDNA clone CBNBDE08 5'
2200	15216	28235	1.76	0.0E+00	AA931691.1	EST_HUMAN	cc32601.st NCI_CGAP_Lus Homo sapiens cDNA clone CBNBDE08 5'
2204	15219	28239	32.02	0.0E+00	BF344434.1	EST_HUMAN	602014823FT NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2205	15220	28240	25.7	0.0E+00	BE748599.1	EST_HUMAN	601572186FT NIH_MGC 35 Homo sapiens cDNA clone IMAGE:3835012 3'
2209	15224	28245	6.56	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2209	15224	28245	6.56	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2213	15887	28250	1.7	0.0E+00	BF313671.1	EST_HUMAN	601800281FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2216	15230	28253	1.26	0.0E+00	BE018750.1	EST_HUMAN	b694602.yt NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN;
2217	15231	28254	1.59	0.0E+00	AA042813.1	EST_HUMAN	2453007.at Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:XB5867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOYE (HUMAN);
2217	15231	28255	1.59	0.0E+00	AA042813.1	EST_HUMAN	2453007.at Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:XB5867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPOYE (HUMAN);
2225	15239	28263	3.38	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2225	15239	28264	3.38	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2230	15244		1.57	0.0E+00	U36289.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2252	15266	28293	7.38	0.0E+00	4557566	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2258	15272	28297	1.33	0.0E+00	7562401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2264	15278	28303	2.29	0.0E+00	BE895281.1	EST_HUMAN	901433325FT NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918507 5'
2266	15280	28305	1.56	0.0E+00	BE905563.1	EST_HUMAN	901435208FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2266	15280	28306	1.56	0.0E+00	BE905563.1	EST_HUMAN	901435208FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2269	15282	28308	1.54	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1383 protein, partial cds
2308	15320	28340	1.32	0.0E+00	BF344756.1	EST_HUMAN	902014009FT NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149770 5'
2308	15320	28341	1.32	0.0E+00	BF344756.1	EST_HUMAN	902014009FT NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149770 5'
2309	15321	28342	4.01	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 8 (DEF8), mRNA
2309	15321	28343	4.01	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 8 (DEF8), mRNA

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2310	15322	28344	2.11	0.0E+00	AJ076404.1	EST_HUMAN	cc0602.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2312	15324	28346	1.43	0.0E+00	AA428001.1	EST_HUMAN	207ba11.r1 Soares fetal_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:759740 5'
2312	15324	28347	1.43	0.0E+00	AA428001.1	EST_HUMAN	207ba11.r1 Soares fetal_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:759740 5'
2314	15328	28349	2.21	0.0E+00	BF347039.1	EST_HUMAN	6020218a6f1.NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157338 5'
2316	14572	27944	1.36	0.0E+00	M16768.1	NT	Human T-cell receptor gamma chain VJ-CJ-CJ1 region mRNA, complete cds
2320	15331	28355	1.09	0.0E+00	U02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2321	15332	28356	1.67	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2327	15338	28361	1.83	0.0E+00	BE676095.1	EST_HUMAN	7122a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3296370 3' similar to TR:094939 094939 KIAA0657 PROTEIN ;
2330	15341	28363	5.18	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PHK42) gene, exon 32
2331	15342	28364	2.11	0.0E+00	AI625542.1	EST_HUMAN	367c08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2283182 3'
2336	15347	28368	1.76	0.0E+00	5603178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2336	15347	28369	1.76	0.0E+00	5603178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2342	15352	28372	1.44	0.0E+00	7652007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2342	15352	28373	1.44	0.0E+00	7652007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2346	15355	28377	0.97	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2346	15355	28378	0.97	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2356	15365	28386	3.71	0.0E+00	5174878	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2360	15368	28390	1.86	0.0E+00	AU131142.1	EST_HUMAN	AU131142.NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2361	15369		8.67	0.0E+00	BE784028.1	EST_HUMAN	801568643.F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2362	15370	28391	1.23	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-e04 SN0033 Homo sapiens cDNA
2363	15371	28392	3.7	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2364	15372	28393	2.27	0.0E+00	4755497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2364	15372	28394	2.27	0.0E+00	4755497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2365	15373		6.34	0.0E+00	AF260107.1	NT	4 (CYP3A4) and cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2367	15375	28396	13.47	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2367	15375	28397	13.47	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2367	15375	28398	13.47	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2368	15376	28399	0.96	0.0E+00	8923089	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2424	15431	28453	1.11	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2426	15433		4.37	0.0E+00	AI042035.1	EST_HUMAN	cc0602.x1 Soares NIHMP1_S1 Homo sapiens cDNA clone IMAGE:1660983 3' similar to TR:008652 008662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ;

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2429	15436		1.2	0.0E+00	BE69605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2439	15446		1.83	0.0E+00	AB005922.1	EST_HUMAN	AB005922.1 HeLa cDNA (T.Homo) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2443	15449	28468	5.37	0.0E+00	6066002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2448	15451	28471	2.23	0.0E+00	D85608.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2448	15451	28472	2.23	0.0E+00	D85608.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2454	15459	28481	3.38	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (IL116) gene, exon 6
2459	15463	28486	1.08	0.0E+00	BF345274.1	EST_HUMAN	602018038F1 NCI_CGAP_Bn57 Homo sapiens cDNA clone IMAGE:4153670 5'
2466	15470	28494	3.44	0.0E+00	5726777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2470	15474	28497	1.27	0.0E+00	BE831003.1	EST_HUMAN	GM6-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2470	15474	28498	1.27	0.0E+00	BE831003.1	EST_HUMAN	GM6-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2475	15479	28502	1.03	0.0E+00	U13668.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2475	15479	28503	1.03	0.0E+00	U13668.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2478	15480	28504	3.72	0.0E+00	BF669144.1	EST_HUMAN	602184598T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300393 3'
2486	15490	28514	2.12	0.0E+00	AW46922.1	EST_HUMAN	h6c4h04.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2872759 3'
2488	15492	28515	3.03	0.0E+00	AW501010.1	EST_HUMAN	U1HF-BF0p-as-c-07-Q-U1r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2513	15516		2.64	0.0E+00	AW813853.1	EST_HUMAN	RC9-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2517	15520	28543	11.9	0.0E+00	BF765542.1	EST_HUMAN	U1H4B14-ec2-b-08-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3946518 5'
2518	15521	28544	1.43	0.0E+00	BF609482.1	EST_HUMAN	Homo sapiens mRNA for membrane transport protein (XK gene)
2521	15524	28546	2.28	0.0E+00	Z32984.2	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
2523	15526		4.59	0.0E+00	5453871	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
2526	15529	28550	3.56	0.0E+00	7657468	NT	Human Sec62 (Sec62) mRNA, complete cds
2627	15530	28551	2.61	0.0E+00	U82239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2533	15538	28557	1.6	0.0E+00	BE866490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909868 5'
2538	15540	28563	6.2	0.0E+00	BE879511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2538	15540	28564	6.2	0.0E+00	BE879511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2539	15541	28565	1.07	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF8
2541	15543	28566	1.11	0.0E+00	AF245505.1	NT	Homo sapiens adiponectin mRNA, complete cds
2558	15560	28576	1.23	0.0E+00	BE536927.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2563	15564	28583	3.18	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2564	15565	28584	3.18	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2564	15565	28585	1.51	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2564	15565	28586	1.51	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2565	15566	28587	1.4	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE_3' similar to TR:000246 000246 HYPOTHETICAL 8.3 KD PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2568	15699	26589	8.56	0.0E+00	AF245505.1	NT	Homo sapiens actinin mRNA, complete cds
2569	15690	26597	1.03	0.0E+00	BE296813.1	EST_HUMAN	601173631FT NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3529159 5'
2606	15627	26626	2.15	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2608	15627	26580	2.15	0.0E+00	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2607	15606		2.35	0.0E+00	BF519835.1	EST_HUMAN	UHHBW1-ramp-1-2-JUL-81 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:4293872 5'
2611	15610	26634	1.01	0.0E+00	BF672818.1	EST_HUMAN	602152653FT NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4293872 5'
2620	15618	26642	1.11	0.0E+00	AJ571737.1	EST_HUMAN	h19508.xt NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2168056 3' similar to gbl20877 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2621	15619	26643	2.57	0.0E+00	5032160	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28KD (TAF2)
2623	15622	26647	7.78	0.0E+00	AB037859.1	NT	mRNA
2624	15623	26648	1.25	0.0E+00	BE795445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2624	15623	26549	1.25	0.0E+00	BE795445.1	EST_HUMAN	601550108FT NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3944304 5'
2634	15633		8.15	0.0E+00	BE792472.1	EST_HUMAN	601554303FT NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3839222 5'
2642	15640	26584	2.66	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2653	15650		1.32	0.0E+00	U75027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
2654	15651	26672	5.99	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2658	15655	26673	110.09	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2661	15658	26676	1.22	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP-4001964 5'
2662	15659	26677	0.92	0.0E+00	MG9225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2664	15661	26679	1.26	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2664	15661	26680	1.26	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2667	15664	26683	2.07	0.0E+00	AW897015.1	EST_HUMAN	RC1-OT0088-220300-011-407 OT0088 Homo sapiens cDNA
2670	15667	26586	1.12	0.0E+00	BF000018.1	EST_HUMAN	7h1505.xt NCI CGAP C678 Homo sapiens cDNA clone IMAGE:3316086 3'
2671	15668	26687	5.39	0.0E+00	BE383165.1	EST_HUMAN	601286714FT NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3628923 5'
2672	15669		3.03	0.0E+00	BE383163.1	EST_HUMAN	601278373FT NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3610267 5'
2709	15703	26719	0.82	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2732	15726		11.44	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2733	15727	26741	1.11	0.0E+00	BE794894.1	EST_HUMAN	601569623FT NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3943591 5'
2739	15733	26748	3.65	0.0E+00	U92853.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2740	15734	26750	1.05	0.0E+00	7659517	NT	Homo sapiens nucleogelin 1 (NRG1),transcript variant SMDF, mRNA
2741	15735	26751	1.6	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2748	15741	28798	9.77	0.0E+00	BE796378.1	EST HUMAN	601561991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2751	15803	28792	13.57	0.0E+00	BE563433.1	EST HUMAN	601335495F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688584 5'
2752	15744		1.22	0.0E+00	AV721647.1	EST HUMAN	AV721647 HTB Homo sapiens cDNA clone HTB8YE59 5'
2754	15748	28795	2.9	0.0E+00	5174496	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2754	15748	28796	2.9	0.0E+00	5174496	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2755	15747	28797	0.98	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477). mRNA
2755	15747	28798	0.98	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477). mRNA
2756	15748	28799	3.23	0.0E+00	AF290195.1	NT	Homo sapiens hypoxanthine-related calcium-regulated gene mRNA, complete cds
2757	15749		48.84	0.0E+00	AV651068.1	EST HUMAN	AV651068 GLG Homo sapiens cDNA clone GLG.D07.3'
2758	15750	28770	8.5	0.0E+00	BF377897.1	EST HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2758	15750	28771	6.5	0.0E+00	BF377897.1	EST HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2762	15754	28774	0.94	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (GDR1) mRNA
2762	15754	28775	0.94	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (GDR1) mRNA
2766	15758	28780	2.96	0.0E+00	BE747193.1	EST HUMAN	601560903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2779	15771		1.71	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2780	15772	28792	4.09	0.0E+00	BF514110.1	EST HUMAN	UI-H-BW1-arnw-e-07-Q-UI lat NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3077340 3'
2786	15778		1.02	0.0E+00	4503098	NT	Homo sapiens chondroclitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2792	15784	28800	1.56	0.0E+00	7705275	NT	Homo sapiens angiodiath-3 (ANG-3), mRNA
2792	15784	28801	1.58	0.0E+00	7705275	NT	Homo sapiens angiodiath-3 (ANG-3), mRNA
2793	15785	28802	4.03	0.0E+00	BF677894.1	EST HUMAN	60208579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248915 5'
2796	15791	28810	1.58	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR), mRNA
2803	15796	28813	15.3	0.0E+00	AV725534.1	EST HUMAN	AV725534 HTG Homo sapiens cDNA clone HTCCOA03 5'
2803	15796	28814	15.3	0.0E+00	AV725534.1	EST HUMAN	AV725534 HTG Homo sapiens cDNA clone HTCCOA03 5'
2806	15797		13.6	0.0E+00	AI879163.1	EST HUMAN	au55604.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2618663 5' similar to SW-RT13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2808	15800	28819	2.83	0.0E+00	BF530661.1	EST HUMAN	60207169F1 NC1 CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4214679 5'
2809	15801	28820	3.53	0.0E+00	BE827268.1	EST HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854942 5'
2811	15803	28821	1.98	0.0E+00	AU131494.1	EST HUMAN	AU131494 NT-2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2811	15803	28822	1.98	0.0E+00	AU131494.1	EST HUMAN	AU131494 NT-2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2812	15804	28823	34.94	0.0E+00	BE300344.1	EST HUMAN	60094794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2812	15804	28824	34.94	0.0E+00	BE300344.1	EST HUMAN	60094794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2817	13290	28216	7.12	0.0E+00	S76830.1	NT	glycoprotein D=bulky group antigen [human, blood, Genomic DNA, 3068 nt]
2820	19811		0.75	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2826	13798	28735	1.8	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2828	13786	28736	1.6	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2830	14089	27037	3.41	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2830	14086	27038	3.41	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2847	15907	28832	2.28	0.0E+00	X85980.1	NT	H sapiens serine hydroxymethyltransferase pseudogene
2848	15908	28844	3.02	0.0E+00	AF038824.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2850	15910		1.6	0.0E+00	AB040660.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2852	15912	28835	1.07	0.0E+00	4502568	NT	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10) mRNA
2852	15912	28836	1.07	0.0E+00	4502568	NT	Homo sapiens caspase 10, apoptosis-related cysteine protease (CASP10) mRNA
2857	15917		0.98	0.0E+00	AJ238952.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2858	15918	28839	3.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2862	15922	28842	1.8	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2865	15925	28844	0.88	0.0E+00	BE154650.1	EST HUMAN	PMO-HT0343-281298-003-e02 HT0343 Homo sapiens cDNA
2865	15925	28846	0.88	0.0E+00	BE154650.1	EST HUMAN	PMO-HT0343-281298-003-e02 HT0343 Homo sapiens cDNA
2867	15927		1.48	0.0E+00	X73428.1	NT	H sapiens d3 gene for HLH type transcription factor
2868	15928		3.61	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2870	15930	28847	1	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2874	15933	28850	25.84	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2874	15933	28851	25.84	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2877	15936	28854	2.34	0.0E+00	AL068857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2878	15937		5.17	0.0E+00	Y10658.1	NT	H sapiens mRNA for nuclear DNA helicase II
2879	15938		1.17	0.0E+00	AF152003.1	NT	Homo sapiens protoadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2880	15939	28855	61.62	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2880	15939	28856	61.62	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2891	15950	28866	2.45	0.0E+00	4507260	NT	Homo sapiens serine/threonine kinase 6 (STKG) mRNA
2894	15953	28870	0.91	0.0E+00	AL047599.1	EST_HUMAN	DKFZp566G0621.1 586 (synonym: tules) Homo sapiens cDNA clone DKFZp566G0621
2895	15954	28871	1.07	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2895	15954	28872	1.07	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2896	15955		2.07	0.0E+00	4503098	NT	Homo sapiens chondroclitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2898	15957	28874	5.43	0.0E+00	BE081898.1	EST_HUMAN	QV2BT0636-130400-138-N03 BT0636 Homo sapiens cDNA
2898	15957	28875	5.43	0.0E+00	BE081898.1	EST_HUMAN	QV2BT0636-130400-138-N03 BT0636 Homo sapiens cDNA
2903	15962	28883	0.63	0.0E+00	6600918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	OFF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2903	15982	28884	0.93	0.0E+00	6808918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2908	15988	28888	2.92	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2908	15985	28889	2.92	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
2907	15986	28890	0.94	0.0E+00	A4215579.1	EST_HUMAN	z99b11.at NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:183517 3' similar to contains Ali
2915	15973		4.07	0.0E+00	Y19210.1	NT	Homo sapiens RH55 gene for hair keratin, exons 1 to 9
2918	15976	28900	1.17	0.0E+00	4758270	NT	Homo sapiens EphA4 (EPHA4) mRNA
2919	15977	28901	23.04	0.0E+00	4803470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2920	15978	28902	0.92	0.0E+00	AI581002.1	EST_HUMAN	t18d07.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2920	15978	28903	0.92	0.0E+00	AI581002.1	EST_HUMAN	t18d07.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2922	15980	28905	0.97	0.0E+00	AF162338.1	NT	Homo sapiens protodactherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2931	15989	28910	1.28	0.0E+00	AI209084.1	EST_HUMAN	SW:CB20_HUMAN_P52289.20 KD NUCLEAR CAP BINDING PROTEIN;
2939	15997	28918	2.92	0.0E+00	AB033083.1	NT	g64904.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1838327 3' similar to
2939	15997	28918	2.92	0.0E+00	AB033083.1	NT	SW:CB20_HUMAN_P52289.20 KD NUCLEAR CAP BINDING PROTEIN;
2940	15998	28920	4.91	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2940	15998	28921	4.91	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2943	16001	28924	2.96	0.0E+00	7861903	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2943	16001	28925	2.56	0.0E+00	7861903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2944	16002	28926	2.73	0.0E+00	5174574	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2944	16002	28926	2.73	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology), translocated to, 4
2944	16002	28927	2.73	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) homology), translocated to, 4
2956	16014	28941	2.96	0.0E+00	4505084	NT	(MLL14) mRNA
2958	16014	28942	2.96	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2958	16023	28948	1.71	0.0E+00	4758827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2958	16024		1.03	0.0E+00	X89404.1	NT	Homo sapiens neuroxin III (NRXN3) mRNA
2971	16029	28982	7.63	0.0E+00	AF106275.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2985	16043		1.1	0.0E+00	AI149880.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 10 variant 4 (ILT10) gene, exon 6
2984	16052	28973	0.97	0.0E+00	4503118	NT	g43069.x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1762806 3'
2985	16053	28974	2.71	0.0E+00	AB004884.1	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3007	16055	28984	1.51	0.0E+00	7862273	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3007	16055	28984	1.51	0.0E+00	7862273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3008	16058	28885	1.96	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3008	16058	28886	1.96	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3016	16074	28894	2.8994	0.0E+00	AF114488.1	NT	Homo sapiens intracellular short isoform (ITSN) mRNA, complete cds
3016	16074	28895	0.95	0.0E+00	AF114488.1	NT	Homo sapiens intracellular short isoform (ITSN) mRNA, complete cds
3038	16093		0.74	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
3040	16098	28014	1.28	0.0E+00	MT4099.1	NT	Human displacement protein (CCAR1) mRNA
3050	16107	29021	0.88	0.0E+00	4508882	NT	Homo sapiens semaphorin 1 (SEMG1) mRNA
3052	16109	29023	0.76	0.0E+00	AW976205.1	EST_HUMAN	EST3388375 MAGE resequences, MAGN Homo sapiens cDNA
3057	16114		4.37	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase F (XNPEP2) gene, complete cds
3060	16117	29031	15.24	0.0E+00	5579469	NT	Homo sapiens heat shock 70KD protein 1 (HSPA1A), mRNA
3060	16117	29032	15.24	0.0E+00	5579469	NT	Homo sapiens heat shock 70KD protein 1 (HSPA1A), mRNA
3062	16119		6.14	0.0E+00	AL359403.1	NT	isoform 2 of a novel human mRNA from chromosome 22
3068	16123	29036	2.48	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
3069	16128		1.86	0.0E+00	AF198779.1	NT	Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel alpha
3084	16141	29052	0.73	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3092	16150	29064	12.09	0.0E+00	X03528.1	NT	Human germline gene 18.1 for Ig lambda L-chain C region (Ig-LC18.1)
3098	16155		1.77	0.0E+00	AF168355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3102	16159	29071	1.71	0.0E+00	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3123	16180	29080	4.2	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3124	16181	29091	4.68	0.0E+00	AF146773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3129	16186	29095	2.83	0.0E+00	7662139	NT	Homo sapiens KIA0469 gene product (KIA0469) mRNA
3130	16187	29096	1.56	0.0E+00	AF042073.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 428) gene, OLFR 428-9110 allele, partial cds
3167	16213	29128	4.32	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3165	16220	29135	22.34	0.0E+00	20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3168	16223	29138	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIA00549 protein, partial cds
3168	16223	29139	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIA00549 protein, partial cds
3174	16229	29145	21.23	0.0E+00	T94870.1	EST_HUMAN	ye32003 s1 Stralagene lung (H937210) Homo sapiens cDNA clone IMAGE:19483 3' similar to SP:529539
3190	16245	29163	1.13	0.0E+00	BF243336.1	EST_HUMAN	801878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3192	16247	29164	1.11	0.0E+00	AI960086.1	EST_HUMAN	wt1210.x1 NCL_CGAP_066 Homo sapiens cDNA clone IMAGE:2516903 3'
3197	16252	29171	4.28	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3197	16252	29172	4.28	0.0E+00	X68922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3207	16262	29183	1.76	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3207	16262	29184	1.16	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3213	16268	29191	9.91	0.0E+00	4504668	NT	Homo sapiens interleukin 1 receptor, type 1 (IL1R1) mRNA
3220	16285	29208	3.9	0.0E+00	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPB1) mRNA, complete cds
3234	16289	29211	1.65	0.0E+00	4502008	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3240	16295	29220	0.98	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubsenstein-Taydi syndrome) (CREBBP) mRNA
3240	16295	29220	0.98	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubsenstein-Taydi syndrome) (CREBBP) mRNA
3242	16307	29221	3.36	0.0E+00	AA74783.1	EST_HUMAN	aa74781.37 Strabagene echiza brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3250	16305	29229	3.98	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3250	16305	29230	3.98	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3261	16316	29236	1.16	0.0E+00	4557560	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3267	16321	29243	1.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3275	16329	29250	1.04	0.0E+00	AF019413.1	NT	Homo sapiens HLA class II region containing tenascin X (tenascin-X) gene, partial cds: cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
3276	16332	29253	4.45	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3288	16312	29281	2.4	0.0E+00	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3288	16312	29282	2.4	0.0E+00	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3303	16356	29276	2.99	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3304	16357	29278	0.96	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3335	16386	29307	2.97	0.0E+00	A1599294.1	EST_HUMAN	f68f08.c2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222635 3' similar to SWRL11_RAT
3343	16394	29315	2.44	0.0E+00	AF129893.1	NT	P29121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element
3343	16394	29316	2.44	0.0E+00	AF129893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3344	16395	29317	0.85	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3344	16395	29318	0.85	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3346	16397	29319	1.11	0.0E+00	4502562	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3346	16397	29320	1.11	0.0E+00	4502562	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3349	16400	29322	10.77	0.0E+00	AF111163.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3351	16402	29324	1.09	0.0E+00	AB040940.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3358	16408	29330	0.85	0.0E+00	BE778039.1	EST_HUMAN	Homo sapiens mRNA for KIAA1507 protein, partial cds
							307464959F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868245 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3369	16419	29344	0.78	0.0E+00	AI032569.1	EST_HUMAN	wb1004.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91928 Q91929
3407	16459	29379	4.18	0.0E+00	AU123654.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3414	16462	29382	1.15	0.0E+00	7363438	NT	AU123654 NT2RM2 Homo sapiens cDNA clone NIT2RM200735 5'
3414	16462	29383	1.15	0.0E+00	7363438	NT	Homo sapiens effector receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3417	16465	29385	8.20	0.0E+00	7706239	NT	Homo sapiens effector receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3417	16465	29385	8.20	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC31594), mRNA
3418	16466	29386	1.51	0.0E+00	AF211188.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
3438	16483	29401	1.13	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3438	16483	29402	1.13	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3437	16484	29403	1.05	0.0E+00	4552398	NT	Homo sapiens beaded filament structural protein 1, flensin (BFSP1) mRNA
3441	16488	29406	2.77	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LLRA2), mRNA
3450	15735	29751	1.38	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3455	16501	29419	2.18	0.0E+00	7857038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3456	16502	29420	1.05	0.0E+00	6453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3456	16502	29421	1.05	0.0E+00	6453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3469	16505	29425	1	0.0E+00	AJ271278.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3459	16505	29426	1	0.0E+00	AJ271278.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3460	16506	29427	5.55	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and hcrA, hcrB, and hcrC
3463	16509	29430	1.31	0.0E+00	7427522	NT	Incompatibility determinants
3469	16515	29435	5.12	0.0E+00	AJ035169.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3469	16515	29435	5.12	0.0E+00	AJ035169.1	EST_HUMAN	NEURAL CELL ADHESION MOLECULE ;
3469	16515	29436	5.12	0.0E+00	AJ035169.1	EST_HUMAN	NEURAL CELL ADHESION MOLECULE ;
3473	16519	29441	1.65	0.0E+00	AJ278120.1	NT	wp14410.x1 NCL CGAP_Lut19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3479	16525	29448	6.24	0.0E+00	6552332	NT	NEURAL CELL ADHESION MOLECULE ;
3479	16525	29450	6.24	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3485	16531	29456	1.06	0.0E+00	M14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3485	16531	29456	1.06	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3490	16544	29469	1.85	0.0E+00	AFO45452.1	NT	Human MDST1 (AML1/MDST1 fusion) mRNA, partial cds
3497	16544	29470	1.85	0.0E+00	AFO45452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3497	16544	29470	1.85	0.0E+00	AFO45452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3504	16551	29478	0.89	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3516	16552	29486	2.29	0.0E+00	BE304791.1	EST_HUMAN	601143653F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3516	16552	29487	2.28	0.0E+00	BE304791.1	EST_HUMAN	601143653F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3519	16555	29490	1.07	0.0E+00	4828785	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNK2) mRNA
3521	16557	29491	1.24	0.0E+00	O14867	SWISSPROT	TRANSRIPTION REGULATOR PROTEIN BACH1 (BTB and CNC HOMOLOG 1) (HA2303)
3526	16572	29495	0.88	0.0E+00	A1384007.1	EST_HUMAN	0035912.x1 Soares_NHMPc.S1 Homo sapiens cDNA clone IMAGE:2068742 3' similar to TRC00498
3529	16576	29498	1.08	0.0E+00	M10976.1	NT	ADA488 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN :
3543	16589	29513	0.92	0.0E+00	AB032979.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3543	16589	29514	0.92	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3551	16597	29523	1.38	0.0E+00	AY701869.1	EST_HUMAN	Homo sapiens mRNA for KIAA1153 protein, partial cds
3552	16598	29523	0.92	0.0E+00	4500884	NT	AY701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3554	16600	29531	1.03	0.0E+00	AF078838.1	NT	Homo sapiens ceromogelin II (SEMG2) mRNA
3563	16609	29531	0.92	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3567	16612	29534	1.21	0.0E+00	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3578	16623	29544	1.33	0.0E+00	8823087	NT	Homo sapiens hypothetical protein FLJ20060 (PLJ20060) mRNA
3588	16633	29551	1.16	0.0E+00	6897248	NT	Homo sapiens esi (Drosophila)-like 1 (SALL1), mRNA
3588	16633	29552	1.16	0.0E+00	6897248	NT	Homo sapiens esi (Drosophila)-like 1 (SALL1), mRNA
3590	16635	29555	1.04	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3595	16640	29555	4.89	0.0E+00	AW852217.1	EST_HUMAN	QVQ-CT0225-230300-186-e01 CT0225 Homo sapiens cDNA
3602	16647	29564	1.35	0.0E+00	AF118848.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLC1C) gene, partial cds
3603	16648	29564	10.81	0.0E+00	BF676393.1	EST_HUMAN	602084933F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248566 5'
3617	16661	29576	1.04	0.0E+00	AW637677.1	EST_HUMAN	QVQ-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3628	16672	29585	1.46	0.0E+00	BF672054.1	EST_HUMAN	602152488F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283645 5'
3629	16672	29586	1.48	0.0E+00	BF672054.1	EST_HUMAN	602152488F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283645 5'
3630	16673	29586	0.84	0.0E+00	4829967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3632	16675	29588	0.84	0.0E+00	AW654693.1	EST_HUMAN	H84g01.x1 Soares_NFL_T_58G_S1 Homo sapiens cDNA clone IMAGE:2976024 3'
3632	16675	29588	0.84	0.0E+00	AW654693.1	EST_HUMAN	H84g01.x1 Soares_NFL_T_58G_S1 Homo sapiens cDNA clone IMAGE:2976024 3'
3638	16678	29593	0.83	0.0E+00	4828763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HSST1) mRNA
3638	16681	29596	1.03	0.0E+00	7662319	NT	Homo sapiens KIA0808 gene product (KIA0808), mRNA
3646	16689	29604	0.87	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3646	16689	29605	0.87	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3651	16704	29618	3.11	0.0E+00	DB7327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3654	16707	29637	10.78	0.0E+00	7889491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD) mRNA
3661	16724	29637	16.15	0.0E+00	AB028542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3885	16728	296939	4.02	0.0E+00	AF124280.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3885	16728	296940	4.02	0.0E+00	AF124280.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3892	16735	296947	1.6	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3892	16735	296948	1.6	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3895	16738	296951	1.34	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281039-005-005 CT0222 Homo sapiens cDNA
3897	16740	296953	2.88	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3899	16742	296955	1.37	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0766 protein, partial cds
3701	16744	296957	0.72	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3703	16746	296958	1.45	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3703	16748	296960	1.45	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3705	16749	296962	1	0.0E+00	7692237	NT	Homo sapiens KIAA0670 protein/ectinus (KIAA0670), mRNA
3705	16749	296963	1	0.0E+00	7692237	NT	Homo sapiens KIAA0670 protein/ectinus (KIAA0670), mRNA
3719	16762	296972	4.6	0.0E+00	AW298134.1	EST_HUMAN	U1-HBW0-ajis-e-12-0-U1.s1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:2733022 3'
3719	16762	296973	4.6	0.0E+00	AW298134.1	EST_HUMAN	U1-HBW0-ajis-e-12-0-U1.s1 NCL_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:2733022 3'
3742	16784	296986	1.47	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen at chain, exon 8
3743	16785	296987	1.06	0.0E+00	AA463659.1	EST_HUMAN	sed0601.r1 Scores_NIHMP_U_S1 Homo sapiens cDNA clone IMAGE:812498 5' similar to SW_KRBA_SHHEEP_P02445 KERA-TIN, HIGH-SULFUR MATRIX PROTEIN, IIB4, [1];
3747	16789	29701	0.76	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3760	16792	29703	3.92	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
3760	16801	29713	0.77	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3772	16814	29723	5.64	0.0E+00	7652163	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3775	16817	29726	19.76	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3781	16822	29729	0.97	0.0E+00	7657085	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3781	16822	29730	0.97	0.0E+00	7657085	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3784	16825	29733	0.92	0.0E+00	4505594	NT	Homo sapiens plasmalogen activator inhibitor, type II (arginine-serpin) (PAI2) mRNA
3834	16874	29776	3.15	0.0E+00	AF178733.1	NT	Pan troglodytes olfactory receptor (PTR203) gene, partial cds
3837	16877	29776	2.76	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
3837	16877	29780	2.76	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
3843	16883	29787	0.91	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3843	16883	29788	0.91	0.0E+00	AF127851.1	EST_HUMAN	GGO71 olfactory receptor (GGO71) gene, partial cds
3844	16884	29789	1.01	0.0E+00	AI377699.1	EST_HUMAN	166210.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3845	16885	29789	1.81	0.0E+00	AF152496.1	NT	Homo sapiens procadherin beta 3 (PCDH-beta3) mRNA, complete cds
3946	16888	29790	0.97	0.0E+00	4759189	NT	Homo sapiens desmoplakin (DP1, DP1L) (DSP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3850	18880	28784	18.28	0.0E+00	578695.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3852	18892	28786	2.25	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3853	18893	28797	1.54	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product [KIAA0569], mRNA
3857	18897	28800	1.1	0.0E+00	4504334	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D), mRNA
3862	18901	28805	1.16	0.0E+00	AB001523.1	NT	Homo sapiens gene for TIME1 and PWP2 complete and partial cds
3862	18901	28806	1.16	0.0E+00	AB001523.1	NT	Homo sapiens gene for TIME1 and PWP2 complete and partial cds
3863	18902	28807	0.77	0.0E+00	5912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3868	18907	28815	7.17	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA
3868	18907	28816	7.17	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA
3870	18909	28819	4.34	0.0E+00	U08412.1	NT	Human zinc finger protein ZNF134, complete cds
3871	18910	28820	1.13	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), mRNA, complete cds
3874	18913	28822	1.29	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
3877	18916	28825	1.3	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3878	18917	28828	2.38	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3880	18919	28828	0.73	0.0E+00	AF069117.1	NT	Homo sapiens amphiphysin gene, partial cds
3889	18929	28838	2.34	0.0E+00	AI864727.1	EST_HUMAN	wk0101_x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR-043340
3892	18932	28842	13.72	0.0E+00	4508742	NT	Q43340 R28830_2, contains element PTR7 repetitive element ;
3897	18937	28848	1.39	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3903	18943	28855	1.34	0.0E+00	6005887	NT	DKFZp434N0413.1 494 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0413 5'
3903	18943	28856	1.34	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3904	18944	28857	1.78	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3906	18946	28857	1.75	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
3910	18950	28861	1.09	0.0E+00	AF149412.1	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1), mRNA
3924	18964	28877	1.17	0.0E+00	450758	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3928	18968	28881	1.3	0.0E+00	4585642	NT	Homo sapiens tyrosine receptor 3 (RYR3), mRNA
3936	18978	28890	1.84	0.0E+00	BF365295.1	EST_HUMAN	Homo sapiens zinc finger protein (KIAA0412), mRNA
3937	18977	28891	1.05	0.0E+00	AW88221.1	EST_HUMAN	RC3-H170865-170800-011-412 HT0868 Homo sapiens cDNA
3937	18977	28892	1.05	0.0E+00	AW88221.1	EST_HUMAN	MARRAS Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1998728 similar to MXRA5
3947	18987	28902	1.85	0.0E+00	AF129533.1	EST_HUMAN	Matrix remodeling associated gene 5
3947	18987	28902	1.85	0.0E+00	AF129533.1	EST_HUMAN	Matrix remodeling associated gene 5
3947	18987	28902	1.85	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B), mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3952	16992	29038	3.36	0.0E+00	BE376602.1	EST_HUMAN	807236565F1.NH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
3951	17091	29916	1.06	0.0E+00	AW590740.1	EST_HUMAN	PV33.L70031-100100-003-R09 L70031 Homo sapiens cDNA
4000	17039	29945	5.21	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4001	17039	29946	5.21	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4010	17048		3.56	0.0E+00	M25910.1	NT	Human IMH class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4013	17052		6.54	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4022	17060	29961	3.12	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4031	17069	29970	1.59	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4036	17074	29974	0.99	0.0E+00	S76653.1	NT	intracemas-related [human, Genomic, 2416 nt]
4047	17085		56.15	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4054	17091		1.47	0.0E+00	AI657076.1	EST_HUMAN	365908.X1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:060309 O60309 KIAA0663 PROTEIN. ;
4057	17093	29988	1.43	0.0E+00	7662183	NT	Homo sapiens KIAA0659 gene product (KIAA0659), mRNA
4058	17094	29989	1.57	0.0E+00	U03056.1	NT	Human zinc finger protein ZNF133
4078	17111	30007	5.87	0.0E+00	AB015510.1	NT	Chlorobacillus ethiops mRNA for ribosomal protein S4X, complete cds
4085	17119		3.81	0.0E+00	AJ238517.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4093	17127	30020	1.14	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4094	17128	30021	2.87	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rpsa-2 (rpsa gene)
4094	17128	30022	2.87	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rpsa-2 (rpsa gene)
4100	17134	30028	7.81	0.0E+00	5032028	NT	Homo sapiens reticuloblastoma-binding protein 4 (RBBP4) mRNA
4111	17145	30039	1.27	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phcsphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
4117	17150	30042	4.96	0.0E+00	4985306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4118	17151	30043	1.32	0.0E+00	AB000825.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4121	17154	30044	7.49	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4122	17155	30045	2.95	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4123	17156		1.21	0.0E+00	AA016975.1	EST_HUMAN	ze5509.r1 Soares retina N264-HR Homo sapiens cDNA clone IMAGE:362820 5' similar to contains Alu repetitive element;
4129	17162	30051	3.26	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4138	14177	27127	1.62	0.0E+00	4829547	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4138	14177	27128	1.62	0.0E+00	4829547	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4143	17175	30053	1.26	0.0E+00	5801005	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4144	17176	30064	1.09	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GBTF1) (GABPA), mRNA

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4144	17176	30065	1.09	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
4145	16598	29523	0.86	0.0E+00	4506984	NT	Homo sapiens senegallin II (SENG2), mRNA
4146	17179	30067	0.8	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4148	17179	30068	0.6	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4153	17184	30071	0.86	0.0E+00	AB02702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4159	17180	30078	4.7	0.0E+00	A1892597.1	EST_HUMAN	Wt04004.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2616975 3'
4169	17180	30079	4.7	0.0E+00	A1892597.1	EST_HUMAN	Wt04004.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2616975 3'
4161	17192	30081	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-H10707-100500-001-e02 HT0707 Homo sapiens cDNA
4161	17192	30082	1.2	0.0E+00	BE184856.1	EST_HUMAN	MR1-H10707-100500-001-e02 HT0707 Homo sapiens cDNA
4165	17186	30087	3.88	0.0E+00	BE274217.1	EST_HUMAN	60112078F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2667660 5'
4170	17201	30087	0.93	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4170	17201	30088	0.93	0.0E+00	AB032951.1	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3), mRNA
4172	17203	30090	1.02	0.0E+00	4507478	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4173	17204	30091	2.84	0.0E+00	5729725	NT	Novel human gene on chromosome 20
4174	17205		1.13	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
4183	17214		5.1	0.0E+00	AW675599.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR :
4188	17219	30106	1.12	0.0E+00	AW408786.1	EST_HUMAN	UHF-BM2-adv-c-02-03-UI-1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4190	17221	30109	1.23	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4190	17221	30110	1.23	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4200	17231		4.37	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog-like (PKDREJ)) mRNA
4220	17249	30133	9.8	0.0E+00	AA401438.1	EST_HUMAN	zu8807.a1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4220	17249	30134	9.8	0.0E+00	AA401438.1	EST_HUMAN	zu8807.a1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element ;
4235	17264	30149	1.04	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4235	17264	30160	1.04	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4258	17271		0.87	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4258	17315	30194	1.26	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4302	17331	30211	2.19	0.0E+00	02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4317	17346	30230	0.87	0.0E+00	AW93689.1	EST_HUMAN	PM2-DT0023-000300-004-e08 DT0023 Homo sapiens cDNA
4322	17351	30236	0.74	0.0E+00	4926827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA

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4322	17351	30237	0.74	0.0E+00	4928827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4324	17353	30239	3.59	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein FB4 (FBL-4) mRNA, partial cds
4332	17360		2.58	0.0E+00	AI189844.1	EST_HUMAN	similar to confins1 MER20 b2 MER20 repetitive element;
4336	17363		5.62	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4347	17374	30254	0.92	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4353	17380	30261	0.71	0.0E+00	6563384	NT	Homo sapiens protein kinase C, $\eta$ (PRKCN), mRNA
4353	17380	30262	0.71	0.0E+00	6563384	NT	Homo sapiens protein kinase C, $\eta$ (PRKCN), mRNA
4359	17386	30268	1.15	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4359	17386	30269	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4359	17395	30275	8.53	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4367	17415		1.12	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (Cx36) gene, complete cds
4382	17420	30303	11.19	0.0E+00	U03601.1	NT	Human Ig light chain VL1 region germline (humv1c25) gene, partial cds
4398	17428	30310	4.52	0.0E+00	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4402	17430	30315	6.75	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4402	17430	30316	6.75	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4408	17438	30322	1.31	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4408	17438	30323	1.31	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4413	17440	30329	9.47	0.0E+00	7662091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4413	17440	30330	9.47	0.0E+00	7662091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4423	17460	30341	1.22	0.0E+00	X82338.1	NT	Homo sapiens Marfan disease gene, exon 4
4428	17453	30345	15	0.0E+00	4885128	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4427	17454	30346	1.23	0.0E+00	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4430	17457	30348	1.01	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1350 protein, partial cds
4463	17489	30376	1.2	0.0E+00	7019450	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4471	17497		6.71	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (AMPEP2) gene, complete cds
4478	17502	30386	1.53	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-actinin 2, exon 10
4478	17502	30387	1.53	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-actinin 2, exon 10
4480	17505	30393	0.88	0.0E+00	W28179.1	EST_HUMAN	24q7 Human telomere cDNA randomly primed sublibrary Homo sapiens cDNA
4480	17505	30394	0.88	0.0E+00	W28179.1	EST_HUMAN	24q7 Human telomere cDNA randomly primed sublibrary Homo sapiens cDNA
4485	17520		2.47	0.0E+00	AF206628.1	NT	Homo sapiens HPS1 gene, intron 5
4514	17539	30424	0.83	0.0E+00	T10233.1	EST_HUMAN	sec1329 b4HBSMA C08-HAP-F1 Homo sapiens cDNA clone b4HBSMA-C07b-HAP-F205 5'
4514	17539	30425	0.83	0.0E+00	T10233.1	EST_HUMAN	sec1329 b4HBSMA C08-HAP-F1 Homo sapiens cDNA clone b4HBSMA-C07b-HAP-F205 5'



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4517	17642		0.9	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4529	17553	30441	3.45	0.0E+00	AW084984.1	EST_HUMAN	xc08603.x1 NCI_OGAP_Es02 Homo sapiens cDNA clone IMAGE:268948 3' similar to SW-AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK;
4531	18318		1.85	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4533	17556	30444	1.09	0.0E+00	AI896938.1	EST_HUMAN	xc56002.x1 NCI_OGAP_P128 Homo sapiens cDNA clone IMAGE:2322603 3' similar to contains MER22 b2 P1R0 repetitive element;
4537	17560		8.50	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4539	17562	30449	1.98	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-01169-002-d03 HT0305 Homo sapiens cDNA
4545	17568	30456	1.2	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4546	17568	30457	1.2	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4547	17570	30459	1.79	0.0E+00	4759497	NT	Homo sapiens G protein-coupled receptor 90 (GPR90) mRNA
4548	17571	30460	2.8	0.0E+00	AF109830.1	NT	Homo sapiens serine-threonine protein kinase (MNIB-H) mRNA, complete cds
4553	17576	30466	0.94	0.0E+00	Z66526.1	NT	H. sapiens pancreatic polypeptide receptor PP1 gene
4554	17877	30487	0.96	0.0E+00	4500982	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminic: alpha-2,8-sialyltransferase, GD3 synthase) (SIA1) mRNA
4559	17882	30473	0.93	0.0E+00	S76884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIK1) gene, exon
4560	17563	30474	1.91	0.0E+00	AF111163.1	NT	Homo sapiens pyrim (MEFV) gene, complete cds
4560	17563	30475	1.91	0.0E+00	AF111163.1	NT	Homo sapiens pyrim (MEFV) gene, complete cds
4570	18319	30488	2.31	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4576	17697	30491	6.31	0.0E+00	AF208181.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4582	17804	30501	1.32	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4585	17616	30510	30.53	0.0E+00	4503470	NT	Homo sapiens chondrocyte transition elongation factor 1 alpha 1 (EEF1A1) mRNA
4605	17626	30518	1.82	0.0E+00	4503068	NT	Homo sapiens chondrocyte transition elongation factor 4 (melanoma-associated) (CSPG4), mRNA
4610	17631	30524	1.4	0.0E+00	4502566	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4614	17635		2.89	0.0E+00	135485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4616	17637	30526	13.95	0.0E+00	7652091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4616	17637	30527	13.95	0.0E+00	7652091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4632	17653	30540	1.97	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4635	17656	30543	10.93	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4635	17656	30544	10.93	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4637	17658	30545	1.21	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0795 protein, partial cds
4645	17666		46.99	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

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4654	17676		1.51	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Stragene fetal retina 637202 Homo sapiens cDNA clone IMAGE:60854.3'
4656	17677		1.02	0.0E+00	7657410	NT	Homo sapiens cdc (O2b)-m, Drosophila) homolog 1 (ODZ1), mRNA
4658	17679		2.05	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4659	17680	30566	0.95	0.0E+00	H82741.1	EST_HUMAN	X62601.s1 Soares, pineal, gland_X3:HPG Homo sapiens cDNA clone IMAGE:231721.3'
4659	17680	30566	0.95	0.0E+00	H82741.1	EST_HUMAN	X62601.s1 Soares, pineal, gland_X3:HPG Homo sapiens cDNA clone IMAGE:231721.3'
4660	17681	30567	1.42	0.0E+00	AF184110.1	NT	Homo sapiens cytoplasmic-related protein (NKR1) gene, complete cds
4661	17682	30568	6.53	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4662	17683		1.84	0.0E+00	AB037521.1	NT	Homo sapiens gene for papiurello protein, partial cds
4664	17685	30569	0.86	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4669	17690	30578	1.04	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4672	17693	30579	1.89	0.0E+00	4557867	NT	Homo sapiens keratin 18 (KRT18) mRNA
4672	17693	30580	1.59	0.0E+00	4557867	NT	Homo sapiens keratin 18 (KRT18) mRNA
4673	17694	30581	1.28	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4682	17703	30582	1	0.0E+00	L76810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4682	17703	30583	1	0.0E+00	L76810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4682	17703	30584	2.41	0.0E+00	L76810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4693	17704	30585	2.03	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4693	17704	30586	2.03	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4698	17709	30592	6.02	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4699	17720		2.24	0.0E+00	AF066641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4704	17725	30619	2.92	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1359 protein, partial cds
4704	17725	30620	2.92	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1359 protein, partial cds
4705	17726	30621	3.31	0.0E+00	M74093.1	NT	Human displacement protein (CCAA1) mRNA
4709	17730	30624	2.42	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4709	17730	30625	2.42	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4711	13244	29174	2.02	0.0E+00	T56945.1	EST_HUMAN	X63304.12 Stragene fetal spleen (4937205) Homo sapiens cDNA clone IMAGE:66310.5'
4711	13244	29174	2.02	0.0E+00	T56945.1	EST_HUMAN	X63304.12 Stragene fetal spleen (4937205) Homo sapiens cDNA clone IMAGE:66310.5'
4711	13244	29176	2.02	0.0E+00	T56945.1	EST_HUMAN	X63304.12 Stragene fetal spleen (4937205) Homo sapiens cDNA clone IMAGE:66310.5'
4713	17733		1.22	0.0E+00	BE27830.1	EST_HUMAN	607158035FF NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3305521.5'
4737	17767	30651	4.85	0.0E+00	5729817	NT	Homo sapiens ectopic viral integration site 2B (EVI2B), mRNA
4737	17767	30652	4.85	0.0E+00	5729817	NT	Homo sapiens ectopic viral integration site 2B (EVI2B), mRNA
4743	17763	30657	5.55	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4746	17766	30660	6.02	0.0E+00	M69167.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4746	17766	30661	6.02	0.0E+00	M69167.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4750	17770	30686	2.21	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4752	17772	30688	24.93	0.0E+00	7692479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4754	17774	30696	2.9	0.0E+00	7692181	NT	Homo sapiens KIAA0953 gene product (KIAA0953), mRNA
4760	17780	30675	0.96	0.0E+00	S71446.1	NT	SCN1A-strain type I sodium channel alpha-subunit (IIIS5 transmembrane region) [human, placenta, Genomic, 1658 nt]
4760	17780	30676	0.96	0.0E+00	S71446.1	NT	SCN1A-strain type I sodium channel alpha-subunit (IIIS5 transmembrane region) [human, placenta, Genomic, 1659 nt]
4765	17785	30681	0.96	0.0E+00	AL096957.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4770	17790		1.25	0.0E+00	X58497.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D8
4781	17801	30691	0.81	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4781	17801	30692	0.81	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4792	17809	30701	1.50	0.0E+00	AF02801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-20
4795	17812	30704	1.12	0.0E+00	6637700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4795	17812	30705	1.12	0.0E+00	6637700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4797	17814	30707	1.12	0.0E+00	7019320	NT	Homo sapiens protein008 (AD013), mRNA
4797	17814	30708	1.12	0.0E+00	7019320	NT	Homo sapiens protein008 (AD013), mRNA
4825	17842	30740	1.49	0.0E+00	AW44637.1	EST_HUMAN	UHHB15-ajw-c-04-Q-U1-1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4831	17848	30749	0.99	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4832	17849		1.83	0.0E+00	AF083242.1	NT	Homo sapiens HSP024-iso mRNA, complete cds
4873	17890	30778	0.98	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4873	17890	30779	0.98	0.0E+00	J00191.1	NT	Human MHC class I transplantation antigen (hla) gene
4879	17896		4.64	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4882	17899	30786	1.0	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4884	17901	30790	0.93	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4885	17902	30781	1.29	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4886	17903	30782	3.04	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4888	17905	30784	13.14	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4889	17906	30795	1.37	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4891	17908	30797	1.65	0.0E+00	8922180	NT	Homo sapiens hypocalcemic protein DKFp762E1312 (DKFp762E1312), mRNA
4894	17911	30801	4.6	0.0E+00	8923080	NT	Homo sapiens hypocalcemic protein FLJ20073 (FLJ20073), mRNA
4898	17915	30805	1.75	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1-J61 segments, and Tor-C-alpha gene, exons 1-4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4898	17915	30806	1.75	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tor-alpha) gene, J1- J61 segments; and Tor-C-alpha gene, exons 1-4
4900	17917	30808	1.49	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4900	17917	30809	1.49	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4903	17920	30812	2.58	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4912	17929	30820	1.16	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 2840 (TAF21) mRNA
4921	17938	30830	1.69	0.0E+00	X92841.1	NT	H.sapiens MICA gene
4923	17940	30832	1.34	0.0E+00	4585842	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4924	17941	30833	0.99	0.0E+00	AB037894.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4925	17942	30834	1.25	0.0E+00	Y08232.1	NT	H.sapiens ferritin alpha pseudogene
4926	17943	30835	1.17	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4927	17944	30836	2.3	0.0E+00	6637848	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zk1), mRNA
4929	17946	30838	1.49	0.0E+00	4758199	NT	Homo sapiens desmoglein (DPI, DPLI) (DSP) mRNA
4930	17947	30839	0.97	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4931	17948	30840	1.15	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA
4932	17949	30841	25.08	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, thered 7
4936	17952	30844	25.15	0.0E+00	AF055068.1	NT	Homo sapiens MHC class 1 region
4938	17954	30847	1.97	0.0E+00	4605508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
4939	17955	30847	2.01	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4941	17957	30851	0.91	0.0E+00	U39965.1	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3) gene, exon 7
4952	17967	30857	0.99	0.0E+00	D63562.1	NT	Homo sapiens COL4A6 gene for a(V) collagen, exon 44 and partial cds
4954	17969	30859	1.02	0.0E+00	4503864	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FPPS) mRNA
4981	17976		0.96	0.0E+00	AJ281129.1	EST_HUMAN	qm15105.x1 NC_CGAP_Lus Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:061632 Q61632 EN-2LACZ FUSION PROTEIN
4972	17987	30876	0.93	0.0E+00	4504082	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
4972	17987	30879	0.93	0.0E+00	4504082	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
4980	18005	30893	1.68	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4995	18010	30897	1.24	0.0E+00	7662318	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
5008	18022	30918	6.04	0.0E+00	U14867.1	NT	Human ribosomal protein L21 mRNA, complete cds
5018	18032	30918	1.08	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5020	18034		2.79	0.0E+00	BE408663.1	EST_HUMAN	601303728P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5023	18037	30922	3.2	0.0E+00	4758199	NT	Homo sapiens desmoglein (DPI, DPLI) (DSP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5330	18044	30828	1.24	0.0E+00	AB028688.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5044	18057	30835	1.97	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5044	18057	30838	1.97	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5057	18068	30847	0.75	0.0E+00	AA001248.1	EST_HUMAN	E239140 SPALT PROTEIN;
5057	18068	30848	0.75	0.0E+00	AA001248.1	EST_HUMAN	not4q09.st NQ1 CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5057	18068	30849	0.75	0.0E+00	AA001248.1	EST_HUMAN	E239140 SPALT PROTEIN;
5074	18084	30874	1.34	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5088	18099	30974	0.8	0.0E+00	U63588.1	NT	Homo sapiens MHC class 1 region
5084	18104		1.27	0.0E+00	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5097	18107		24.84	0.0E+00	D60657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG3P) pseudogene
5122	18132	31009	3.45	0.0E+00	X62988.1	NT	Bacillus amyloqueliciens sacB gene for levansucrase (EC 2.4.1.10)
5141	18150	31029	0.98	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5141	18150	31030	0.98	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
6142	18161	31031	0.95	0.0E+00	6454163	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5171	18180	31057	1.07	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5171	18180	31058	1.07	0.0E+00	Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5178	18185	31062	1.31	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5208	18217	31092	0.84	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC615897), mRNA
5208	18217	31093	0.84	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC615897), mRNA
5218	18227	31101	1.13	0.0E+00	U26555.1	NT	Human vesican V2 core protein precursor splice-variant mRNA, complete cds
5221	18229	31103	1.01	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5221	18229	31104	1.01	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5236	18244	31116	1.11	0.0E+00	4826777	NT	Homo sapiens jumonji (mouse) homolog (JMJ) mRNA
5257	18265		1.35	0.0E+00	U05367.1	NT	Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ectopic viral integration site 2B (EV12B) exons 1-2; ecotropic viral integration site 2A (EV12A) exons 1-2; adenylate kinase (AK3) exons 1-2
5264	18272		1.08	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
5295	18301	31161	0.93	0.0E+00	AB035356.1	NT	Homo sapiens mRNA for neurixin-1 alpha protein, complete cds
5305	18308		2.09	0.0E+00	AL040249.1	EST_HUMAN	DKFZp4340713.J1.434 (synonym: hnc3) Homo sapiens cDNA clone DKFZp4340713.5
5313	18329		3.2	0.0E+00	AF030938.1	NT	Homo sapiens acornase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5324	18430	31181	2.03	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5324	18430	31182	2.03	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5346	18451	31322	1.18	0.0E+00	AU934954.1	EST_HUMAN	wp0608.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464084 3'
5349	18454	31325	1.2	0.0E+00	9256579	NT	Homo sapiens probocardin alpha 13 (PCDH13), mRNA
5364	18469	31340	4.04	0.0E+00	BE031080.1	EST_HUMAN	RC3-GN0076-31080-013-403 GN0076 Homo sapiens cDNA
5368	18473	31344	2.83	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDCL2) mRNA, complete cds
5368	18473	31345	2.83	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDCL2) mRNA, complete cds
5376	18480	31354	32.34	0.0E+00	X68163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5376	18480	31355	32.34	0.0E+00	X68163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5457	18559	31470	8.37	0.0E+00	BE075498.1	EST_HUMAN	7110c08.x1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:3294250 3'
5458	18560	31471	1.72	0.0E+00	BE220783.1	EST_HUMAN	h09a02.x1 NCI_CGAP_Luz2 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN
5459	18561	31472	1.69	0.0E+00	BE784412.1	EST_HUMAN	P42684 HYPOTHETICAL PROTEIN KIAA0054.1
5459	18561	31473	1.69	0.0E+00	BE784412.1	EST_HUMAN	601589422FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5460	18562	31474	0.63	0.0E+00	AI189142.1	EST_HUMAN	601589422FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5464	18566	31477	18.78	0.0E+00	M28908.1	NT	q04a04.x1 Soares placenta_806weeks_2NHIP809W Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:172D3_DROME P48846 TRANSCRIPTION INITIATION FACTOR TFIID 85 KD SUBUNIT; Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5468	18570	31480	0.56	0.0E+00	AI791363.1	EST_HUMAN	h08a09.v5 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG
5478	25539	31486	4.25	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR VJ REGION (HUMAN); Homo sapiens Sp4 transcription factor (SF4), mRNA
5488	18588	31488	1.72	0.0E+00	BF655982.1	EST_HUMAN	602118928FT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276254 5'
5489	18589	31499	0.77	0.0E+00	AU134408.1	EST_HUMAN	AU134408 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5489	18589	31500	0.71	0.0E+00	AU134408.1	EST_HUMAN	AU134408 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5495	18595	31507	0.04	0.0E+00	BE536857.1	EST_HUMAN	60108108FT NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5504	18604	31533	1.22	0.0E+00	BE257784.1	EST_HUMAN	601105891FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2968310 5'
5509	18609	31539	2.05	0.0E+00	BF626328.1	EST_HUMAN	602071972FT NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5509	18609	31540	2.05	0.0E+00	BF626328.1	EST_HUMAN	602071972FT NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5528	20048	33350	2.31	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5532	18630	31567	1.03	0.0E+00	AB007695.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
5532	18630	31568	1.03	0.0E+00	AB007695.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
5536	18633	31572	4.26	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5538	18633	31573	4.26	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5550	18647	31589	1.18	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5550	18647	31590	1.18	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-16)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5568	18683	31623	1.8	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5572	18698	31628	1.55	0.0E+00	Z39133.1	NT	H.sapiens mRNA for myobin
5591	18687	31655	0.87	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5591	18687	31658	0.87	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05 5'
5594	18690	31680	3.21	0.0E+00	BF529631.1	EST_HUMAN	602042322FT NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4178888 5'
5594	18690	31681	3.21	0.0E+00	BF529631.1	EST_HUMAN	502042322FT NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4178888 5'
5599	18695	31665	2.24	0.0E+00	BF313139.1	EST_HUMAN	6011897659FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5610	18706	31853	3.88	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5626	18722	31881	0.57	0.0E+00	A1928161.1	EST_HUMAN	w065602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5626	18722	31882	0.57	0.0E+00	A1928161.1	EST_HUMAN	w065602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5944	18740	31805	1.24	0.0E+00	BE260777.1	EST_HUMAN	075054 KIAA0466 PROTEIN ;
5953	18749	31807	7.42	0.0E+00	AW667316.1	EST_HUMAN	601160253FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602809 5'
5968	18763	31932	2.41	0.0E+00	BE262889.1	EST_HUMAN	MRQ-SN0037-030400-001-H07 SN0037 Homo sapiens cDNA
5968	18763	31933	2.41	0.0E+00	BE262889.1	EST_HUMAN	601105291FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5989	18784	31955	1.79	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5989	18784	31956	1.79	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5997	18782	31984	4.3	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5997	18792	31985	4.3	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5704	18769	31975	2.98	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5704	18769	31976	2.98	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5735	18629	32007	0.7	0.0E+00	A1198515.1	EST_HUMAN	q64g10.x1 Soares_pleocita_R108week_2NBP89c9w Homo sapiens cDNA clone IMAGE:1757730 3'
5739	18633	32013	7.46	0.0E+00	A65719.1	EST_HUMAN	similar to SW-CADC_HUMAN_P65289 BRAIN-CADHERIN PRECURSOR ;
5748	18640	32022	5.85	0.0E+00	AW405472.1	EST_HUMAN	UH-FP-BLO-ech-4-02-0-U1 r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3081656 5'
5769	18652	32032	1.19	0.0E+00	Z28299.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 14 spid 15
5771	18653	32042	1.87	0.0E+00	AW351877.1	EST_HUMAN	PM3-CT0263-091286-007-H05 CT0263 Homo sapiens cDNA
5771	18653	32043	1.87	0.0E+00	AW351877.1	EST_HUMAN	PM3-CT0263-091286-007-H05 CT0263 Homo sapiens cDNA
5771	18653	32044	1.87	0.0E+00	AW351877.1	EST_HUMAN	PM3-CT0263-091286-007-H05 CT0263 Homo sapiens cDNA
5774	18656	32047	0.84	0.0E+00	AB035268.1	NT	Homo sapiens mRNA for neurxin II, complete cds
5774	18656	32048	0.84	0.0E+00	AB035268.1	NT	Homo sapiens mRNA for neurxin II, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5776	18969	32061	2.24	0.0E+00	U30281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5811	18901	32084	1.13	0.0E+00	AB046961.1	NT	Homo sapiens mRNA for KIAA1841 protein, partial cds
5833	18923	32107	0.93	0.0E+00	A1114926.1	EST_HUMAN	HAT435 Human fetal liver cDNA library Homo sapiens cDNA
5873	18992	32151	2.4	0.0E+00	AA189505.1	EST_HUMAN	395511.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:627633 5' similar to gb: X03740
5874	18993	32162	1.22	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
5874	18993	32163	1.22	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQ171 gene
5883	18972	32165	1.32	0.0E+00	AJ207616.1	EST_HUMAN	Homo sapiens KVLQ171 gene
5905	18991	32182	5.12	0.0E+00	11416801	NT	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5910	18996	32185	1.25	0.0E+00	BE791173.1	EST_HUMAN	Homo sapiens protocadherin beta 2 (PCDH2) mRNA
5920	19006	32198	1.09	0.0E+00	9998943	NT	601684032FT NIH_MGC-7 Homo sapiens cDNA clone IMAGE:3935551 5'
5921	19007	32198	7.99	0.0E+00	BE960982.1	EST_HUMAN	Homo sapiens ameliorite-sensitive cation channel 1, neuronal (degenerin) (ACONT1), mRNA
5922	19008	32200	1.33	0.0E+00	10048478	NT	601345141FT NIH_MGC-8 Homo sapiens cDNA clone IMAGE:3677843 5'
5923	19009	32201	3.06	0.0E+00	U66961.1	NT	Mus musculus ezonin (Ac2) mRNA
5923	19009	32202	3.06	0.0E+00	U66961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5942	19028	32222	1.81	0.0E+00	BF338835.1	EST_HUMAN	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5946	19032	32225	0.97	0.0E+00	AF142621.1	NT	602036927FT NCL_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4184321 5'
5947	19033	32226	2.82	0.0E+00	BEZ79983.1	EST_HUMAN	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
5959	19044	32243	1.14	0.0E+00	BE503058.1	EST_HUMAN	601104462FT NIH_MGC-14 Homo sapiens cDNA clone IMAGE:3347483 5'
5963	19048	32249	1.79	0.0E+00	BF569005.1	EST_HUMAN	h283411.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084
5968	19053	32253	1.11	0.0E+00	AA464642.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING :
6004	19087	32287	2.27	0.0E+00	AF217289.1	NT	602185555FT NIH_MGC-45 Homo sapiens cDNA clone IMAGE:4310076 5'
6006	19089	32289	2.43	0.0E+00	BE828144.1	EST_HUMAN	26894008.at Soares_NHNPMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6011	19094	32294	0.91	0.0E+00	BE958536.1	EST_HUMAN	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6017	19100	32302	0.53	0.0E+00	AJ268880.1	NT	RC5-ET10027-210600-022-G10 ET10027 Homo sapiens cDNA
6030	19113	32315	0.61	0.0E+00	BE673966.1	EST_HUMAN	601845287FT NIH_MGC-56 Homo sapiens cDNA clone IMAGE:3830453 5'
6030	19113	32316	0.61	0.0E+00	BE673966.1	EST_HUMAN	Homo sapiens KIA0851 gene (partial), X13 gene and LZ1FL1 gene
6030	19113	32316	0.61	0.0E+00	BE673966.1	EST_HUMAN	7872811.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3276540 3' similar to SW:DAX1_HUMAN
6035	19118	32322	0.8	0.0E+00	AW276760.1	EST_HUMAN	P712911.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3276540 3' similar to SW:DAX1_HUMAN
6035	19118	32322	0.8	0.0E+00	AW276760.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1, [1];
6035	19118	32322	0.8	0.0E+00	AW276760.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1, [1];
6035	19118	32322	0.8	0.0E+00	AW276760.1	EST_HUMAN	XP0503.x1 NCL_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335
6035	19118	32322	0.8	0.0E+00	AW276760.1	EST_HUMAN	GUANYLATE KINASE ASSOCIATED PROTEIN, [1];



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit: Descriptor
6047	19128	32336	0.67	0.0E+00	BF031742.1	EST_HUMAN	60158090F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6047	19128	32337	0.67	0.0E+00	BF031742.1	EST_HUMAN	60158090F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6059	19140	32352	1.27	0.0E+00	AW470848.1	EST_HUMAN	h834406.x1 NC1 CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR-Q921N3
6072	19153	32364	0.95	0.0E+00	BF155670.1	EST_HUMAN	Q821N3 MYOSIN-RHO GAP PROTEIN, MYR 7 ;
6072	19153	32365	0.95	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-290900-389-410 HT0894 Homo sapiens cDNA
6080	19160	32371	1.38	0.0E+00	W33069.1	EST_HUMAN	QV4-HT0894-290900-389-410 HT0894 Homo sapiens cDNA
6080	19160	32372	1.38	0.0E+00	W33069.1	EST_HUMAN	z08b06.r1 Scavenger parathyroid tumor_NBRIPA Homo sapiens cDNA clone IMAGE:321755 5'
6081	19161		2.28	0.0E+00	AF012818.1	NT	z08b06.r1 Scavenger parathyroid tumor_NBRIPA Homo sapiens cDNA clone IMAGE:321755 5'
6084	19164	32376	2.82	0.0E+00	BE280187.1	EST_HUMAN	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6091	19170	32385	2.31	0.0E+00	BE89810.1	EST_HUMAN	60113651F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6093	19172	32388	0.53	0.0E+00	BE38867.1	EST_HUMAN	601512630F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3914238 5'
6109	19185	32408	0.53	0.0E+00	AW752848.1	EST_HUMAN	601286330F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6112	19190	32410	1.48	0.0E+00		NT	IL3-CT0220-111166-028-E04 CT0220 Homo sapiens cDNA
6113	19191	32412	1.12	0.0E+00	BE601608.1	EST_HUMAN	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6113	19191	32413	1.12	0.0E+00	BE601608.1	EST_HUMAN	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6113	19191	32414	1.12	0.0E+00	BE601608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6129	25654	32431	9.98	0.0E+00	9789986	NT	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6132	19209	32434	1.43	0.0E+00	AA163506.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6132	19209	32435	1.43	0.0E+00	AA163506.1	EST_HUMAN	z460101.r1 Scavenger_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to
6155	19230	32460	11.54	0.0E+00	U34625.1	NT	SW-Y05_HUMAN_P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5 ;
6155	19230	32461	11.54	0.0E+00	U34625.1	NT	SW-Y05_HUMAN_P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5 ;
6157	19232	32463	0.54	0.0E+00	AW853983.1	EST_HUMAN	Human T cell surface glycoprotein CD-8 mRNA, complete cds
6157	19232	32464	0.54	0.0E+00	AW853983.1	EST_HUMAN	Human T cell surface glycoprotein CD-8 mRNA, complete cds
6187	19271	32506	1.14	0.0E+00	BE268330.1	EST_HUMAN	RC9-CT0254-110300-027-409 CT0254 Homo sapiens cDNA
6207	19281	32514	1.24	0.0E+00	BE156591.1	EST_HUMAN	RC9-CT0254-110300-027-409 CT0254 Homo sapiens cDNA
6217	19291	32524	0.53	0.0E+00	M38107.1	NT	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3365665 5'
6254	19327	32568	1.71	0.0E+00	BE370007.1	EST_HUMAN	QVQ-HT0389-090200-099-409 HT0389 Homo sapiens cDNA
6260	19333	32584	1.16	0.0E+00	AW137772.1	EST_HUMAN	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6282	19354	32590	3.66	0.0E+00	U45982.1	NT	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
							AU197772 PLACE1 Homo sapiens cDNA clone IMAGE:1007201 5'
							Human G protein-coupled receptor GPR-9-8 gene, complete cds

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6311	19382	32622	4.53	0.0E+00	AA204740.1	EST_HUMAN	z481403.r1 Stratiagene INT neuron (4637233) Homo sapiens cDNA clone IMAGE:648005 5' similar to
6312	19383	32623	4.05	0.0E+00	11545913	NT	TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN ;
6312	19383	32624	4.05	0.0E+00	11545913	NT	Homo sapiens xycyltransferase II (XT2), mRNA
6331	19401	32642	0.56	0.0E+00	U07228.1	NT	Homo sapiens xycyltransferase II (XT2), mRNA
6349	19418	32659	8.33	0.0E+00	11428367	NT	Human beta2-chimerin mRNA, complete cds
6353	19422	32664	3.66	0.0E+00	BE257173.1	EST_HUMAN	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6369	19437		0.97	0.0E+00	AI686048.1	EST_HUMAN	197110.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:22419339 3' similar to TR:Q14839 Q14839
6373	19441	32683	1.29	0.0E+00	U35920.1	NT	ML-2 PROTEIN ;
6382	19450	32691	1.29	0.0E+00	BE787395.1	EST_HUMAN	Human anion exchanger (AE1) gene, exons 1-20
6382	19450	32692	1.29	0.0E+00	BE787395.1	EST_HUMAN	601597971FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6393	19461	32707	0.85	0.0E+00	AI198025.1	EST_HUMAN	601597971FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6393	19461	32708	0.85	0.0E+00	AI198025.1	EST_HUMAN	q150b11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1865901 3' similar to TR:Q12838 Q12838
6396	19464	32710	1	0.0E+00	BF357123.1	EST_HUMAN	TFIIIC ALPHA SUBUNIT ;
6404	19472	32720	1.71	0.0E+00	11435930	NT	q150b11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1865901 3' similar to TR:Q12838 Q12838
6414	19482	32729	0.79	0.0E+00	D55649.1	NT	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6432	19498	32751	1	0.0E+00	AW178142.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6453	19518	32768	0.74	0.0E+00	BE674544.1	EST_HUMAN	13-HT0682-010999-GT4-A04 HT0682 Homo sapiens cDNA
6458	19523	32774	0.88	0.0E+00	7662039	NT	76d212.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302 3' similar to SW:Y178_HUMAN
6472	19537	32795	3.68	0.0E+00	AV650020.1	EST_HUMAN	Q1481 HYPOTHETICAL PROTEIN KIAA0176 ;
6481	19546	32795	3.68	0.0E+00	AW675988.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6484	19540	32798	6.02	0.0E+00	H01255.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6483	19559	32809	1.16	0.0E+00	11428283	NT	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6488	19562	32814	0.93	0.0E+00	X15377.1	NT	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6500	19584	32816	0.72	0.0E+00	AA466375.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6501	19565	32817	1.23	0.0E+00	AI612841.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6507	19571	32823	3.93	0.0E+00	BE735989.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6507	19571	32824	3.93	0.0E+00	BE735989.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds
6511	19576	32830	0.78	0.0E+00	AW748995.1	EST_HUMAN	Human alpha mannosidase II (alpha-mannosidase II) isozyme, complete cds

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6511	19575	32831	0.78	0.0E+00	AW748593.1	EST_HUMAN	MRO-ET0284-221189-002411 BT0254 Homo sapiens cDNA
6512	19576		0.67	0.0E+00	U77629.1	NT	Homo sapiens Achele-Scute homologue 2 (ASCL2) gene, complete cds
6514	19578	32833	28.27	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1003960 5'
6514	19578	32834	28.27	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1003960 5'
6519	19582	32840	0.88	0.0E+00	BE780453.1	EST_HUMAN	601489712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
6520	19583	32841	1.02	0.0E+00	G92217.1	NT	H sapiens germline immunoglobulin heavy chain, variable region, (13-2)
6537	19599	32862	1.64	0.0E+00	AI989483.1	EST_HUMAN	w25c07.X1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2498220 3'
6551	19612	32873	1.78	0.0E+00	BE263153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987663 5'
6551	19612	32874	1.78	0.0E+00	BE263153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987663 5'
6626	19644	32912	0.71	0.0E+00	BE807687.1	EST_HUMAN	6011443175F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3847291 5'
6626	19644	32962	1.2	0.0E+00	AW408348.1	EST_HUMAN	UI-HF-BLO-eco-h-02-0-UI.H1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058931 5'
6626	19644	32963	1.2	0.0E+00	AW408348.1	EST_HUMAN	UI-HF-BLO-eco-h-02-0-UI.H1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058931 5'
6650	19717	32984	0.59	0.0E+00	AV719444.1	EST_HUMAN	AU719444 GL G Homo sapiens cDNA clone GLOEHC08 5'
6659	19726	33001	1.27	0.0E+00	BE868340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6659	19726	33002	1.27	0.0E+00	BE868340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6672	19726	33005	2.18	0.0E+00	AF190890.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav1.1a (CACNA1G) mRNA, complete cds
6675	19732	33008	0.84	0.0E+00	L48546.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6677	19734	33009	1.11	0.0E+00	11420658	NT	Homo sapiens transformation/transcription domain-associated protein (TRRAP), mRNA
6684	19741	33016	3.24	0.0E+00	AW163640.1	EST_HUMAN	au8808.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR-O15390 O15390 GT24 (3) TR-O43940 TR-O43206;
6684	19741						au8808.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR-O15390 O15390 GT24 (3) TR-O43940 TR-O43206;
6688	19746	33017	3.24	0.0E+00	AW163640.1	EST_HUMAN	TR-O15390 O15390 GT24 (3) TR-O43940 TR-O43206;
6688	19746	33020	0.85	0.0E+00	W37163.1	EST_HUMAN	2520e06.r1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW-ZN45_HUMAN Q02388 ZINC FINGER PROTEIN 45;
6688	19746	33021	0.85	0.0E+00	W37163.1	EST_HUMAN	2520e06.r1 Scores_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW-ZN45_HUMAN Q02388 ZINC FINGER PROTEIN 45;
6706	19762	33041	1.19	0.0E+00	BE794853.1	EST_HUMAN	60158371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6713	19769	33048	4.81	0.0E+00	BE795873.1	EST_HUMAN	60158371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6714	19770	33049	3.07	0.0E+00	BE707655.1	EST_HUMAN	QV1-GN0095-140905-318-hc2 GN0095 Homo sapiens cDNA
6714	19770	33050	3.07	0.0E+00	BE707655.1	EST_HUMAN	QV1-GN0095-140905-318-hc2 GN0095 Homo sapiens cDNA
6718	19774	33053	7.16	0.0E+00	BE86813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6718	19774	33054	7.16	0.0E+00	BE86813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6727	19783	33062	5.42	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6732	19786	33066	2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6732	19786	33067	2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6738	19794	33074	3.67	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZF3A), mRNA
6741	19796	33076	3.87	0.0E+00	AI059412.1	EST	h3111.x1 NCI_GCAP_G08 Homo sapiens cDNA clone IMAGE2242413 3' similar to SW-WNT3_MOUSE
6743	19798	33078	1.41	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR. ;
6755	19809	33090	0.78	0.0E+00	AW650430.1	EST	HUMAN UL-HF-BNO-ama-c-01-01 r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6757	19811	33091	3.98	0.0E+00	AA434584.1	EST	HUMAN 2453203.r1 Soares, total, fetus, NbcHFB_Sw Homo sapiens cDNA clone IMAGE:773668 5'
6771	19828	33101	1.13	0.0E+00	BF2177200.1	EST	HUMAN 60186331Tf1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4703693 5'
6775	19830	33113	1.68	0.0E+00	BE026976.1	EST	HUMAN QVA-BN0047-300800-278-c08 BN0047 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6808	19862	33149	0.75	0.0E+00	11428758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6808	19862	33150	0.76	0.0E+00	11428758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6826	19880	33171	2.04	0.0E+00	AU126928.1	EST	HUMAN AUI28928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6828	19882	33173	0.84	0.0E+00	BE101434.1	EST	HUMAN PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6828	19882	33174	0.84	0.0E+00	BE101434.1	EST	HUMAN PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6851	19894	33169	1.46	0.0E+00	BE142363.1	EST	HUMAN RCM-BN0121-280300-032-c04 BN0121 Homo sapiens cDNA
6873	19926	33222	1.01	0.0E+00	BE060612.1	EST	HUMAN RCS-BN0121-280300-032-c04 BN0121 Homo sapiens cDNA
6873	19926	33223	1.01	0.0E+00	BE060612.1	EST	HUMAN PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6901	19963	33250	7.7	0.0E+00	BE109131.1	EST	HUMAN IL5-GN0332-185900-145-c07 GN0332 Homo sapiens cDNA
6903	19956	33252	3.49	0.0E+00	BF085687.1	EST	HUMAN zp89e03.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE-627292 5'
6943	20167	33490	3.27	0.0E+00	AA190766.1	EST	HUMAN Human salivary peroxidase mRNA, complete cds
6954	20178	33504	1.04	0.0E+00	U39573.1	NT	7649607.x1 NCI_GCAP_G08 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z865 Q9Z865
6958	20189	33506	0.7	0.0E+00	BE671087.1	EST	HUMAN TEKTIN.1 ;
6970	20193	33520	6.96	0.0E+00	AI0840821.1	EST	HUMAN IL3-ST10024-230769-001-B01 ST10024 Homo sapiens cDNA
6970	20193	33521	6.96	0.0E+00	AI0840821.1	EST	HUMAN IL3-ST10024-230769-001-B01 ST10024 Homo sapiens cDNA
6984	20207	33537	1.98	0.0E+00	11435928	NT	Homo sapiens CD6 antigen (CD6), mRNA
6988	20124	33438	1.01	0.0E+00	AL042443.1	EST	HUMAN DKFZp454I20201.1 434 (synonym: h3ac3) Homo sapiens cDNA clone DKFZp434I20201 5'
6999	20123	33440	47.69	0.0E+00	X656163.1	NT	H sapiens immunoglobulin heavy chain gene, variable region
7002	20128	33443	0.84	0.0E+00	AI169270.1	EST	HUMAN h10d001.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1965761 3' similar to
7002	20133	33448	0.82	0.0E+00	BE734087.1	EST	HUMAN TR:Q26623 Q26623 TEKTIN C1.1 ;
7007	20133	33448	0.82	0.0E+00	BE734087.1	EST	HUMAN PM1567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3942090 5'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7030	18362	31248	1.17	0.0E+00	BE666381.1	EST_HUMAN	601336977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682287 5'
7040	18372	31259	12.91	0.0E+00	BE887889.1	EST_HUMAN	601449667F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3847697 5'
7040	18372	31260	12.91	0.0E+00	BE887889.1	EST_HUMAN	601449667F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3847697 5'
7046	20070	33376	1.94	0.0E+00	BE550162.1	EST_HUMAN	714903.1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
7048	20070	33377	1.94	0.0E+00	BE550162.1	EST_HUMAN	714903.1 NCI CGAP_L124 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
7074	20068	33406	2.29	0.0E+00	BF088376.1	EST_HUMAN	CGA:HT0877:406900:397:q11 HT0877 Homo sapiens cDNA
7081	20102	33413	1.41	0.0E+00	AA195103.1	EST_HUMAN	z34g03.1 Sources_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5'
7088	20022		11.47	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7090	20024	33326	0.91	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7092	20026	33326	0.78	0.0E+00	BE313075.1	EST_HUMAN	601150682F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
7092	20026	33330	0.78	0.0E+00	BE313075.1	EST_HUMAN	601150682F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503391 5'
7106	20040	33342	3.08	0.0E+00	BF569605.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310078 5'
7114	20048	33350	0.61	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7122	20058		2.02	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
7132	20108	33419	3.33	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7132	20108	33420	3.33	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7133	20109	33421	1.77	0.0E+00	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x6
7146	18378	31266	3.02	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7147	18379	31267	0.67	0.0E+00	AI410666.1	EST_HUMAN	SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN, 1
7147	18379	31268	0.57	0.0E+00	AI410666.1	EST_HUMAN	SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN, 1
7152	18384	31272	0.86	0.0E+00	BE256708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
7173	18404	31202	1.21	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone IMAGE:1003678 5'
7176	18407	31206	5.02	0.0E+00	BE262841.1	EST_HUMAN	601148954F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3501829 5'
7177	18408	31207	2.28	0.0E+00	Z37976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7177	18408	31208	2.26	0.0E+00	Z37976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7178	18409	31209	3.32	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7178	18409	31210	3.32	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7185	18416	31217	1.33	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7187	18418	31218	0.59	0.0E+00	BF130916.1	EST_HUMAN	601819722F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4051709 5'

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Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7192	20218	33546	0.57	0.0E+00	BE762770.1	EST_HUMAN	QV5-NT0022-140600-223-01 NT0022 Homo sapiens cDNA
7198	20222	33553	2.39	0.0E+00	BF696903.1	EST_HUMAN	602185682F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4310076 5'
7200	20224	33555	0.68	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dylin heavy chain (DNAH8 gene)
7202	20226	33556	0.68	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dylin heavy chain (DNAH8 gene)
7204	20228	33558	4.32	0.0E+00	LO1878.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7209	20232	33565	1.49	0.0E+00	AW502382.1	EST_HUMAN	UIHF-BR0P-ska-d-10-Q-U171 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7209	20232	33566	1.49	0.0E+00	AW502382.1	EST_HUMAN	UIHF-BR0P-ska-d-10-Q-U171 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7218	20240	33574	0.63	0.0E+00	AL039591.1	EST_HUMAN	DKFZ43402221.1 1 434 (synonym: Hies3) Homo sapiens cDNA clone DKFZ-43402211 5'
7218	20240	33575	0.93	0.0E+00	AL039591.1	EST_HUMAN	DKFZ43402221.1 1 434 (synonym: Hies3) Homo sapiens cDNA clone DKFZ-43402211 5'
7227	20249	33583	6.16	0.0E+00	BF306996.1	EST_HUMAN	601868823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7233	20254		2.16	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A5) and (CDM) paralogous genes, complete cds
7275	20010	33312	1.21	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7315	20266	33627	0.59	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7315	20266	33628	0.69	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7320	20281	33634	0.68	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7320	20281	33635	0.68	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7326	20297	33641	1.23	0.0E+00	AW054809.1	EST_HUMAN	EST336676 MAGC resequences, MAGC Homo sapiens cDNA
7327	20298	33642	1.14	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354585 5'
7340	20311	33654	1.23	0.0E+00	LO1873.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7345	20318	33664	0.68	0.0E+00	AB007635.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7348	20318	33665	0.68	0.0E+00	AB007635.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7354	20324	33672	1.38	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT25P4 Homo sapiens cDNA clone NT25P4001568 5'
7370	20340	33692	1	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7375	20346		2.24	0.0E+00	AU143706.1	EST_HUMAN	AU143708 Y79AAT1 Homo sapiens cDNA clone Y79AAT1002865 5'
7376	20346	33697	0.66	0.0E+00	4758839	NT	Homo sapiens nefrin 1 (NTN1), mRNA
7385	20355	33704	1.34	0.0E+00	BE891285.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917194 5'
7385	20355	33707	1.34	0.0E+00	BE891285.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917194 5'
7407	18430	31181	2.28	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7419	20368	33736	0.7	0.0E+00	BE47231.1	EST_HUMAN	Homo sapiens keratin 12 (KRT12) gene, complete cds
7419	20368	33737	0.7	0.0E+00	BE47231.1	EST_HUMAN	601680948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7432	20398	33751	4.41	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7432	20398	33752	4.41	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descrip
7447	20413	33766	0.65	0.0E+00	AF22744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform aa (CACNA1G) mRNA, complete cds
7469	20435	33791	36.24	0.0E+00	AI128344.1	EST_HUMAN	q6b7a07.x1 Soares, placenta, 8to6weeks, 2NHP8t0c9w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR; contains element HGR repetitive element;
7469	20435	33791	36.24	0.0E+00	AI128344.1	EST_HUMAN	q6b7a07.x1 Soares, placenta, 8to6weeks, 2NHP8t0c9w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR; contains element HGR repetitive element;
7469	20435	33791	36.24	0.0E+00	AI128344.1	EST_HUMAN	q6b7a07.x1 Soares, placenta, 8to6weeks, 2NHP8t0c9w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR; contains element HGR repetitive element;
7472	20438	33795	0.82	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7472	20438	33795	0.82	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7475	20441	33799	5.42	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7475	20441	33799	5.42	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7475	20441	33800	5.42	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7478	20444		13.74	0.0E+00	BF337375.1	EST_HUMAN	602035099.F1 NCJ_OGAP_Brr64 Homo sapiens cDNA clone IMAGE:4182839 5'
7480	20446	33802	2.76	0.0E+00	AA128463.1	EST_HUMAN	z60609.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562801 5' similar to TR:G806562 G806562 NEBULIN ;
7480	20460	33808	0.75	0.0E+00	AL079497.1	EST_HUMAN	DKFZp43480226_r1 434 (synonym: hhex3) Homo sapiens cDNA clone DKFZp43480226 5'
7485	20450	33809	0.75	0.0E+00	AL079497.1	EST_HUMAN	DKFZp43480226_r1 434 (synonym: hhex3) Homo sapiens cDNA clone DKFZp43480226 5'
7486	20461	33821	0.87	0.0E+00	AJ270988.1	NT	Homo sapiens partial mRNA for LTRPC3 protein (LTRPC3 gene)
7530	20493	33855	1.12	0.0E+00	BE265499.1	EST_HUMAN	60174576.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529764 5'
7532	20495	33856	0.9	0.0E+00	11427865	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20281), mRNA
7533	20498		1.46	0.0E+00	AU116507.1	EST_HUMAN	AU116507 HEMBA1 Homo sapiens cDNA clone HEMBA1003669 5'
7536	20499	33859	2.02	0.0E+00	AF05213.1	NT	Homo sapiens ankryrin 1 (ANK1) mRNA, complete cds
7536	20499	33860	2.02	0.0E+00	AF05213.1	NT	Homo sapiens ankryrin 1 (ANK1) mRNA, complete cds
7547	20510	33868	0.85	0.0E+00	AF245505.1	NT	Homo sapiens edicin mRNA, complete cds
7555	20518	33873	7.23	0.0E+00	X70172.1	NT	H.sapiens DNA for ZNGP2 pseudogene, exon 4
7557	20520	33875	6.94	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7557	20520	33876	6.94	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7570	20533	33891	0.81	0.0E+00	AW65603.1	EST_HUMAN	EST1368573 MAGE resequences, MAGE Homo sapiens cDNA
7572	20535	33893	2.85	0.0E+00	AW65616.1	EST_HUMAN	EST1362688 MAGE resequences, MAGE Homo sapiens cDNA
7599	20560	33920	0.79	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7599	20560	33921	0.79	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7599	20560	33922	0.79	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7623	20583		0.62	0.0E+00	N80394.1	NT	Human BTFS3 protein homolog gene, complete cds
7624	20584	33947	0.72	0.0E+00	BE408263.1	EST_HUMAN	601302879.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:5637434 5'

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7635	20585	33958	0.5	0.0E+00	AW402542.1	EST_HUMAN	UI-HF-BK0-445-q-07-QJ1.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054924 5'
7653	20613		1.3	0.0E+00	R87430.1	EST_HUMAN	ym8h110.11 Soares adult brain N244-HB557 Homo sapiens cDNA clone IMAGE:190051 5'
7654	20614	33978	2.42	0.0E+00	AW239326.1	EST_HUMAN	x39a05.v1 NCL CGAP Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7676	20634		1.21	0.0E+00	AU117553.1	EST_HUMAN	HNF3FH TRANSCRIPTION FACTOR GENESIS:
7678	20636	33968	3.92	0.0E+00	11427135	NT	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7697	20655	34019	1.78	0.0E+00	AA211693.1	EST_HUMAN	z166f02.11 Stralagene muscled 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7703	20660	34024	0.58	0.0E+00	BF228235.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7710	20667	34034	0.62	0.0E+00	AW696409.1	EST_HUMAN	WRO-AN0083-270900-004-07 AN0083 Homo sapiens cDNA
7713	20670	34037	0.81	0.0E+00	L32832.1	NT	QV3-BN0046-220300-129-a04 BN0046 Homo sapiens cDNA
7740	20694	34058	1.17	0.0E+00	BF306998.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7746	20694	34059	1.17	0.0E+00	BF306998.1	EST_HUMAN	601889923.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123943 5'
7750	20703	34071	1.24	0.0E+00	AU118767.1	EST_HUMAN	601889923.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123943 5'
7782	20735	34107	0.49	0.0E+00	AW499551.1	EST_HUMAN	AU118767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
7809	20768	34132	0.64	0.0E+00	ABC02355.1	NT	UI-HF-BR0p-sj1-q-10-DJ1.1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074778 5'
7810	20769	34133	4.06	0.0E+00	A1762561.1	EST_HUMAN	Human mRNA for KIAA0357 gene, partial cds
7810	20769	34133	4.06	0.0E+00	A1762561.1	EST_HUMAN	cm17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm17d05 random
7810	20769	34134	4.06	0.0E+00	A1762561.1	EST_HUMAN	cm17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm17d05 random
7879	20823	34200	0.53	0.0E+00	AA398959.1	EST_HUMAN	zu8b007.r1 Soares testis NIH Homo sapiens cDNA clone IMAGE:743125 5'
7879	20823	34201	0.53	0.0E+00	AA398959.1	EST_HUMAN	zu8b007.r1 Soares testis NIH Homo sapiens cDNA clone IMAGE:743125 5'
7880	20824	34202	0.53	0.0E+00	AL048472.2	EST_HUMAN	DKFZp434J087.r1 434 (synonym: hhes) Homo sapiens cDNA clone DKFZp434J087 5'
7887	20840	34221	1.22	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7897	20840	34222	1.22	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7935	20848	34233	1.06	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7919	20862	34250	0.58	0.0E+00	BE438545.1	EST_HUMAN	HTMT-163F1 HTMT Homo sapiens cDNA
7920	20863	34251	1.03	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7939	20881	34271	0.5	0.0E+00	BF659005.1	EST_HUMAN	602185652.F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7950	20891	34282	0.73	0.0E+00	A1825504.1	EST_HUMAN	w617605.x1 NCL_GGAP_GC8 Homo sapiens cDNA clone IMAGE:2306976 5' similar to TR:O75863 O75863



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7950	20891	34293	0.73	0.0E+00	A1823504.1	EST_HUMAN	w617g06.ct NCL_CGAP_GCB Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR-075563 O75563 A1BC1.1
7958	20896	34292	3.09	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7955	20904	34296	0.96	0.0E+00	N76128.1	EST_HUMAN	zab6a05.ct Scapex fetal lung, NIH/19W Homo sapiens cDNA clone IMAGE:299456 3'
7971	20910	34300	5.4	0.0E+00	BF217605.1	EST_HUMAN	001854065F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
7976	20915	34306	0.93	0.0E+00	BF56882.1	EST_HUMAN	602785080F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310258 5'
7981	20920	34311	3.6	0.0E+00	AU128622.1	EST_HUMAN	001854062 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
8006	20923	34338	0.97	0.0E+00	AW059274.1	EST_HUMAN	cr42a09.x1 Jle bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42a09 3'
8006	20933	34339	0.97	0.0E+00	AW059274.1	EST_HUMAN	cr42a09.x1 Jle bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42a09 3'
8010	20948	34341	6.98	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8017	20955	34348	1.05	0.0E+00	AV758467.1	EST_HUMAN	AU758467 BM Homo sapiens cDNA clone BMBFGG05 5'
8020	20957	34350	5.84	0.0E+00	BE739870.1	EST_HUMAN	601563166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8020	20957	34351	5.84	0.0E+00	BE739870.1	EST_HUMAN	601563166F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
8021	20958	34352	0.88	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1, actin receptor interacting protein 1 (KIAA0705), mRNA
8021	20958	34353	0.88	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1, actin receptor interacting protein 1 (KIAA0705), mRNA
8022	20959	34354	3.3	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8022	20959	34355	3.3	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
8048	20985	34381	2.13	0.0E+00	BF560267.1	EST_HUMAN	rib22a04.x1 Scapex NSF_F8_3W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3263214 3' similar to contains element TARI1 repetitive element
8060	20997	34393	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8060	20997	34394	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
8101	21037	34437	0.94	0.0E+00	AW695307.1	EST_HUMAN	EST306377 MAOE reserquenes, MAGD Homo sapiens cDNA
8123	21060	34458	0.92	0.0E+00	Y16765.1	NT	Homo sapiens pathH1Aa pseudogene
8129	21069	34466	0.49	0.0E+00	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8130	21067	34467	0.99	0.0E+00	AU117353.1	EST_HUMAN	AU117353 HEMBA1 Homo sapiens cDNA clone HEMBA1001176 5'
8131	21068	34468	0.92	0.0E+00	BE613963.1	EST_HUMAN	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905733 5'
8146	21083	34482	4.38	0.0E+00	AW68044.1	EST_HUMAN	EST3380119 MAOE reserquenes, MAGI Homo sapiens cDNA
8147	21084	34483	0.75	0.0E+00	AU1133435.1	EST_HUMAN	HAB2043 Homo fetal liver cDNA library Homo sapiens cDNA
8186	21156	34595	0.64	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
8231	21200	34620	0.65	0.0E+00	BF217200.1	EST_HUMAN	001854071F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
8244	21213	34620	0.87	0.0E+00	BE313013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
8256	21225	34636	1.09	0.0E+00	AA149791.1	EST_HUMAN	600160611 Stralene codon (#637204) Homo sapiens cDNA clone IMAGE:566410 5'

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8268	21237	34648	0.88	0.0E+00	BF026628.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
8281	21250	34662	0.62	0.0E+00	AA017021.1	EST_HUMAN	z633908.r1 Soares telomere N2B4HR Homo sapiens cDNA clone IMAGE:360891 5'
8299	21288	34680	2.26	0.0E+00	BE735046.1	EST_HUMAN	601303563F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3659603 5'
8314	21283	34695	2.42	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8314	21283	34696	2.52	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8344	21313	34727	0.74	0.0E+00	AW674581.1	EST_HUMAN	b634d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652 F17K2.29 PROTEIN. ;
8344	21313	34728	0.74	0.0E+00	AW674581.1	EST_HUMAN	b634d02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652 F17K2.29 PROTEIN. ;
8351	21320	34734	2.47	0.0E+00	AA397551.1	EST_HUMAN	z631604.r1 Stralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
8356	21325	34735	0.92	0.0E+00	AW387131.1	EST_HUMAN	MRO-3T0031-061099-003-at11 ST0031 Homo sapiens cDNA
8356	21325	34735	0.92	0.0E+00	AB020691.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
8357	21328	34737	7.99	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y76A3.1 Homo sapiens cDNA clone Y76A4.1000277 5'
8361	21330	34741	1.12	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8361	21330	34742	1.12	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8376	21346	34756	0.46	0.0E+00	7657276	NT	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8378	21347	34758	0.92	0.0E+00	W95278.1	EST_HUMAN	z605001.r1 Soares fetal heart NBH119W Homo sapiens cDNA clone IMAGE:359081 5'
8378	21347	34759	0.92	0.0E+00	W95278.1	EST_HUMAN	z605001.r1 Soares fetal heart NBH119W Homo sapiens cDNA clone IMAGE:359081 5'
8380	21349	34760	17.98	0.0E+00	BF673096.1	EST_HUMAN	602153006F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284128 5'
8384	21353	34776	0.95	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARG1 Homo sapiens cDNA clone OVARG1001296 5'
8398	21387	34776	1.71	0.0E+00	BF52534.1	EST_HUMAN	602069832F1 NCI CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8398	21387	34777	1.71	0.0E+00	BF52534.1	EST_HUMAN	602069832F1 NCI CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4212727 5'
8430	21399	34810	1.65	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8430	21399	34811	1.65	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8473	21442	34811	1.24	0.0E+00	BE677863.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:368773 5'
8497	21655	34881	1.91	0.0E+00	AW50549.1	EST_HUMAN	U1HF-BND-ak4-c1-10JL11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
8505	21473	34887	10.07	0.0E+00	AW157233.1	EST_HUMAN	ad3608x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783769 5' similar to TR:O60468 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1] ;
8523	21491	34906	0.67	0.0E+00	AW072395.1	EST_HUMAN	xcu7d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2897639 5' similar to contains element OFR repetitive element. ;
8541	21609	34926	1.06	0.0E+00	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8544	21612	34926	0.83	0.0E+00	W01616.1	EST_HUMAN	z636005.r1 Soares fetal liver spleen NF1S Homo sapiens cDNA clone IMAGE:294633 5'

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8546	21514	34931	1.26	0.0E+00	BE746597.1	EST_HUMAN	601678105F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:382698 5'
8546	21514	34932	1.26	0.0E+00	BE746597.1	EST_HUMAN	601678105F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:382698 5'
8559	21527	34946	1.2	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8578	21548	34985	0.44	0.0E+00	DA5032.1	NT	Human DNA for ceruloplasmin, exon 5
8599	21587	34983	1.08	0.0E+00	AI387350.1	EST_HUMAN	q36512.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:1969334 3' similar to TR:Q14673 Q14673 KIA00184 PROTEIN. ;
8610	21578	34984	2.6	0.0E+00	BE074157.1	EST_HUMAN	747640.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O85793 Q95793 STAU7EN PROTEIN. ;
8612	21580	34988	1.22	0.0E+00	AI885871.1	EST_HUMAN	M60510.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
8625	21593	35012	1.29	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8625	21593	35013	1.29	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8633	21601	35023	1.93	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8633	21601	35024	1.93	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8635	21603	35026	1.35	0.0E+00	AA403192.1	EST_HUMAN	z669102.11 Soares_tibial_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798619 5' similar to TR:G1304132 G1304132 TPRD. ;
8635	21603	35027	1.35	0.0E+00	AA403192.1	EST_HUMAN	z669102.11 Soares_tibial_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798619 5' similar to TR:G1304132 G1304132 TPRD. ;
8678	21644		3.69	0.0E+00	AA39851.1	EST_HUMAN	z73408.61 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:585655 PROHIBITIN (HUMAN);
8685	21653	35076	0.93	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0094-120600-013-07 FN0094 Homo sapiens cDNA
8685	21654	35077	1.25	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8686	21654	35078	1.25	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8705	21673	35097	1.28	0.0E+00	BE512596.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858179 5'
8705	21673	35098	1.28	0.0E+00	BE612596.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858179 5'
8720	21688	35116	1.65	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8720	21688	35116	1.65	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8730	21698	35123	0.7	0.0E+00	AI894477.1	EST_HUMAN	nm3341.1x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O16457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
8737	21705	35128	0.85	0.0E+00	AA502294.1	EST_HUMAN	nc25610.at NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1196434 G1136434 KIAA0187 PROTEIN. ;
8742	21710		0.97	0.0E+00	11416759	NT	Homo sapiens proteolipid protein beta 3 (PCDH3), mRNA
8748	21717	35140	0.99	0.0E+00	AI580780.1	EST_HUMAN	hs0411.x1 Soares_pregnant_fetus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8752	21720		1.97	0.0E+00	BE860797.1	EST_HUMAN	601431288F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:391699 5'

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8778	21745	35168	0.55	0.0E+00	AW245765.1	EST_HUMAN	2822701.5p1r1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701.5'
8778	21745	35167	0.55	0.0E+00	AW245765.1	EST_HUMAN	2822701.5p1r1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701.5'
8779	21746	35168	2.62	0.0E+00	47586953	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8779	21746	35168	2.62	0.0E+00	47586953	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8783	21760	35172	0.52	0.0E+00	U89084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8783	21760	35173	0.52	0.0E+00	U89084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8851	21818	35238	1.02	0.0E+00	AJ251760.1	NT	Homo sapiens NESP5, GNA51 antisense (partial) and Xlaiphas (partial) genes
8851	21823	35244	3	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8851	21823	35245	3	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8858	21823	35248	3	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8871	21838	35280	1.82	0.0E+00	U82979.1	NT	Human Immunoglobulin-like transcript-3 mRNA, complete cds
8913	21879	35305	1.16	0.0E+00	AF022955.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8913	21879	35306	1.16	0.0E+00	AF022955.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8916	21882	35308	0.68	0.0E+00	AU131671.1	EST_HUMAN	AU131671.1 NT26P3 Homo sapiens cDNA clone NT26P303016.5'
8931	21897	35325	0.81	0.0E+00	11426572	NT	Homo sapiens Immunoglobulin superfamily, member 2 (IGSF2), mRNA
8935	21901		1.53	0.0E+00	AW513513.1	EST_HUMAN	601472196F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874912.5'
8937	21903		0.55	0.0E+00	BE78322.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
8938	21904	35328	11.32	0.0E+00	D52650.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-084C02
8969	21935	35391	3.89	0.0E+00	BE378495.1	EST_HUMAN	601236498F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3508709.5'
8975	21941	35395	3.98	0.0E+00	AA410545.1	EST_HUMAN	Z326d4.1 Sources ovary tumor N87H7 Homo sapiens cDNA clone IMAGE:724052.5'
8977	21943		3.27	0.0E+00	BF913946.1	EST_HUMAN	601600571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744.5'
8984	21950	35374	1.37	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
8989	21956	35379	1.38	0.0E+00	AW139673.1	EST_HUMAN	UIH-HB1-adr-e-12-DJL1 NCL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717887.3'
8989	21955	35380	1.38	0.0E+00	AW139673.1	EST_HUMAN	UIH-HB1-adr-e-12-DJL1 NCL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2717887.3'
8994	21980		0.61	0.0E+00	AI640160.1	EST_HUMAN	wa30b10.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2269579.3' similar to TR-O15044
9013	21979	35398	9.23	0.0E+00	BF377897.1	EST_HUMAN	OM1-TN0141-250800-439-b08 TN0141 Homo sapiens cDNA
9022	21986	35410	0.45	0.0E+00	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9028	21994	35414	2.93	0.0E+00	BE260272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836.5'
9033	21999	35418	2.98	0.0E+00	BF700766.1	EST_HUMAN	602127684F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:2264542.5'
9033	21999	35419	2.98	0.0E+00	BF700766.1	EST_HUMAN	602127684F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:2264542.5'

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## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit Database BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6033	21989	35420	2.98	0.0E+00	BF700165.1	EST_HUMAN	602127694F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284542 5'
6047	22013	35436	0.63	0.0E+00	AI458722.1	EST_HUMAN	IK13111.1x1 NCL_CGAP_LU24 Homo sapiens cDNA clone IMAGE:2150949 3'
6076	22042	35465	0.7	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Sleavrides GS) Homo sapiens cDNA
6084	22050	35472	12.98	0.0E+00	AA962527.1	EST_HUMAN	cc6002.61 NCL_CGAP_LU5 Homo sapiens cDNA clone IMAGE:1602164 3' similar to gb:MA6072 80S
6090	22056	35480	4.78	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN);
6090	22056	35481	4.78	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
6114	22080	35508	1.23	0.0E+00	Y1107.3	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
6114	22080	35510	2.41	0.0E+00	BE278677.1	EST_HUMAN	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
6126	22092		3.32	0.0E+00	AV718377.1	EST_HUMAN	601158330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
6132	22098	35525	3.36	0.0E+00	AW33277.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAP11 5'
6138	22104	35530	1.56	0.0E+00	AU724051.1	EST_HUMAN	xw73-07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone NT2RM2201575 5'
6214	22160	35611	0.88	0.0E+00	AU140704.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
6224	22160	35620	0.55	0.0E+00	AB007923.1	EST_HUMAN	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'
6229	22165	35624	0.51	0.0E+00	R17132.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
6229	22165	35625	0.61	0.0E+00	R17132.1	EST_HUMAN	yg09e09.11 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31674 5'
6233	22169	35627	5.11	0.0E+00	AW592233.1	EST_HUMAN	H48a09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:31674 5'
6233	22169	35628	5.11	0.0E+00	AW592233.1	EST_HUMAN	H48a09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
6269	22235	35664	0.46	0.0E+00	AU128904.1	EST_HUMAN	H48a09.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
6281	22247	35676	0.89	0.0E+00	AV714764.1	EST_HUMAN	AU128904.1 NT2P2 Homo sapiens cDNA clone NT2P2004265 5'
6286	22262	35680	3.01	0.0E+00	AL040428.1	EST_HUMAN	AV714764 DGB Homo sapiens cDNA clone DCBAUA06 5'
6296	22262	35681	3.01	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814.31 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
6302	22267	35687	1.27	0.0E+00	AF133901.1	NT	DKFZp434C1814.31 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814 3'
6304	22269	35700	1.89	0.0E+00	AB040645.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
6310	22275	35707	2.24	0.0E+00	BF075505.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
6312	22277		0.92	0.0E+00	BF068289.1	EST_HUMAN	702b03.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:4274708 6'
6342	22307	35733	4.64	0.0E+00	11422857	NT	S GAG ;
6352	22317	35743	1.44	0.0E+00	K01241.1	NT	Homo sapiens tumor protein p73 (TP73), mRNA
6361	22326	35754	4.23	0.0E+00	AB020630.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
6361	22326	35755	4.23	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
6366	22331	35781	1.71	0.0E+00	AB060739.1	EST_HUMAN	Homo sapiens mRNA for KIAA0823 protein, partial cds
6366	22331	35781	1.71	0.0E+00	AB060739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLOC12 3'

Table 4

## Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9372	22337	35767	3.07	0.0E+00	7708638	NT	Homo sapiens polyoma-L (PKOL), mRNA
9377	22342	35772	2.22	0.0E+00	BE793328.1	EST_HUMAN	601588304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
9378	22343	35773	0.46	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
9378	22343	35774	0.48	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
9391	22358	35774	0.98	0.0E+00	H73937.1	EST_HUMAN	6003908.11 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:232767 5'
9401	22366	35798	4.19	0.0E+00	BE315402.1	EST_HUMAN	60141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9411	22366	35799	4.19	0.0E+00	BE315402.1	EST_HUMAN	60141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9411	22370	35814	0.59	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9411	22370	35815	0.59	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9414	22370	35815	0.52	0.0E+00	M89983.1	NT	Human polymorphic loci in Xq28
9416	22381	35919	1.74	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9433	22397	35935	0.5	0.0E+00	AU127096.1	EST_HUMAN	AU127096 NT2RP2 Homo sapiens cDNA clone NT2RP2000579 5'
9437	22401	35939	1.29	0.0E+00	AI061395.1	EST_HUMAN	an29d04.x1 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9442	22406	35943	1.98	0.0E+00	AI854807.1	EST_HUMAN	w334412.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MG83_HUMAN
9447	22411	35948	4.1	0.0E+00	9255595	NT	O19460 MELANOMA-ASSOCIATED ANTIGEN B3
9459	22422	35980	1.18	0.0E+00	AW958311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9468	22432	35970	4.72	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9484	22448	35888	1.44	0.0E+00	AU142862.1	EST_HUMAN	AU142862 Y76A31 Homo sapiens cDNA clone Y76A31000578 5'
9489	22463	35604	1.48	0.0E+00	1143895	NT	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9500	22484	35604	0.8	0.0E+00	BE410768.1	EST_HUMAN	601301679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636163 5'
9513	22476	35621	1.29	0.0E+00	BF002024.1	EST_HUMAN	7697H12.x1 NCI_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9LH82
9527	22490	35937	1.28	0.0E+00	AB011150.1	NT	Q9LH82 HYPOPHYSICAL 42.5 KD PROTEIN ;
9528	22491	35938	4.85	0.0E+00	BE794823.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9534	22497	35945	1.04	0.0E+00	AU136220.1	EST_HUMAN	601569294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
9539	22502	35950	1.38	0.0E+00	BE883943.1	EST_HUMAN	AU136220 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9539	22502	35951	1.36	0.0E+00	BE883943.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911985 5'
9557	22519	35967	0.77	0.0E+00	AB011166.1	NT	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911985 5'
9591	22523	35971	3.53	0.0E+00	AA344601.1	EST_HUMAN	Homo sapiens mRNA for KIAA0594 protein, partial cds
9561	22523	35972	3.53	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder1 Homo sapiens cDNA 5' end
9519	22553	36011	1.02	0.0E+00	AW673469.1	EST_HUMAN	h654d08.x3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O60275 O60275 KIAA0922 PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9619	22563	36012	1.02	0.0E+00	AW167469.1	EST_HUMAN	baf5408.3 NIH_MGC.10 Homo sapiens cDNA clone IMAGE:2600367 5' similar to TR:060275 O60275 KIAA0522 PROTEIN;
9653	22566	36044	4.71	0.0E+00	BE207063.1	EST_HUMAN	baf905.y1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2623873 5' similar to gbL35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9653	22566	36045	4.71	0.0E+00	BE207063.1	EST_HUMAN	baf905.y1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2623873 5' similar to gbL35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9654	22621	36275	1.77	0.0E+00	BF348013.1	EST_HUMAN	902023150F1 NC1 CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4169300 5'
9700	22653	36107	2.9	0.0E+00	BE712515.1	EST_HUMAN	QV2-H10898-250700-282-508 HT10808 Homo sapiens cDNA
9732	22760	36213	0.86	0.0E+00	BF034377.1	EST_HUMAN	801455116F1 NIH_MGC.68 Homo sapiens cDNA clone IMAGE:3859035 5'
9732	22760	36214	0.86	0.0E+00	BF034377.1	EST_HUMAN	801455116F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3859035 5'
9738	22768	36221	0.53	0.0E+00	AB068551.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA
9741	22769	36223	3.69	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and TIM domains), member 5 (LILR95), mRNA
9741	22769	36224	3.69	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and TIM domains), member 5 (LILR95), mRNA
9751	22892	36149	2.54	0.0E+00	AL042278.1	EST_HUMAN	DKFZP434L0120.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZP434L0120 5'
9756	22727	36183	2.35	0.0E+00	AL098043.1	EST_HUMAN	aw60101.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 KIAA0171 PROTEIN;
9793	21118	34515	0.85	0.0E+00	BF306932.1	EST_HUMAN	501802245F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4139066 5'
9795	21118	34518	2.84	0.0E+00	11580151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9795	21118	34519	2.84	0.0E+00	11580151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9797	21120	34522	20.82	0.0E+00	AL290909.1	EST_HUMAN	qtm08a0.6.x1 NC1 CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL28_HUMAN P23916 60S RIBOSOMAL PROTEIN L23A;
9797	21120	34523	20.82	0.0E+00	AL290909.1	EST_HUMAN	qtm09a0.6.x1 NC1 CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1881288 3' similar to SW:RL28_HUMAN P23916 60S RIBOSOMAL PROTEIN L23A;
9798	21121	34524	3.57	0.0E+00	AW953836.1	EST_HUMAN	EST368028 IMAGE: resseques, MAGC Homo sapiens cDNA
9825	22674	36129	3.43	0.0E+00	AF163486.1	NT	Homo sapiens polyoma kidney disease 2-like protein (PKD2L) gene, exon 8
9828	22671	36133	0.60	0.0E+00	BE695128.1	EST_HUMAN	901510892F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3912165 5'
9828	22671	36134	0.60	0.0E+00	BE695128.1	EST_HUMAN	901510892F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3912165 5'
9837	22773	36231	2.22	0.0E+00	BE258629.1	EST_HUMAN	80110942F1 NIH_MGC.16 Homo sapiens cDNA clone IMAGE:3350722 5'
9840	22776	36232	1.36	0.0E+00	BE781382.1	EST_HUMAN	801466828F1 NIH_MGC.67 Homo sapiens cDNA clone IMAGE:3870007 5'
9840	22776	36232	1.36	0.0E+00	BE781382.1	EST_HUMAN	801466828F1 NIH_MGC.67 Homo sapiens cDNA clone IMAGE:3870007 5'
9843	22779	36234	30.94	0.0E+00	AW163778.1	EST_HUMAN	ab6604.y1 Schneider field brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gbL36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);





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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10153	23078	36554	1.71	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
10152	23087	36564	0.82	0.0E+00	BE208710.1	EST_HUMAN	b52601.x1 NIH_MGC 5 Homo sapiens cDNA clone IMAGE:2964000 3'
10178	23103	36583	2.6	0.0E+00	AJ132349.1	EST_HUMAN	AJ132349 NT28P3 Homo sapiens cDNA clone NT2RP3004260 5'
10178	23103	36584	2.8	0.0E+00	AJ132349.1	EST_HUMAN	AJ132349 NT28P3 Homo sapiens cDNA clone NT2RP3004260 5'
10187	23112	36598	1.82	0.0E+00	AW500936.1	EST_HUMAN	UHRF-BPou-405-Q171 NIH_MGC 51 Homo sapiens cDNA clone IMAGE:3072897 5'
10193	23118	36602	18.11	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3949383 5'
10193	23118	36603	18.11	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3949383 5'
10194	23119	36604	0.45	0.0E+00	AB030357.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
10194	23119	36605	0.46	0.0E+00	AB030357.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
10206	23131	36618	1.76	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
10224	23149	36538	3.6	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434B2418.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2418 5'
10229	23154	36544	0.71	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2418.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2418 5'
10238	23164	36551	2.57	0.0E+00	AJ132349.1	EST_HUMAN	AJ132349 NT28P3 Homo sapiens cDNA clone NT2RP3004260 5'
10240	23165	36552	2.44	0.0E+00	AF152308.1	NT	Homo sapiens proteodherin alpha 12 (PODH-alpha12) mRNA, complete cds
10268	23193	36580	5.52	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10268	23193	36581	5.52	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10284	23209	36594	2.5	0.0E+00	BF092698.1	EST_HUMAN	NR4-TN0114-110900-101-404 TN0114 Homo sapiens cDNA
10314	23238	36720	2.73	0.0E+00	BE280793.1	EST_HUMAN	601159227F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3138798 5'
10323	23247	36728	1.2	0.0E+00	BE388700.1	EST_HUMAN	601288355F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3613045 5'
10323	23247	36727	1.2	0.0E+00	BE388700.1	EST_HUMAN	601288355F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3613045 5'
10332	23247	36727	1.2	0.0E+00	BE388700.1	EST_HUMAN	601288355F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3613045 5'
10332	23256	36733	3.64	0.0E+00	AW236269.1	EST_HUMAN	xn72901.x1 NCI_CGAP_CvML1 Homo sapiens cDNA clone IMAGE:2699877 3' similar to gb-X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10353	23287	36734	0.75	0.0E+00	AA341305.1	EST_HUMAN	EST146740 Fetal kidney II Homo sapiens cDNA 5' end
10342	23268	36745	0.63	0.0E+00	11427235	NT	Homo sapiens Chondrak-Higashi syndrome 1 (CHS1), mRNA
10363	23286	36763	0.76	0.0E+00	AW864113.1	EST_HUMAN	EST376186 IMAGE:resequenc, MAGH Homo sapiens cDNA
10376	23299	36774	7.08	0.0E+00	AJ143673.1	EST_HUMAN	AJ143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10376	23299	36775	7.08	0.0E+00	AJ143673.1	EST_HUMAN	AJ143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10376	23302	36778	13.11	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIR3C gene, exons 2, 3, and 4
10382	23304	36780	2.8	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10382	23304	36781	2.8	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10416	23338	36824	3.43	0.0E+00	AJ136637.1	EST_HUMAN	AJ136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10416	23338	36825	3.43	0.0E+00	AJ136637.1	EST_HUMAN	AJ136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10432	23354	36839	2.24	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10432	23354	36840	2.24	0.0E+00/AJ29844.1	NT		Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
10437	23359	36847	0.75	0.0E+00/AV695712.1	EST_HUMAN		AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
10437	23359	36848	0.75	0.0E+00/AV695712.1	EST_HUMAN		AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
10443	23365	36855	0.76	0.0E+00/AF072408.1	NT		Homo sapiens killer cell inhibitory receptor KIR3J gene, exons 2, 3, and 4
10445	23367	36858	2.64	0.0E+00/AA196387.1	EST_HUMAN		z897h11.1 Strategene muscle 83/209 Homo sapiens cDNA clone IMAGE:628197 5'
10470	23392	36887	1.78	0.0E+00/AA131248.1	EST_HUMAN		z897h11.1 Scores_pregnant_uterus_NbJPU Homo sapiens cDNA clone IMAGE:503545 5'
10470	23392	36888	1.78	0.0E+00/AA131248.1	EST_HUMAN		z897h11.1 Scores_pregnant_uterus_NbJPU Homo sapiens cDNA clone IMAGE:503545 5'
10517	23439	36937	1.79	0.0E+00/AF179308.1	NT		Homo sapiens KIF4 (KIF4) mRNA, complete cds
10581	23483	36978	0.88	0.0E+00/BE980588.1	EST_HUMAN		801491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3853657 5'
10573	23496	36987	11.49	0.0E+00/BE730772.1	EST_HUMAN		801570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10573	23496	36988	11.49	0.0E+00/BE730772.1	EST_HUMAN		801570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10578	23500	36992	0.82	0.0E+00/AU127403.1	EST_HUMAN		AU127403 NT2R2P2 Homo sapiens cDNA clone NT2R2P201212 5'
10588	23510	37003	0.86	0.0E+00/BE958511.1	EST_HUMAN		801645134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930177 5'
10588	23510	37004	0.88	0.0E+00/BE958511.1	EST_HUMAN		801645134F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930177 5'
10605	23527	37023	0.88	0.0E+00/BE907487.1	EST_HUMAN		801432313F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10616	23538	37037	0.88	0.0E+00/AA311624.1	EST_HUMAN		EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10617	23539	37038	0.56	0.0E+00/4758827	NT		Homo sapiens neuroxin III (NRXN3) mRNA
10629	23551	37051	0.78	0.0E+00/BE991113.1	EST_HUMAN		801432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917698 5'
10632	23564	37054	1.19	0.0E+00/11660161	NT		Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10642	23564	37060	1.39	0.0E+00/AB029290.1	NT		Homo sapiens mRNA for actin binding protein ABP820, complete cds
10643	23565	37061	0.6	0.0E+00/BE304522.1	EST_HUMAN		801105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10643	23565	37062	0.6	0.0E+00/BE304522.1	EST_HUMAN		801105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10650	23572	37067	4.13	0.0E+00/AB000590.1	NT		Homo sapiens mRNA for estrogen receptor beta, complete cds
10650	23572	37068	4.13	0.0E+00/AB000590.1	NT		Homo sapiens mRNA for estrogen receptor beta, complete cds
10658	23580	37077	1.27	0.0E+00/AA704457.1	EST_HUMAN		gbM14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10660	23582	37078	1.19	0.0E+00/M22921.1	NT		Human beta 1.4-galactosyl-transferase mRNA, complete cds
10662	23584	37081	4.52	0.0E+00/BF340331.1	EST_HUMAN		802037045F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
10662	23584	37082	4.62	0.0E+00/BF340331.1	EST_HUMAN		802037045F1 NCL CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
10687	23609	37103	5.24	0.0E+00/BE987149.1	EST_HUMAN		801439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10687	23609	37104	5.24	0.0E+00/BE987149.1	EST_HUMAN		801439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10719	23641	37134	0.48	0.0E+00/AV16271.1	EST_HUMAN		AV176271 DCS Homo sapiens cDNA clone DCSBD009 5'
10719	23641	37135	0.48	0.0E+00/AV16271.1	EST_HUMAN		AV176271 DCS Homo sapiens cDNA clone DCSBD009 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10750	23672	37167	1.13	0.0E+00	A1631818.1	EST_HUMAN	w3d5603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE
10750	23672	37168	1.13	0.0E+00	A1631818.1	EST_HUMAN	w3d5603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204 Q61204 NOTCH2-LIKE
10764	23685	37181	2	0.0E+00	T03078.1	EST_HUMAN	F823A4 Fetal brain, Stratagene Homo sapiens cDNA clone F823A4 3'end
10769	23710	37212	0.67	0.0E+00	AU122429.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10765	23716	37218	0.43	0.0E+00	6005621	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
10817	23738	37241	2.63	0.0E+00	BF406218.1	EST_HUMAN	hnb45a12.x1 Scores_NSF_Eb_9W_OT_P_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10818	23739		1.3	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLC2Z007 3'
10837	23757	37257	5.03	0.0E+00	AW517850.1	EST_HUMAN	ku74601.x1 NCI_CGAP_K48 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gbM59066 MOESIN (HUMAN);
10841	23761	37261	18.38	0.0E+00	BE546213.1	EST_HUMAN	61017874F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10858	23768	37278	0.84	0.0E+00	11436003	NT	Homo sapiens hydrolytic protein DKFZp781P1010 (DKFZp781P1010), mRNA
10863	23803	37307	0.44	0.0E+00	X68856.1	NT	H1 sapiens myRNA for NK receptor (183 Act)
10884	23804	37308	4.15	0.0E+00	BE781742.1	EST_HUMAN	610487419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3970700 5'
10903	23823	37334	3.07	0.0E+00	BE082720.1	EST_HUMAN	RC2-B10842-012-003 B10842 Homo sapiens cDNA
10903	23823	37356	3.07	0.0E+00	BE082720.1	EST_HUMAN	RC2-B10842-160200-012-003 B10842 Homo sapiens cDNA
10910	23830	37353	0.96	0.0E+00	Y08032.1	NT	Homo endogenous retrovirus-K, LTR US and gag gene
10915	23835	37341	0.7	0.0E+00	A1656890.1	EST_HUMAN	11654007.x1 NCI_CGAP_G038 Homo sapiens cDNA clone IMAGE:2244812 3'
10922	23842	37358	1.6	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10925	23845	37361	0.67	0.0E+00	BE617655.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10946	23865	37380	0.55	0.0E+00	X39805.1	EST_HUMAN	6014477231 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845685 3'
10960	23880	37393	0.48	0.0E+00	AW748117.1	EST_HUMAN	6014477231 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845685 3'
10972	23892	37400	1.16	0.0E+00	D87675.1	NT	QV6-B10107-2307599-007-006 B10107 Homo sapiens cDNA
10973	23893	37407	0.48	0.0E+00	AF081364.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10994	23914	37430	0.46	0.0E+00	AW342141.1	EST_HUMAN	Synthetic construct Q350 ligand-ecotactin A fusion protein (Q350L-E1A fusion), partial cds
10994	23914	37431	0.46	0.0E+00	AW342141.1	EST_HUMAN	EST 00007 Human differential display products Homo sapiens cDNA clone UNCCD7
10994	23914	37431	0.46	0.0E+00	AW342141.1	EST_HUMAN	EST 00007 Human differential display products Homo sapiens cDNA clone UNCCD7
10999	23965	37469	1.72	0.0E+00	AW711075.1	EST_HUMAN	AW711075 Cu Homo sapiens cDNA clone CUAAKG05 6'
10999	23965	37469	1.72	0.0E+00	AW711075.1	EST_HUMAN	AW711075 Cu Homo sapiens cDNA clone CUAAKG05 6'
11001	23967	37460	3.28	0.0E+00	AW813783.1	EST_HUMAN	RC3-S10197-170200-015-403 S10197 Homo sapiens cDNA
11007	23972	37460	0.97	0.0E+00	AW695563.1	EST_HUMAN	EST3776638 A1P-binding cassette, sub-family A (ABC1), member 3 (ABCAC3), mRNA
11019	23984	37510	1.81	0.0E+00	11431124	NT	Homo sapiens A1P-binding cassette, sub-family A (ABC1), member 3 (ABCAC3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11019	23984	37511	1.81	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11023	23988	37515	1.76	0.0E+00	AW057621.1	EST_HUMAN	wy1109.x1 Soares_NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR-Q60568 Q60568 VDX.
11029	23993	37520	1.86	0.0E+00	BE245270.1	EST_HUMAN	TCAAPDQ0917 Podiatric acute myelogenous leukemia cell (FAB M1) Bayer-HGSC project-TCAA Homo sapiens cDNA clone TCAAP0917
11030	23994	37521	2.64	0.0E+00	AI652239.1	EST_HUMAN	wb28412.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element
11030	23994	37522	2.64	0.0E+00	AI652239.1	EST_HUMAN	MSR1 MSR1 repetitive element
11034	23998	37525	2.73	0.0E+00	BF306542.1	EST_HUMAN	MSR1 MSR1 repetitive element
11041	24005	37531	3.83	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
11041	24005	37532	3.83	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
11055	24018	37541	5.31	0.0E+00	AW404795.1	EST_HUMAN	ULHF-BL0-acm-d-04-0-J1.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
11058	24021	37544	2.69	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
11059	24022	37545	7.34	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
11059	24022	37546	7.34	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
11080	24023	37547	2.71	0.0E+00	AI691827.1	EST_HUMAN	wb2806.x1 Soares_Dickgraefer_colon_NHCO Homo sapiens cDNA clone IMAGE:3906885 5'
11083	24026	37551	1.64	0.0E+00	BE982109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906885 5'
11086	24029	37553	21.37	0.0E+00	BE991630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918636 5'
11098	24031	37554	4.89	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11098	24031	37555	4.89	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
11098	24031	37555	4.89	0.0E+00	8923939	NT	z95611.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:627833 5' similar to gb:X03740
11083	18962	32151	5.67	0.0E+00	AA165905.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11103	24063	37586	100.2	0.0E+00	AA609080.1	EST_HUMAN	hw7008.s1 NCI_CGAP_G080 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57809 IG
11104	24064	37587	4.22	0.0E+00	BE763498.1	EST_HUMAN	LAMBDA CHAIN C REGIONS (HUMAN);
11113	24073	37595	15.77	0.0E+00	AV727382.1	EST_HUMAN	601598928F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945015 5'
11113	24073	37596	15.77	0.0E+00	AV727382.1	EST_HUMAN	AV727382 HTc Homo sapiens cDNA clone HTCAQH06 5'
11126	24086	37613	14.2	0.0E+00	AA464313.1	EST_HUMAN	AV727382 HTc Homo sapiens cDNA clone HTCAQH06 5'
11129	24089	37618	24.26	0.0E+00	AW516055.1	EST_HUMAN	z978012.r1 Soares_ova1 NihO1 Homo sapiens cDNA clone IMAGE:809878 5' similar to gb:X72467
11129	24089	37618	24.26	0.0E+00	AW516055.1	EST_HUMAN	IG KAPPA CHAIN PRECURSOR V-J REGION (HUMAN);
11134	24094	37623	1.88	0.0E+00	AU135741.1	EST_HUMAN	xy0410.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2862226 3' similar to gb:M60854_40S
11134	24094	37623	1.88	0.0E+00	AU135741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
11134	24094	37623	1.88	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11139	24099	37626	3.36	0.0E+00	AW593333.1	EST_HUMAN	hg13cd02.x1 Scores_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSRT1 repetitive element;
11139	24099	37627	3.36	0.0E+00	AW593333.1	EST_HUMAN	hg13cd02.x1 Scores_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSRT1 repetitive element;
11139	24099	37628	3.36	0.0E+00	AW593333.1	EST_HUMAN	hg13cd02.x1 Scores_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSRT1 repetitive element;
11141	24101	37629	1.68	0.0E+00	Z34897.1	NT	H.sapiens mRNA for HT histamine receptor
11142	24102	37630	2.54	0.0E+00	F13059.1	EST_HUMAN	HSC3C3C3 normalized infant brain cDNA
11159	24117	37643	2.4	0.0E+00	M2751.1	NT	Homo sapiens immunoglobulin kappa-chain A14 V-region precursor (IGKV) gene, partial cds
11159	24117	37644	2.4	0.0E+00	M2751.1	NT	Homo sapiens immunoglobulin kappa-chain A14 V-region precursor (IGKV) gene, partial cds
11167	24125	37654	40.1	0.0E+00	AW338094.1	EST_HUMAN	xw6601.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 (G MU CHAIN C REGION (HUMAN);
11168	24126	37655	3.64	0.0E+00	AW451230.1	EST_HUMAN	U1H-B13-alt-e-01-01.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11168	24126	37656	3.54	0.0E+00	AW451230.1	EST_HUMAN	U1H-B13-alt-e-01-01.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11170	19318	37674	8.04	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11184	24140	37682	2.07	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3029219 5'
11189	24151	37686	2.13	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
11199	24154	37686	1.69	0.0E+00	Z20556.1	NT	Homo sapiens cDNA for cardiac alpha-myosin heavy chain gene
11206	24160	37690	1.68	0.0E+00	BE294695.1	EST_HUMAN	601168324F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3539012 5'
11214	24167	37696	1.62	0.0E+00	BE792155.1	EST_HUMAN	601168204F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3636639 5'
11215	24168	37698	70.33	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4302432 5'
11217	24170	37698	7.68	0.0E+00	AU118398.1	EST_HUMAN	AU118398 HEMBA1 Homo sapiens cDNA clone HEMBA1003488 5'
11218	24171		2.51	0.0E+00	AW236269.1	EST_HUMAN	x72b01.x1 NCI CGAP_OML1 Homo sapiens cDNA clone IMAGE:2689077 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11223	24176	37702	4.92	0.0E+00	A1149506.1	EST_HUMAN	q43cd03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'
11223	24176	37703	4.92	0.0E+00	A1149506.1	EST_HUMAN	q43cd03.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1762772 3'
11234	24177	37704	2.09	0.0E+00	AW351937.1	EST_HUMAN	QV4-ST0234-121199-032-006 S10234 Homo sapiens cDNA
11234	24187		1.94	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11238	24191	37710	9.23	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
11244	24197	37716	145.99	0.0E+00	AW804516.1	EST_HUMAN	QVQ-UM0093-170400-191-d08 UM0093 Homo sapiens cDNA
11244	24197	37717	145.99	0.0E+00	AW804516.1	EST_HUMAN	QVQ-UM0093-170400-191-d08 UM0093 Homo sapiens cDNA
11245	24198	37718	3.26	0.0E+00	BF340308.1	EST_HUMAN	602307014F1 NCI CGAP_BnB4 Homo sapiens cDNA clone IMAGE:4184978 5'
11247	24200	37721	49.07	0.0E+00	BE281209.1	EST_HUMAN	601146357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:316310 5'
11251	24204	37726	1.74	0.0E+00	AB026040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11256	24208	37731	8.12	0.0E+00	U50328.1	NT	Human protein kinase C substrate 60K-H (PRKCSH) gene, exon 15-17
11257	24209	37732	1.72	0.0E+00	Z20656.1	NT	Homo sapiens cDNA alpha-myosin heavy chain gene
11260	24212	37735	6	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT10134-17/0700-012-07 FT10134 Homo sapiens cDNA
11260	24212	37736	6	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT10134-17/0700-012-07 FT10134 Homo sapiens cDNA
11263	24233	37759	89.91	0.0E+00	AA740782.1	EST_HUMAN	363287.01 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSRT1 repetitive element
11285	24235	37762	38.54	0.0E+00	AW465922.1	EST_HUMAN	hcd404.4x1 NCL CGAP_Kid2 Homo sapiens cDNA clone IMAGE:2372759 3'
11291	24241	37768	2.95	0.0E+00	AF262303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
11304	24254	37780	1.84	0.0E+00	BE268478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11304	24254	37781	1.84	0.0E+00	BE268478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11307	24257	37783	7.6	0.0E+00	C05039.1	EST_HUMAN	C05088 Homo sapiens cDNA (YNAKamure) Homo sapiens cDNA clone 3NHQ4817
11313	24263	37789	1.91	0.0E+00	AA746375.1	EST_HUMAN	ca55901.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11313	24263	37790	1.91	0.0E+00	AA746375.1	EST_HUMAN	ca55901.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11321	24271	37796	1.66	0.0E+00	BF353523.1	EST_HUMAN	Q12-HT0688-020800-285-007 HT0688 Homo sapiens cDNA
11322	24272	37799	5.79	0.0E+00	AL157608.1	EST_HUMAN	DKFZP761J2116_11 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761J2116 5'
11333	24283	37807	6.83	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
11347	24297	37825	1.54	0.0E+00	AU132437.1	EST_HUMAN	AU132437 NT2RP3 Homo sapiens cDNA clone NT2RP3004422 5'
11367	18868	32047	2.84	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neuritin II, complete cds
11367	18868	32048	2.84	0.0E+00	AB035268.1	NT	Homo sapiens mRNA for neuritin II, complete cds
11371	24318	37846	2.4	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-000500-002-E05 HT0645 Homo sapiens cDNA
11371	24318	37847	2.4	0.0E+00	BE182360.1	EST_HUMAN	PMO-HT0645-000500-002-E05 HT0645 Homo sapiens cDNA
11372	24319	37848	1.48	0.0E+00	AV701162.1	EST_HUMAN	AV701162 ADA Homo sapiens cDNA clone ADAAA06 5'
11372	24319	37863	75.44	0.0E+00	AV701162.1	EST_HUMAN	U1HF-B10-acc-2-09-0-U11 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060089 5'
11387	24334	37865	2.81	0.0E+00	BE96423.1	EST_HUMAN	601436092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
11387	24342	37874	2.26	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BND-alg-d-02-0-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11387	24342	37875	2.26	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BND-alg-d-02-0-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11397	24342	37875	2.26	0.0E+00	AW500307.1	EST_HUMAN	U1HF-BND-alg-d-02-0-U11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb-Y00345_cds1
11398	24343	37876	7.11	0.0E+00	BE018293.1	EST_HUMAN	POLYADENYLATE BINDING PROTEIN (HUMAN); gb-X85553 M.musculus mRNA for poly(A) binding protein (MOUSE);
11417	24361	37896	14.92	0.0E+00	X59314.1	NT	H.sapiens gene for Ig kappa light chain variable region "011"
11421	24365	37900	2.3	0.0E+00	AU121677.1	EST_HUMAN	AU121677 MAMMA1 Homo sapiens cDNA clone MAMMA1000731 5'
11430	24374	37913	4.14	0.0E+00	BE807653.1	EST_HUMAN	601440448F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11431	24375	37914	1.99	0.0E+00	AA459545.1	EST_HUMAN	ac86g11.X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11431	24375	37916	1.68	0.0E+00	AA459545.1	EST_HUMAN	ac86g11.X1 meningioma Homo sapiens cDNA clone IMAGE:1952804 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11441	24384	37924	4.83	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120.5'
11446	24389	37931	4.18	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #836215, Homo sapiens cDNA clone 77E12
11446	24389	37932	4.18	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #836215, Homo sapiens cDNA clone 77E12
11474	24417	37987	2.85	0.0E+00	4758827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
11475	24418	37965	3.38	0.0E+00	BF205561.1	EST_HUMAN	601870802F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4101433 5'
11478	24421	37970	12.88	0.0E+00	AW207734.1	EST_HUMAN	U1H-B12-agg-h-01-q-U1 s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11479	24422	37971	5.09	0.0E+00	AW604975.1	EST_HUMAN	RCQ-CT0380-210100-032-ct10 CT0380 Homo sapiens cDNA
11479	24422	37972	5.09	0.0E+00	AW604975.1	EST_HUMAN	RCQ-CT0380-210100-032-ct10 CT0380 Homo sapiens cDNA
11483	24426	37975	2.81	0.0E+00	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11483	24426	37976	2.91	0.0E+00	AB018280.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11484	24427	37977	3.54	0.0E+00	BE208846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
11484	24427	37978	3.54	0.0E+00	BE208846.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
11508	24448	37998	2.13	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11509	24870	34037	1.82	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A), mRNA
11513	24454	38003	3.74	0.0E+00	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-104 HT0230 Homo sapiens cDNA
11513	24454	38004	3.74	0.0E+00	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-104 HT0230 Homo sapiens cDNA
11523	24464	38017	7.84	0.0E+00	AA195905.1	EST_HUMAN	z95511.1 Stratagene muscle 837209 Homo sapiens cDNA clone IMAGE:627693 5' similar to gb:303740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11531	24472	38023	1.51	0.0E+00	AW973469.1	EST_HUMAN	bio4408.v1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN. ;
11531	24472	38024	1.51	0.0E+00	AW973469.1	EST_HUMAN	bio4408.v1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN. ;
11549	24490	38046	5.23	0.0E+00	BF507876.1	EST_HUMAN	U1H-B14-ask-b-10-q-U1 s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11549	24490	38047	5.23	0.0E+00	BF507876.1	EST_HUMAN	U1H-B14-ask-b-10-q-U1 s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11556	24496	38052	3.54	0.0E+00	AU135570.1	EST_HUMAN	AU13570 PLACE1 Homo sapiens cDNA clone PLACE101381 5'
11560	24500	38056	1.84	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271630 5'
11560	24500	38057	1.84	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271630 5'
11561	24501	38058	17.24	0.0E+00	BE878401.1	EST_HUMAN	901486828F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3889207 5'
11561	24501	38059	17.24	0.0E+00	BE878401.1	EST_HUMAN	901486828F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3889207 5'
11567	24507	38064	2.9	0.0E+00	DB7682.1	NT	Human mRNA for KIAA0241 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11571	24510		5.42	0.0E+00	BF240538.1	EST_HUMAN	601875530F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4069710 5'
11582	24520	38076	1.69	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11582	24520	38076	1.68	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11588	24524	38079	3.41	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11588	24524	38080	3.41	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11590	24528	38085	2.06	0.0E+00	BE122784.1	EST_HUMAN	23_08 Human Epidermal Keratinocyte Subtraction Library. Upregulated Transcripts Homo sapiens cDNA clone 23_08_5 similar to Homo sapiens cyclin B2 (CCNB2)
11591	24529	38086	3.23	0.0E+00	BE017890.1	EST_HUMAN	bb73905.v1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048057 5' similar to SW:CD97_HUMAN
11595	24533	38089	2.69	0.0E+00	AA772837.1	EST_HUMAN	P48960 LELUCOCYTE ANTIGEN CD97 PRECURSOR. [1];
11605	24543	38103	6.4	0.0E+00	4603844	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11612	24553	38110	2.25	0.0E+00	BF576297.1	EST_HUMAN	802134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11615	24553	38114	5.5	0.0E+00	AW328173.1	EST_HUMAN	dr04005.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11620	24558		83.29	0.0E+00	ME50983.1	NT	Human gamma actin-like pseudogene, complete cds
11624	24562	38123	159.29	0.0E+00	AI960908.1	EST_HUMAN	wf20s1.1; Soares_Dickgreafe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:MB8789 IG GAMMA-1 CHAIN C REGION (HUMAN);
11625	24563	38124	2.3	0.0E+00	BF306996.1	EST_HUMAN	601889623F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11625	24563	38125	2.3	0.0E+00	BF306996.1	EST_HUMAN	601889623F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11632	24569	38133	59.51	0.0E+00	BF362442.1	EST_HUMAN	QV2-NN0054-230800-333-404 NN0054 Homo sapiens cDNA
11648	24585	38154	2.42	0.0E+00	U38284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11648	24585	38155	2.42	0.0E+00	U38284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11654	24591		4.74	0.0E+00	BE897051.1	EST_HUMAN	801439805F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11655	24601	38177	1.54	0.0E+00	8923698	NT	Homo sapiens poligin-like protein (GLP), mRNA
11658	24604		2.24	0.0E+00	BF207682.1	EST_HUMAN	601185194F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4081715 5'
11668	24605		4.82	0.0E+00	BE237744.1	EST_HUMAN	601116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357384 5'
11682	24646	38225	4.13	0.0E+00	BE208948.1	EST_HUMAN	ba04007.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 E1B; 55KDA-ASSOCIATED PROTEIN. ;
11682	24648	38226	4.13	0.0E+00	BE208946.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN. ;
11684	24650	38228	3.8	0.0E+00	AW175028.1	EST_HUMAN	Q1V0-CT0225-01259-071-08 CT0225 Homo sapiens cDNA
11689	24655		4.96	0.0E+00	AA558707.1	EST_HUMAN	rh42008.s1 NCL CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11660	18451	31322	3.12	0.0E+00	AI934954.1	EST_HUMAN	wf05g08.x1 NCL CGAP_KIR12 Homo sapiens cDNA clone IMAGE:2464094 3'
11691	24656	38234	9.26	0.0E+00	AW327895.1	EST_HUMAN	dr02008.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846819 5'





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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11898	24760	38367	1.48	0.0E+00	AL043705.1	EST_HUMAN	DKFZp434L1227.1 434 (synonym: hae3) Homo sapiens cDNA clone DKFZp434L1227.6
11904	24765	38374	3.35	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261095-012-503 ST0118 Homo sapiens cDNA
11904	24765	38376	3.35	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261095-012-503 ST0118 Homo sapiens cDNA
11910	24797		2.43	0.0E+00	AW883777.1	EST_HUMAN	MR3-SN0010-310300-107-h3 SN0010 Homo sapiens cDNA
11927	24808	38402	4.22	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11927	24808	38403	4.22	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11932	24813	38409	5.01	0.0E+00	U36253.1	NT	Human beta-prime-adipin (BAM22) gene, exon 5
11934	24813	38411	2.03	0.0E+00	BE372554.1	EST_HUMAN	601237691FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609633.5
11934	24815	38412	2.03	0.0E+00	BE372554.1	EST_HUMAN	601237691FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609633.5
11946	20655	34019	2.41	0.0E+00	AA211963.1	EST_HUMAN	z16502.11 Stratagene muscle 937203 Homo sapiens cDNA clone IMAGE:562203.6 similar to gb-X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
11947	24828	38421	2.36	0.0E+00	AA468994.1	EST_HUMAN	sa55611.1st NCI CGAP_GCR1 Homo sapiens cDNA clone IMAGE:824900.3 similar to gb-X37768 B-LYMPHOCTE ACTIVATION MARKER BLAST-1 PRECURSOR (HUMAN);
11952	24831	38427	2.35	0.0E+00	BE794768.1	EST_HUMAN	601590588FT NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708.5
11953	24832	38428	160.82	0.0E+00	BE794768.1	EST_HUMAN	601491821FT NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220.5
11955	24844	38439	12.65	0.0E+00	BE400963.1	EST_HUMAN	601289403FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629444.5
11958	24845	38440	2.25	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
11958	24845	38441	2.25	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
11957	18647	31589	2.21	0.0E+00	D26533.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11957	18647	31590	2.21	0.0E+00	D26533.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11958	24846	38442	4.01	0.0E+00	BF081641.1	EST_HUMAN	602155722FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4266725.5
11958	24846	38443	4.01	0.0E+00	BF081641.1	EST_HUMAN	602155722FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4266725.5
11974	18348	31294	1.51	0.0E+00	AF272693.1	NT	Homo sapiens gephyrin mRNA, complete cds
11976	24853	38451	1.57	0.0E+00	AJ132840.1	EST_HUMAN	AU132840 NT2RP4 Homo sapiens cDNA clone NT2RP4000620.5
11978	24856	38453	4.83	0.0E+00	BE903372.1	EST_HUMAN	601676357FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935.5
11992	24869	38464	3.47	0.0E+00	BF312552.1	EST_HUMAN	601897524FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069.5
11992	24869	38465	3.47	0.0E+00	BF312552.1	EST_HUMAN	601897524FT NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069.5
11994	24871	38467	34.13	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11994	24871	38468	34.13	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12006	24883		3.04	0.0E+00	BE906402.1	EST_HUMAN	601439308FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900398.5
12007	24884		1.52	0.0E+00	BE906402.1	EST_HUMAN	601439308FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900398.5
12035	25708		58.85	0.0E+00	BF309120.1	EST_HUMAN	601890934FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131419.5

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12037	24912	38505	2.38	0.0E+00	BE698881.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
12037	24912	38506	2.38	0.0E+00	BE698881.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
12040	24915	38500	60.15	0.0E+00	BE207175.1	EST_HUMAN	60117407F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3532988 5'
12048	24921	38517	1.81	0.0E+00	BE744311.1	EST_HUMAN	60157652F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3837222 5'
12048	24921	38518	1.81	0.0E+00	BE744311.1	EST_HUMAN	60157652F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3837222 5'
12062	24935	38531	1.81	0.0E+00	7669505.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
12062	24935	38532	1.81	0.0E+00	7669505.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
12067	24940	38535	1.08	0.0E+00	11024711.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
12071	24944	38537	2.41	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #36215. Homo sapiens cDNA clone
12071	24944	38538	2.41	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #36215. Homo sapiens cDNA clone
12077	24949	38544	8.46	0.0E+00	BE545535.1	EST_HUMAN	60107039F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3456407 5'
12080	24952	38547	3.24	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12080	24952	38548	3.24	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12118	24988	38590	2.15	0.0E+00	Z20556.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
12124	24993	38595	2.27	0.0E+00	BE204968.1	EST_HUMAN	60119382F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3537774 5'
12124	24993	38596	2.27	0.0E+00	BE204968.1	EST_HUMAN	60119382F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3537774 5'
12131	25000	38605	8.45	0.0E+00	11418020.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA
12131	25000	38606	8.45	0.0E+00	11418020.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA
12146	25072	31289	1.81	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3503020 5'
12161	25819		1.43	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12163	25828		8.62	0.0E+00	AI160693.1	NT	gc17612x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
12173	25922		1.33	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
12192	25937		2.28	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12201	25944		5.82	0.0E+00	11417662.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12218	25958		3.47	0.0E+00	5802073.1	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
12251	25788	31523	2.06	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12295	25768		4.42	0.0E+00	AL041831.1	EST_HUMAN	DKFZp34K0819_r1 434 (synonym: hess3) Homo sapiens cDNA clone DKFZp34K0819 5'
12291	25940		3.76	0.0E+00	11418316.1	NT	Homo sapiens S-2 and S-phase expressed 1 (STSE1), mRNA
12289	25110		5.98	0.0E+00	AL048544.1	EST_HUMAN	DKFZp34G219_r1 434 (synonym: hess3) Homo sapiens cDNA clone DKFZp34G219 5'

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12314	25834		1.98	0.0E+00	AI030497.1	EST_HUMAN	IL-BT030-27/068-001 BT030 Homo sapiens cDNA
12357	25862		1.82	0.0E+00	N54484.1	EST_HUMAN	SW40608.st Scores fetal liver spleen INFL Homo sapiens cDNA clone IMAGE:245222 3' similar to yw-pOL_BAEVIM P-10272 POL POLYPROTEIN ;
12371	25167		5.69	0.0E+00	AF106558.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12374	13960	26857	3.44	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12374	13960	26858	3.44	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12383	25837		2.59	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
12411	13620		2.52	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arylidic acid dermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12504	25767	31621	3.54	0.0E+00	AW59082.1	EST_HUMAN	hg31068.LX1 NCL CGAP_GCC Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
12534	25797		1.41	0.0E+00	L20483.1	NT	Homo sapiens gamma-glutamyl transpeptidase mRNA, complete cds
12581	25831		2.82	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SS1R3) gene, 5' flanking region and partial cds
12597	25300		2.72	0.0E+00	9635487	NT	Homo sapiens endogenous retrovirus, complete genome
12635	25823		1.47	0.0E+00	AI204914.1	EST_HUMAN	hnc0304.X1 Strategene ichizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12683	15027	28034	1.88	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12683	15027	28035	1.88	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12701	25361	31787	1.82	0.0E+00	AF033585.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12712	14723	27705	4.49	0.0E+00	H30132.1	EST_HUMAN	yc59a08.r1 Scores breast 3NHBat Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M84099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12712	14723	27706	4.49	0.0E+00	H30132.1	EST_HUMAN	yc59a08.r1 Scores breast 3NHBat Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M84099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12724	25377		52.89	0.0E+00	D56559.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG9) pseudogene
12726	25378	31743	3.53	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12726	25378	31744	3.63	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12739	15120	28141	2.42	0.0E+00	4769469	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12780	25415		1.39	0.0E+00	AW66499.1	EST_HUMAN	h18a06.X1 Scores NFL_T_GBC S11 Homo sapiens cDNA clone IMAGE:2976154 3'
12818	25440	31721	1.51	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP-4468
12817	25446		1.55	0.0E+00	11529291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12849	18338	31287	3.07	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12858	19346	31292	1.68	0.0E+00	6089718	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12863	25400		2.17	0.0E+00	ABC29900.1	NT	Homo sapiens GST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5

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Table 4  
Single Exon Probes Expressed in Bone Marrow

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12902	25488	31733	2.53	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 180kD subunit (CPSF1), mRNA
12927	25994		3.32	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21O048
12935	13692	26809	2.65	0.0E+00	6805918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12986	14499	27473	1.32	0.0E+00	6912467	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
13018	25598		3.02	0.0E+00	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
13051	25590	31685	1.36	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
13082	25913		1.63	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV8)
13103	14203	27156	1.41	0.0E+00	6868844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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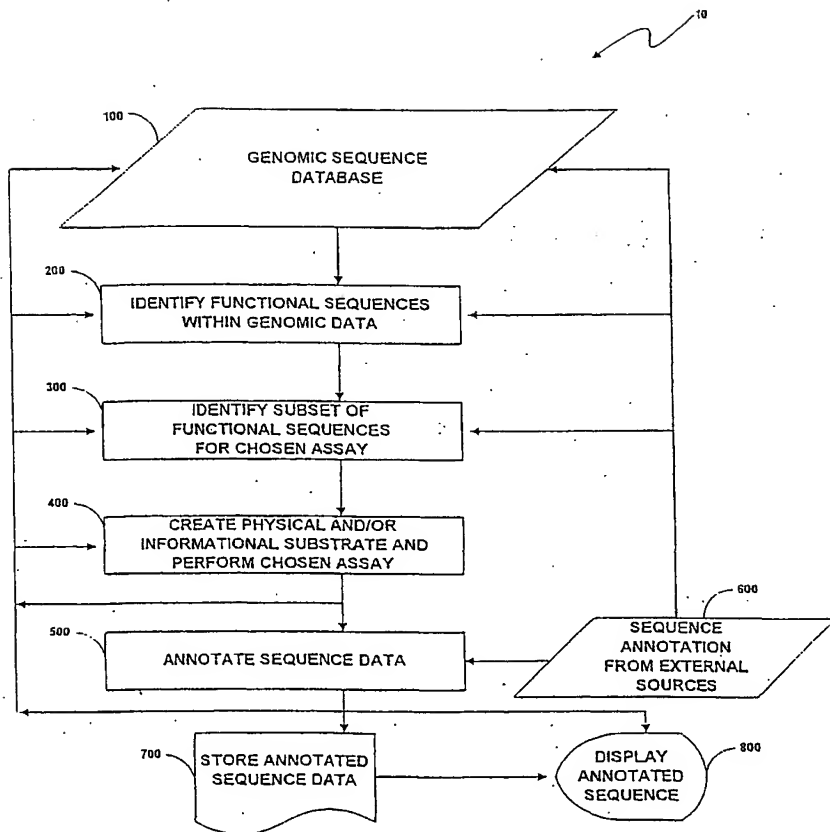


Fig. 1

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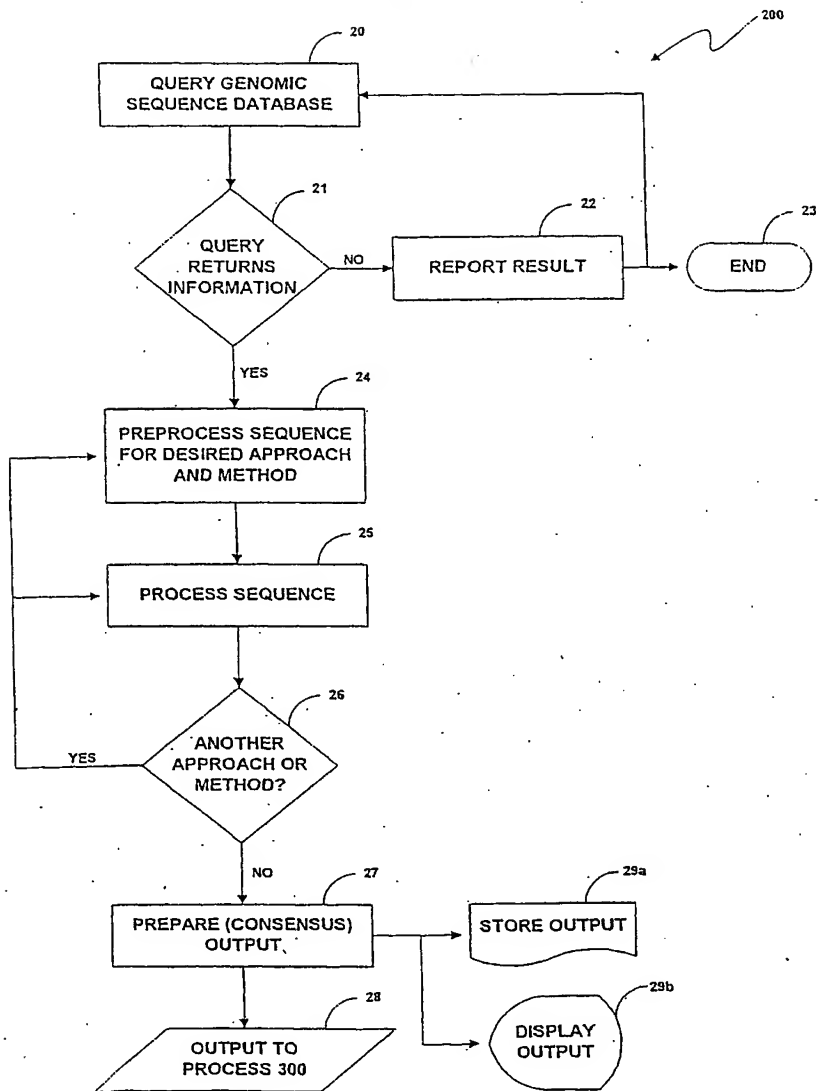


Fig. 2

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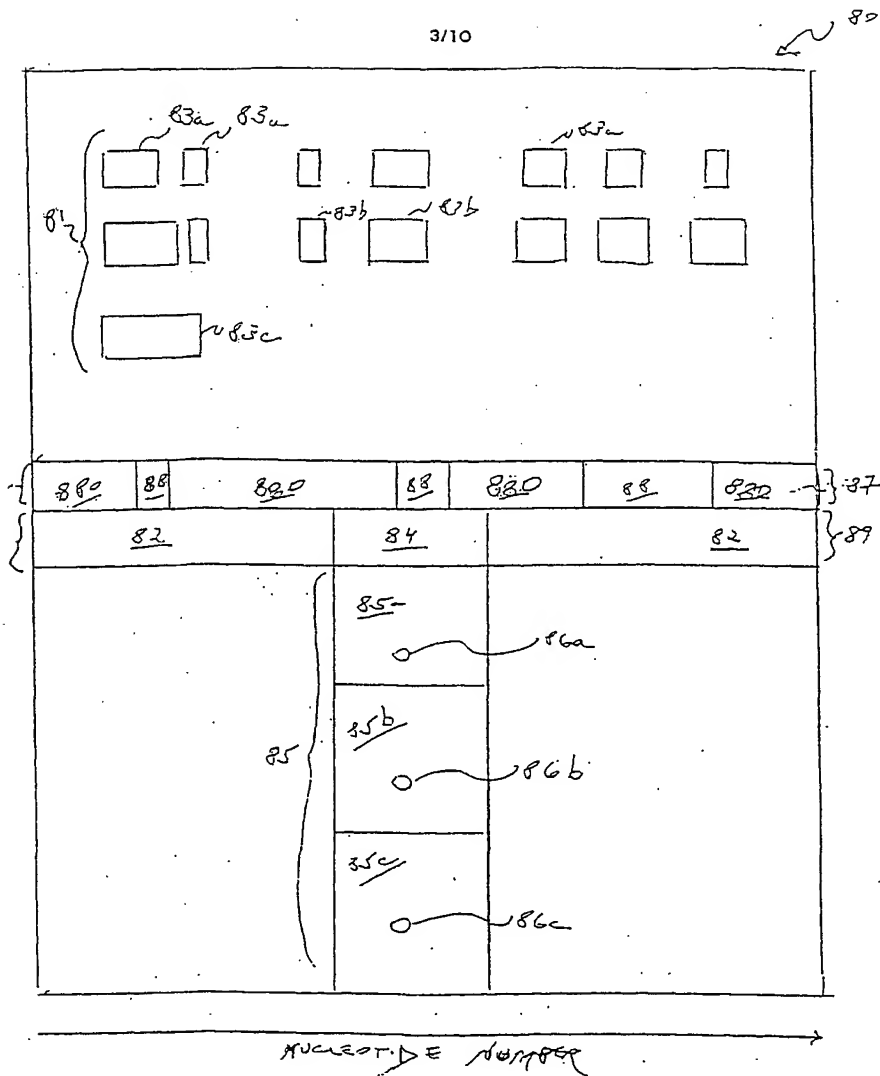


Fig. 3



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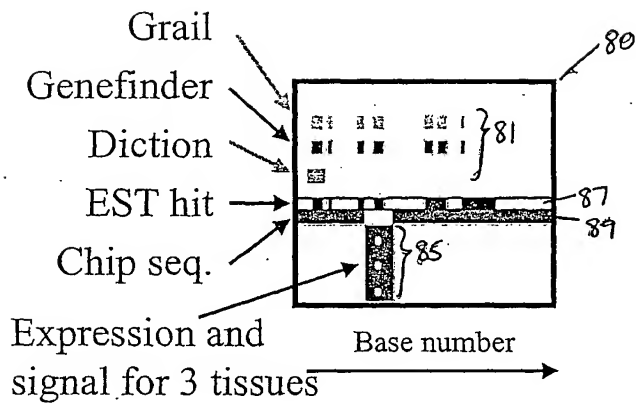


Fig. 4

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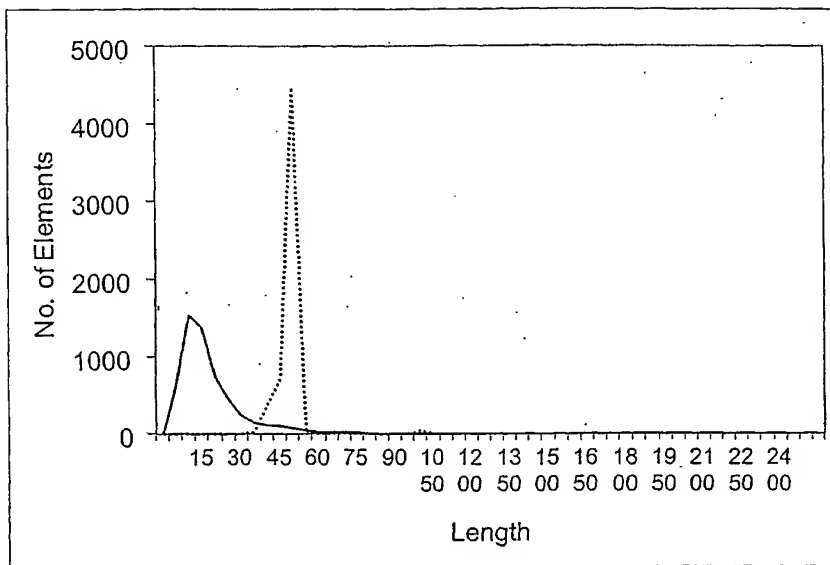


Fig. 5

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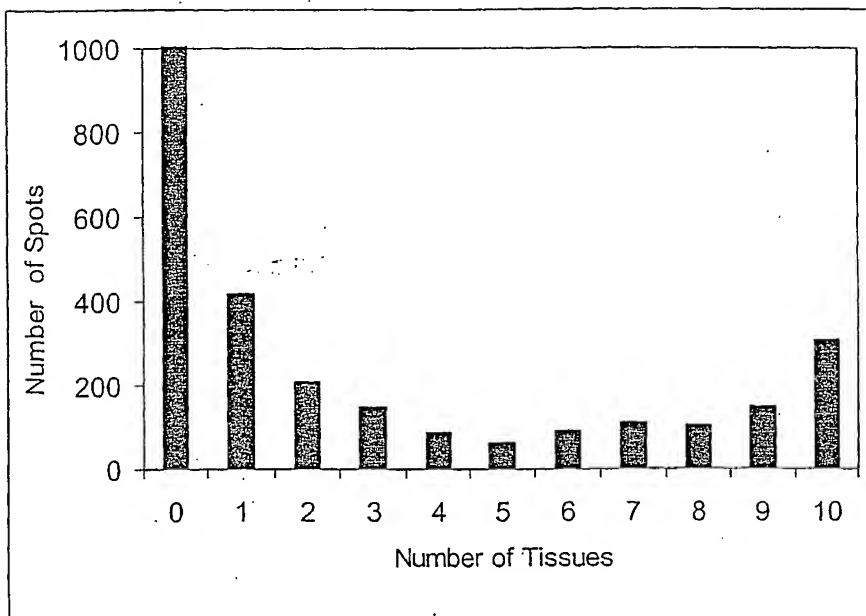


Fig. 6

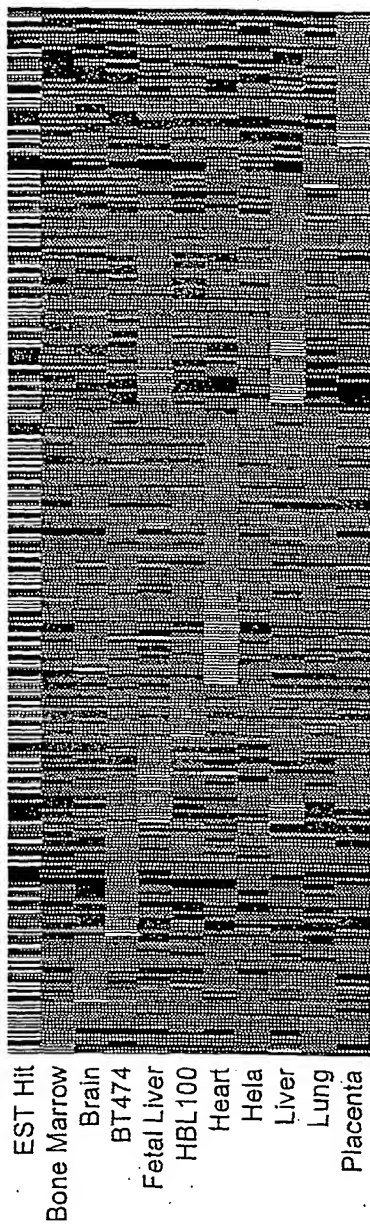


Fig. 7a

ratio legend

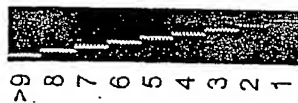


Fig. 7b

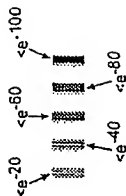


Fig. 7c

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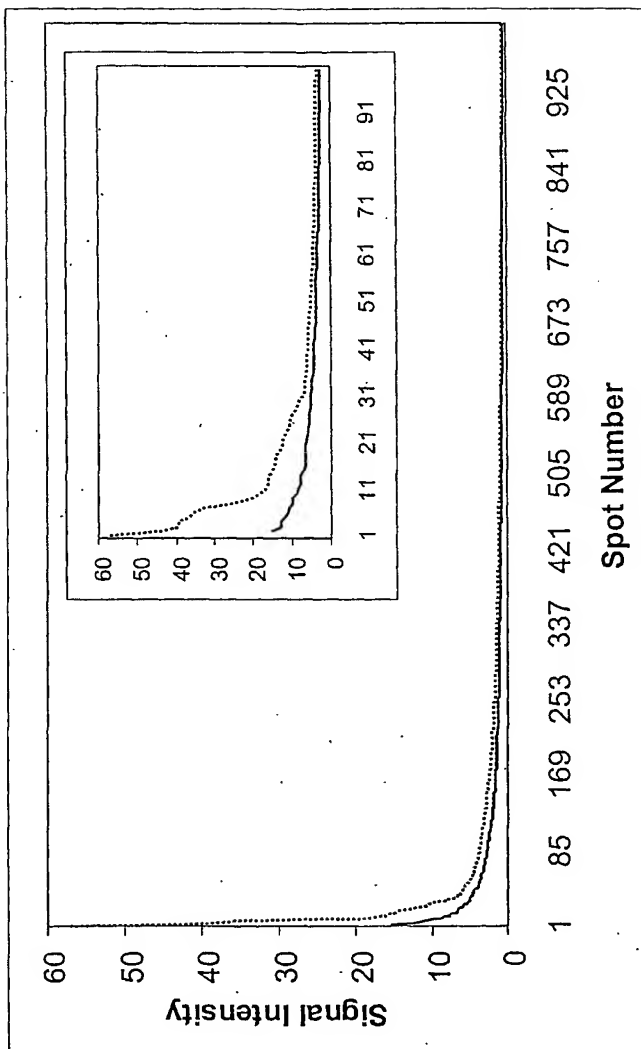


Fig. 8

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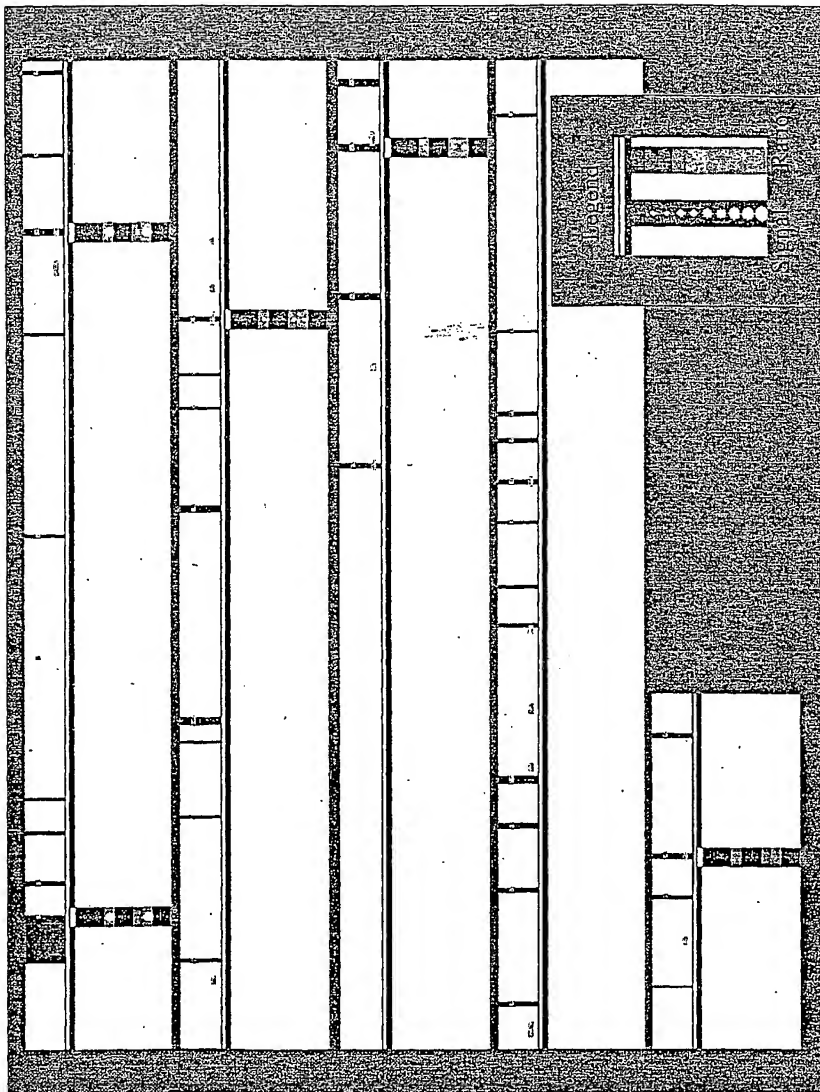
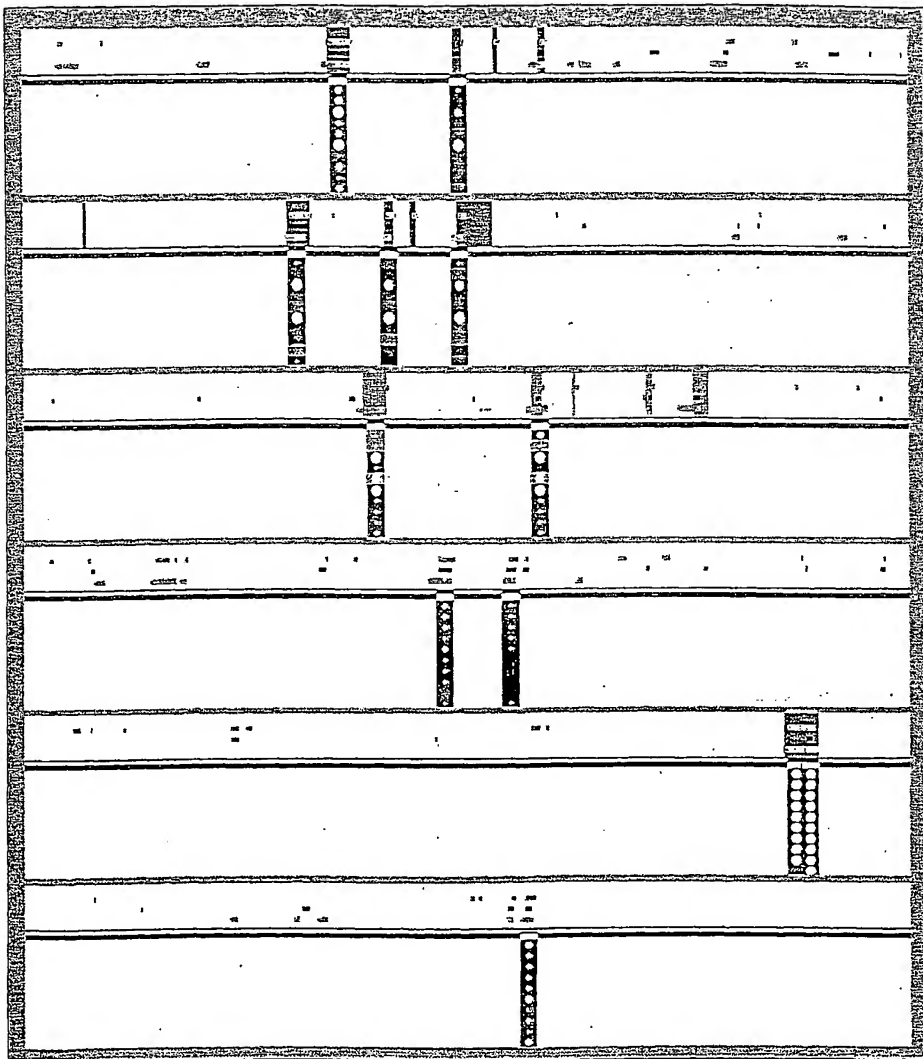


Fig. 9

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Fig. 10



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| 0024263.6  | 4 October 2000 (04.10.2000)    | GB |
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- (72) Inventors; and
- (75) Inventors/Applicants (for US only): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 988 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).
- (74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. Also described are single exon nucleic acid probes expressed in the bone marrow and their use in methods for detecting gene expression.



WO 01/057276 A3



## INTERNATIONAL SEARCH REPORT

In ☐ National Application No.  
PCT/US 01/00668

A. CLASSIFICATION OF SUBJECT MATTER  
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>STAUDER R ET AL: "Different CD44 splicing patterns define prognostic subgroups in multiple myeloma." BLOOD, (1996). VOL. 88, NO. 8, PP. 3101-8. JOURNAL CODE: A86. ISSN: 0006-4971., XP002182129 Basel Institute for Immunology, Switzerland. the whole document</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p>	13

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

\* Special categories of cited documents:

- 'A' document defining the general state of the art which is not considered to be of particular relevance
- 'E' earlier document but published on or after the International filing date
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- 'O' document relating to an oral disclosure, use, exhibition or other means
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'G' document member of the same patent family

Date of the actual completion of the International search

2 August 2002

Date of mailing of the International search report

05.09.02

Name and mailing address of the ISA

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## INTERNATIONAL SEARCH REPORT

In Application No  
PCT/US 01/00668

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	MACKAY C R ET AL: "EXPRESSION AND MODULATION OF CD44 VARIANT ISOFORMS IN HUMANS" JOURNAL OF CELL BIOLOGY, ROCKEFELLER UNIVERSITY PRESS, NEW YORK, US, US, vol. 124, no. 1/2, 1994, pages 71-82, XP000471699 ISSN: 0021-9525 the whole document	13
X	SCREATON G R ET AL: "GENOMIC STRUCTURE OF DNA ENCODING THE LYMPHOCYTE HOMING RECEPTOR CD44 REVEALS AT LEAST 12 ALTERNATIVELY SPLICED EXONS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 89, no. 24, 15 December 1989 (1989-12-15), pages 12160-12164, XP000470187 ISSN: 0027-8424 abstract; table 1	13
X	DATABASE EBI 'Online! EMBL; Accession Number HSPA10C6 (Z77862), 5 August 1996 (1996-08-05) MUNGALL AJ ET AL.: "H. sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10C6" XP002182130 abstract	13
X	O'CONNOR H E ET AL: "Abnormalities of the ETV6 gene occur in the majority of patients with aberrations of the short arm of chromosome 12: a combined PCR and Southern blotting analysis." LEUKEMIA, (1998 JUL) 12 (7) 1099-106., XP001022502 p. 1099, col. 2, last par.-p. 1101, col. 2, 1st full par. column 2; figure 1	13
X	DATABASE EBI 'Online! EMBL; Accession Number AC007372, 27 April 1999 (1999-04-27) XP002182131 abstract	13
A	WO 99 33979 A (CHIRON CORP) 8 July 1999 (1999-07-08) page 1, line 19 -page 8, line 26; claims 19-21	1,12

-/-

## INTERNATIONAL SEARCH REPORT

 Int Application No  
 PCT/US 01/00668

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5 618 671 A (LINDSTROEM PER) 8 April 1997 (1997-04-08) column 1, line 60 -column 2, line 19 column 4, line 36 -column 5, line 29; claims ----	1-27
A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document ----	1,12
A	WO 92 13075 A (GENETICS INST) 6 August 1992 (1992-08-06) page 28, line 4 - line 6; claims ----	1,12,13
A	SOLOVYEV V V ET AL: "PREDICTING INTERNAL EXONS BY OLIGONUCLEOTIDE COMPOSITION AND DISCRIMINANT ANALYSIS OF SPLICEABLE OPEN READING FRAMES" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 22, no. 24, 1994, pages 5156-5163, XP002915964 ISSN: 0305-1048 the whole document ----	1-27
A	GUAN ET AL: "GRAIL: an integrated artificial intelligence system for gene recognition and interpretation" PROCEEDINGS OF THE CONFERENCE ON ARTIFICIAL INTELLIGENCE APPLICATIONS. MONTEREY, MAR. 2 - 6, 1992, LOS ALAMITOS, IEEE COMP. SOC. PRESS, US, vol. CONF. 8, 2 March 1992 (1992-03-02), pages 9-13, XP010027422 ISBN: 0-8186-2690-9 the whole document ----	1-27
P,X	PENN S G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, (2000 NOV) 26 (3) 315-8., XP002183793 the whole document ----	1

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## INTERNATIONAL SEARCH REPORT

Int. Application No.  
PCT/US 01/00668

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EBI 'Online! 9 May 1997 (1997-05-09) MARRA M. ET AL.: "The WashU-HHMI mouse EST project; vc72c02.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 780098" Database accession no. AA414703 XP002208274 abstract</p>	13,14, 18,20,21
X	<p>DATABASE EBI 'Online! 16 October 1997 (1997-10-16) MARRA M. ET AL.: "The WashU_HHMI mouse EST project; v160c06.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 976618" XP002208275 abstract</p>	13,14, 16,18, 20,21
A	<p>DATABASE EBI 'Online! 27 April 1999 (1999-04-27) DICKHOFF R. ET AL.: "Sequencing of human chromosome 14q31 region" XP002208276 abstract</p>	13,14,18

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 01/00668

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☒ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
1-27
  
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 1 (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13115 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 1), microarrays comprising said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons (claim 23) and a method for assigning exons to a single gene (claim 24) comprising using the said arrays, a peptide encoded by SEQ ID 1 or 13115 (claims 26-27), in particular having the sequence SEQ ID 26013, which is the translation from SEQ ID 13115 (see p. 74 of the description).

2. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13116 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sequence, a method for measuring gene expression, a method for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 13116, in particular having the sequence SEQ ID 26014, which is the translation from SEQ ID 13116 (see p. 74 of the description).

...Inventions 3-13114: similar subject-matter as above related to SEQ IDs 3-13114.

## Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject-matter for which a search has been performed and which has been identified as inventions 1 and 2 in PCT form 206.

1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description pages 10, 1. 15-22).

2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID 1 or 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and conciseness (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID 1 and 2 as such.

3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID 1 and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. 26013 and 26014 (Art. 6 PCT).

4) Claims 15-21 relate to nucleic probes, solely defined in that they code for a polypeptide having the sequence SEQ ID 26013 or 26014. However, a peptide is potentially coded by an extremely large number of nucleic acid sequences. Hence, claims 15-21 lack clarity and conciseness to such an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID 1, 2, 13115 and 13116.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

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